

# Interlaboratory Comparison on POPs in Food 2011



## Twelfth Round of an International Study

Veronica Horpestad Liane

Georg Becher



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# Summary

In 2011, the twelfth round of the Interlaboratory Comparison on POPs in Food was conducted on the determination of the 2,3,7,8-chlorinated dibenzo-p-dioxins (PCDDs) and dibenzofurans (PCDFs) as well as dioxin-like non-ortho and mono-ortho chlorinated biphenyls (dl-PCBs) in three different food items. In addition laboratories could voluntarily determine and report six Indicator PCBs, polybrominated diphenyl ethers (PBDEs) and hexabromocyclododecane (HBCD). The objectives of this interlaboratory comparison study were a) to offer a quality assurance instrument for the participating laboratories, b) to assess the between laboratory reproducibility and c) to assess the readiness of expert laboratories world-wide to determine levels of chlorinated and brominated persistent organic pollutants in regular foodstuffs.

The 2011 study was performed on sample homogenates of salmon filet, mozzarella cheese and eggs. In addition, six standard solutions were provided containing known concentrations of 1) PCDDs/PCDFs, 2) non-ortho PCBs, 3) mono-ortho PCBs, 4) PBDEs, 5) Indicator PCBs and 6)  $\alpha$ -HBCD. The testing materials were sent to 103 laboratories in January 2011, and results were returned from 101 laboratories in 31 different countries by the deadline in April. Most laboratories analyzed all the three food items. A draft report was made available on the Internet in August and was discussed among the participants at the Waters New Technology Forum during the DIOXIN 2011 Symposium in Brussels, Belgium.

This report presents the submitted results for: all seventeen 2,3,7,8-substituted PCDDs/PCDFs, the non-ortho substituted PCBs #77, 81, 126 and 169 and the eight mono-ortho substituted PCBs #105, 114, 118, 123, 156, 157, 167, 189 in the three food items on a fresh weight and lipid weight basis. In addition, the results for eight PBDEs #28, 47, 99, 100, 153, 154, 183 and 209, six Indicator PCBs #28, 52, 101, 138, 153 and 180, and total HBCD as well as the  $\alpha$ -,  $\beta$ - and  $\gamma$ -isomers were reported from those laboratories that voluntarily determined their concentrations. Non-detected congeners were assigned a concentration corresponding to the reported detection limit except for PBDEs, Indicator PCBs and HBCD where non-detects were removed from the data set. The consensus concentration (assigned value) for each analyte in the three food samples was determined as follows: The median of all reported concentrations for each analyte was calculated. All values above two times the median were removed from the calculation. The consensus median and consensus mean plus standard

deviation (SD) were calculated from the remaining data. Toxic equivalents (TEQs) were calculated from the consensus values of individual congeners using the toxic equivalency factors derived by WHO in 1998 and 2005. Z-scores for PCDD/PCDF TEQs were calculated for each laboratory using  $\pm 20\%$  of the consensus TEQs (WHO-1998TEQs) as a value for target standard deviation ( $\sigma$ ). Further, Z-scores were calculated for the non-ortho PCB TEQ, the mono-ortho PCB TEQ, the total TEQ, the sum of six Indicator PCBs, the sum of eight PBDEs, total HBCD, and the three isomers of HBCD and for each single congener in all three matrices.

The consensus values for the standard solutions were calculated as mentioned above except that values outside  $\pm 50\%$  of the median of all values were removed prior to the final calculation of the consensus median and mean. The consensus values for the lipid content were calculated by first excluding results deviating more than two SD from the mean of all values and then recalculating the median, mean and SD.

For the determination of total TEQs in the three food samples, Z-scores within  $\pm 1$  were obtained by 76-85% of the laboratories. The majority of the laboratories (88-90%) reported results for total TEQ with a trueness of  $\pm 40\%$  for all food samples (Z-score  $\pm 2$ ). The relative standard deviation (RSD) calculated for the total TEQ after removal of outliers was 11-13%. It is therefore concluded that the performance of laboratories world-wide in determining dioxin-like compounds is generally good for the food samples included in this study.

For the different food samples, between 55-68 laboratories reported results for the six Indicator PCBs, 31-41 laboratories reported concentrations for the seven tetra- to hepta-BDEs and 22-27 laboratories reported concentrations for BDE-209. The concentrations of the sum of seven PBDEs on fresh weight basis were 2130 (28%), 220 (33%) and 258 (31%) pg/g in salmon, Mozzarella and eggs, respectively, with average RSD given in parentheses. The consensus concentrations for BDE-209 were 42 (n=27), 28 (n=25) and 111 (n=22) pg/g fresh weight in salmon filet, Mozzarella cheese and eggs, respectively. The corresponding RSD on fresh weight basis were 48, 62 and 36%. The consensus concentrations calculated for HBCD are just indicative values as only few laboratories reported results. The sums of concentrations on fresh weight basis for six Indicator PCBs were 32.3 ng/g (26%) in salmon, 0.92 (37%) ng/g in Mozzarella cheese and 1.45 (33%) ng/g in eggs. Average RSDs are given in parentheses.

# Introduction

In order to ensure consumer protection and reduce human exposure to dioxins and dioxin-like PCBs through food consumption, many countries request frequent monitoring of the presence of these toxic pollutants in food and feed. Thus, there is a large demand for chemical laboratories that are able to determine these contaminants at low levels in food and feed. It is usually required by the authorities that laboratories performing such measurements are accredited according to ISO standards and prove their competence by successful participation in interlaboratory studies.

This study is the twelfth round of a world-wide interlaboratory comparison study on halogenated persistent organic pollutants in food organized by the Department of Analytical Chemistry, Division of Environmental Medicine, Norwegian Institute of Public Health, Oslo, Norway.

The exercise took place from January 2011, when the samples were shipped to the laboratories for analysis, to the reporting deadline in April 2011, when the last reports on the results were received. A draft report

was made available to the participants on the new webpage (<http://www.fhi.no/ILC>) in August and was discussed during the Waters New Technology Forum at the DIOXIN 2011 Symposium in Brussels, Belgium.

The main objective of this exercise was to assess the between laboratory reproducibility of dioxin-like compounds analyses in frequently consumed foods and provide a QA/QC instrument for each participating laboratory to contribute to its proficiency. Participants were also asked to voluntarily determine the concentrations of eight PBDEs, six Indicator PCBs and HBCD in the food samples in order to assess the readiness of laboratories to analyze these persistent organic pollutants.

All of the participants from previous rounds of this series of "Interlaboratory Comparisons on POPs in Food" were invited to participate. In addition, several other laboratories announced their participation. There was no limit to the total number of participating laboratories. The 101 laboratories that submitted results, and thereby contributed to the study results, are presented in Table 1.

**Table 1.**

**Participants that reported results in the twelfth round of Interlaboratory Comparison on POP's in food 2011**

<b>Agenzia Regionale Protezione Ambiente Del Piemonte, Polo Microinquinanti</b> Grugliasco (Torino), Italy	<b>Chemisches und Veterinäruntersuchungsamt (CVUA)</b> Freiburg, Germany
<b>AGRIPARADIGMA</b> Ravenna, Italy	<b>China CDC</b> Beijing, China
<b>ALS Czech Republic, s.r.o.</b> Pardubice, Czech Republic	<b>Consorzio Interuniversitario Nazionale la Chimica per l'Ambiente</b> Marghera (VE), Italy
<b>ALS Laboratory Group (Center of Excellence)</b> Edmonton, Alberta, Canada	<b>CVUA-MEL Münster</b> Münster, Germany
<b>Analytical Perspectives</b> Wilmington, NC, USA	<b>Danish Veterinary and Food Administration</b> Ringsted, Denmark
<b>ARPAT Agenzia Regionale per la Protezione Ambientale della Toscana</b> Firenze, Italy	<b>Chinese Academy of Inspection and Quarantine</b> Beijing, China
<b>ASAE (Food Safety and Economic Authority)</b> Lisboa, Portugal	<b>Environmental Laboratory</b> Barcelona, Spain
<b>AsureQuality Limited - Wellington Laboratory</b> Wellington, New Zealand	<b>Eurofins GfA GmbH</b> Hamburg, Germany
<b>BioDetection Systems</b> Amsterdam, The Netherlands	<b>FDA, Arkansas Regional Lab</b> Jefferson, USA
<b>Canadian Food Inspection Agency</b> Calgary, Canada	<b>Federal Environment Agency (UBA)</b> Berlin, Germany
<b>CARSO-LSEHL</b> Lyon Cedex 07, France	<b>Federal Institute for Risk Assessment (BfR)</b> Berlin, Germany
<b>CART, University of Liège</b> Liège, Belgium	<b>Food GmbH Jena Analytik &amp; Consulting</b> Jena, Germany
<b>CCL Nutricontrol</b> Veghel, The Netherlands	<b>Government Laboratory</b> Hong Kong SAR, China
<b>Central Lab of Residue Analysis of Pesticides and Heavy Metals in Foods</b> Giza, Egypt	<b>Gruppo CSA S.p.A.</b> Rimini (RN), Italy
<b>CHELAB SRL , Unità Locale di Lusciano</b> Lusciano (CE), Italy	<b>Guangdong Test Center of Product Quality Supervision (GDQT)</b> Shunde, China
<b>Chemisches und mikrobiologisches Institut UEG GmbH</b> Wetzlar, Germany	<b>Health Canada</b> Ottawa, Ontario, Canada



<b>Health Canada</b> Toronto, Ontario, Canada	<b>Laboratory of Vendee (LEVA)</b> La Roche sur Yon, France
<b>Hong Kong Baptist University</b> Hong Kong, China	<b>Landesamt für Umweltschutz Sachsen-Anhalt</b> Halle, Germany
<b>Hong Kong Government Laboratory</b> Hong Kong, China	<b>Landesuntersuchungsamt Institut für Lebensmittelchemie</b> Speyer, Germany
<b>Institute of Aquaculture</b> Stirling, Scotland, UK	<b>LUFÄ Rostock der LMS</b> Rostock, Germany
<b>Institute of Environmental Assessment and Water Research (IDAEA-CSIC)</b> Barcelona, Spain	<b>mas   münster analytical solutions gmbh</b> Münster, Germany
<b>Instituto "G. CAPORALE"</b> Teramo, Italy	<b>Medved's Institute of Ecohygiene and Toxicology</b> Kiev, Ukraine
<b>Istituto Zooprofilattico Sperimentale delle regioni Lazio e Toscana</b> Rome, Italy	<b>MicroPolluants Technologie</b> Thionville, France
<b>Istituto Zooprofilattico Sperimentale Lombardia Emilia Romagna</b> Bologna (BO), ITALY	<b>National Cheng Kung University</b> Tainan, Taiwan, R.O.C.
<b>Italian National Institute for Health</b> Rome, Italy	<b>National Institute for Health and Welfare</b> Kuopio, Finland
<b>Japan Food Research Laboratories</b> Japan	<b>National Institute of Nutrition and Food Safety</b> Beijing, China
<b>Korea Food and Drug Administration, National Institute of Food and Drug Safety Evaluation</b> Chungbuk, Republic of Korea	<b>National Measurement Institute</b> Sydney, Australia
<b>La Drome Laboratoire</b> Valence, France	<b>National Tsing Hua University</b> Hsinchu, Taiwan
<b>LABERCA</b> Nantes Cedex 3, France	<b>NCSR "Demokritos"</b> Athens, Greece
<b>Laboratoire De Rouen</b> Rouen, France	<b>NEOTRON SPA</b> Modena, Italy
<b>Laboratorio CSMO Magistrato Alle Acque di Venezia</b> Padova, Italy	<b>Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit</b> Oldenburg, Germany
<b>Laboratory of SGS Bulgaria Ltd.</b> Varna, Bulgaria	<b>Shanghai Municipal Center for Disease Control and Prevention</b> Shanghai, China
<b>NIFES- National Institute of Nutrition and Seafood Research</b> Bergen, Norway	<b>Shenzhen Center for Disease Control &amp; Prevention</b> Shenzhen, Guangdong, China

<b>Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit</b> Braunschweig, Germany	<b>Shimadzu Techno-Research, INC.</b> Kyoto, Japan
<b>Norwegian Institute for Air Research</b> Kjeller, Norway	<b>T.C. TARIM ve KÖYİŞLERİ BAKANLIĞI</b> Ankara, Turkey
<b>Nofalab BV</b> Schiedam, The Netherlands	<b>TestAmerica</b> West Sacramento, CA, USA
<b>NOFER Institute Of Occupational Medicine</b> Lodz, Poland	<b>The Food and Environment Research Agency (FERA)</b> York, UK
<b>Oekometric</b> Bayreuth, Germany	<b>TLR International laboratories</b> Rotterdam, The Netherlands
<b>QLIP N.V</b> Zutphen , The Netherlands	<b>UIS Umweltinstitut synlab GmbH, Institut für Industrie und Umweltanalytik</b> Linz, Austria
<b>R&amp;C LAB SRL</b> Altavilla Vicentina , Italy	<b>Umeå University</b> Umeå, Sweden
<b>Research and Productivity Council</b> Fredericton, New Brunswick, Canada	<b>Umweltbundesamt GmbH</b> Vienna, Austria
<b>RIKILT</b> Wageningen, The Netherlands	<b>VITO</b> Mol, Belgium
<b>Scientific Analysis Laboratories</b> Manchester, UK	<b>Wellington Laboratories Inc.</b> Guelph, Ontario, Canada
<b>Servizos De Apoyo Á Investigación</b> A Coruña, Spain	<b>Wessling Laboratorien GmbH</b> Altenberge, Germany
<b>SGS Belgium NV</b> Antwerpen, Belgium	<b>Western Region Laboratory</b> Burnaby, British Columbia, Canada
<b>SGS Institut Fresenius GmbH</b> Bayreuth, Germany	<b>Worthies Engineering Consultants Corp.</b> Taichung, Taiwan
<b>SGS North America Inc.</b> Wilmington, NC, USA	<b>Zavod za zdravstveno varstvo Maribor Institut za varstvo okolja</b> Maribor, Slovenia
<b>Sun Dream Environmental Technology Corporation</b> Taichung City, Taiwan	<b>Zdravotní ústav se sídlem s Ostravě</b> Czech Republic
<b>Super Micro Mass Research &amp; Technology Center</b> Niaosong Township, Kaohsiung County, Taiwan	<b>Zhejiang Provincial Center for Disease Control and Prevention (ZJCDC)</b> HangZhou, China
<b>State Laboratory</b> County Kildare, Ireland	

# Design and practical implementation

## Study design and reporting of results

As in the previous rounds of this interlaboratory comparison studies, the test material chosen represented naturally contaminated food samples. The analytes to be determined by each participating laboratory were all seventeen 2,3,7,8-substituted PCDDs/PCDFs, the four non-ortho substituted PCBs #77, 81, 126 and 169 and the eight mono-ortho substituted PCBs #105, 114, 118, 123, 156, 157, 167 and 189. In addition, laboratories were asked to determine on a voluntary basis eight PBDEs #28, 47, 99, 100, 153, 154, 183 and 209, six Indicator PCBs #28, 52, 101, 138, 153 and 180, total HBCD and its three isomers ( $\alpha$ -,  $\beta$ -,  $\gamma$ -HBCD). The six PCB congeners belong together with the mono-ortho PCB #118 to the selection of PCBs commonly referred to as ICES-7.

The analysis should be performed using the laboratories' own methods for sample preparation and instrumental analysis, their own standards and quantification procedures and their own method for lipid determination.

It was recommended that laboratories determine as many as possible of the 2,3,7,8-substituted PCDDs/PCDFs, dioxin-like PCBs, PBDEs, Indicator PCBs and HBCD. The report was to include the determined lipid percent for the test samples. Also the actual sample and lipid amount (g) for each determination should be reported. For each sample, laboratories were to report the found concentration on fresh weight basis for each congener which was detected (e.g.  $S/N \geq 3$ ) as well as the limit of determination (LOD, e.g.,  $S/N = 3$ ). Non-detected congeners (e.g.  $S/N < 3$ ) were to be marked "ND" in the comments column of the Report form.

In addition, six standard solutions containing known concentrations of 1) seventeen 2,3,7,8-substituted PCDDs/PCDFs, 2) four non-ortho PCBs, 3) eight mono-ortho PCBs, 4) eight PBDEs, 5) six Indicator PCBs and 6)  $\alpha$ -HBCD were to be analyzed using the laboratory's own quantification standards and methods. The results were reported on separate forms.

The test materials consisted of salmon filet, mozzarella cheese and eggs. The laboratories could choose to analyze one, two or all three food samples.

Each participating laboratory was given a specific code by the co-coordinators. In the present report, the participants are presented in the tables and figures by

their laboratory codes. Participants had access to their own code only and laboratory codes were not revealed to third parties.

On receipt by the co-coordinators, the raw data from the laboratories were entered into a database. The draft final report was generated and made available to all participants on the Internet in August 2011. The draft of the final report was discussed at the Waters users' meeting at DIOXIN 2011 in August in Brussels, Belgium.

## Collection, preparation, and distribution of samples

Samples shipped to the participants comprised one to three of the following:

- Salmon filet: Obtained from the Baltic Sea (115 g)
- Mozzarella cheese: Obtained from Italy (50 g)
- Egg: Obtained from The Netherlands (70 g)

The test materials consisted of three natural products not fortified with standards.

Homogenization of the salmon and mozzarella cheese was performed by repeatedly grinding portions of the food item in a grinder and homogenizing these portions in a mixer. The homogeneity of these materials was tested using an approach developed at NIPH. The rationale for and description of the test method is given in Appendix E. The egg sample was carefully warmed to 30°C, filtered through gauze, thoroughly mixed by stirring and subsequently subdivided. Sub-samples of at least 115 g of salmon filet (S), 50 g of Mozzarella cheese (M) and 70 g of eggs (E) were placed into carefully cleaned screw-cap glass bottles. All samples were stored at -20 °C until shipment. The frozen samples were shipped to the participating laboratories marked as test material S, M and E.

## Statistical analysis

Based on experiences from previous rounds, we have chosen the following approach for the calculation of the consensus concentrations for each of the congeners:

For PCDDs/PCDFs and dioxin-like PCBs congener-by-congener medians were calculated from the food sample data of all reporting laboratories using the detection limit as concentration for non-detected congeners (upperbound concentration). For PBDEs, Indicator PCBs and HBCD, non-detected congeners were removed from the data set prior to consensus calculation. Outliers were defined as those values above two times the median of all values and were removed from the data set. The consensus values were defined as the median of the remaining data for each congener. In addition, the consensus mean and SD were calculated from this data set for each congener. Those congener data which had been removed prior to consensus calculation are marked in the tables presenting the individual results.

For the standard solutions, outliers were defined as those values outside  $\pm 50\%$  of the median of all reported values. Consensus median, mean and SD were calculated from the remaining data. The consensus of the lipid content was calculated as the mean after removal of values outside  $\pm 2SD$ .

TEQs were calculated from the consensus values for PCDDs/PCDFs, non-ortho PCBs, and mono-ortho PCBs, using the toxic equivalency factors derived by WHO in 1998 and 2005. As the detection limit was used for the concentration of non-detects, these TEQs represent upper bound concentrations.

Z-scores for PCDD/PCDF TEQ as well as for the non-ortho PCB TEQ, the mono-ortho PCB TEQ, the total TEQ (WHO1998TEQs) the sum of six Indicator PCBs, the sum of eight PBDEs, total HBCD and for each congener were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

Where  $x$  = reported value;  $X$  = consensus value (assigned value);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. Z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

## The final report and certificate

The draft of the final report was prepared by the co-coordinators and published on the web in August 2011. The draft was discussed at the Waters Users' Meeting at the DIOXIN2011 Symposium in August in Brussels, Belgium.

A certificate, stating the participant's code, will be sent to each participant contributing to the results at the end of 2011. The final report will be made available to the participants in pdf format at [www.fhi.no/ILC](http://www.fhi.no/ILC).

## Co-ordination

The study was initiated and carried out by the Department of Analytical Chemistry, Division of Environmental Medicine, Norwegian Institute of Public Health, Oslo, Norway. Members of the co-ordination committee were:

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# Results

The results are presented in the following chapters. A participating laboratory will be able to compare its performance congener by congener with the other laboratories. Since variations in performances are based on several factors, it is recommended that each laboratory carefully evaluates the factors that, favorably or unfavorably, have contributed to its performance. A general reader of the report, who has no access to the laboratory codes, will be able to get a picture of the analytical performance of laboratories world-wide for determining dioxins, dioxin-like PCBs, Indicator PCBs, PBDEs and HBCD in regular foods.

## Presentation in the report

Results were submitted from 101 laboratories from 31 different countries. In Appendix C, the consensus statistics are given on fresh and lipid weight basis for concentrations and TEQ values of individual congeners, a summary of TEQ values for each food item, and the Z-score plots based on a target deviation of  $\pm 20\%$ . Further, the results of the lipid determinations are presented. Finally, individual results reported by the laboratories for each congener are given for salmon filet, Mozzarella cheese and eggs in Appendix 2, 3 and 4.

## Summarising comments on results

### *PCDDs/PCDFs*

#### Analyte solution

Concentrations for PCDDs/PCDFs were reported by 86 laboratories. The average RSD for the 17 congeners was 9.3% ranging from 7.3% for 1,2,3,7,8-PeCDD to 12% for OCDF. The calculation of Z-scores for the TEQs (target 13.6 pg TEQ/ $\mu$ l) of the PCDD/PCDF standard solution showed that 95% of the labs were within the range of  $\pm 20\%$  of the consensus value. This demonstrates the high quality of the calibration solutions used by the laboratories.

#### Salmon filet

For the salmon filet sample, PCDD/PCDF results from 88 laboratories were received. The consensus TEQ was 8.1 pg TE/g fresh weight and 93 pg TE/g lipid. The average RSD was 34% ranging from 23-60%. Z-scores within  $\pm 1$  were obtained by 85% of the laboratories and 90% of the laboratories had Z-scores within  $\pm 2$ . About 96% percent of the PCDD/PCDF TEQ is made up by the four congeners 2,3,7,8-TCDD, 1,2,3,7,8-PeCDD, 2,3,7,8-TCDF and 2,3,4,7,8-PeCDF.

#### Mozzarella cheese

PCDD/PCDF concentrations in the Mozzarella cheese sample were reported by 73 laboratories. The consensus TEQ was 1.2 pg TE/g fresh weight and 4.3 pg TE/g lipid. The average RSD was 36% ranging from 23-70%. Z-scores were within  $\pm 1$  for 76% of the laboratories and within  $\pm 2$  for 88% of the laboratories. About 77% percent of the PCDD/PCDF TEQ is made up by the four congeners 2,3,7,8-TCDD, 1,2,3,7,8-PeCDD, 2,3,7,8-TCDF and 2,3,4,7,8-PeCDF.

#### Eggs

For the egg sample, 74 laboratories determined PCDD/PCDF concentrations. The consensus TEQ was 0.76 pg/g fresh weight and 7.8 pg/g lipid. The average RSD was 30% ranging from 18-50%. Z-scores for PCDD/PCDF TEQ within  $\pm 1$  were obtained by 83% of the laboratories and 90% had Z-scores within  $\pm 2$ . About 78% percent of the PCDD/PCDF TEQ is made up by the four congeners 2,3,7,8-TCDD, 1,2,3,7,8-PeCDD, 2,3,7,8-TCDF and 2,3,4,7,8-PeCDF.

### *Dioxin-like PCBs*

#### Analyte solution

The 12 dioxin-like PCBs in the analyte solution were analyzed and reported by 82 to 86 laboratories. The RSDs for the different congeners were 8.2-11% with an average of 9.3%.

#### Salmon filet

Dioxin-like PCB concentrations were reported from 86 to 90 laboratories. The concentrations of the 12 congeners varied between 2.2 pg/g fresh weight (CB-81) and 4816 pg/g fresh weight (CB-118). The dioxin-like PCBs contribute 62% to the total TEQ in the sample with CB-

126 as the main contributor (47%). The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 27% ranging from 22% for CB-105 to 48% for CB-123.

#### Mozzarella cheese

The number of laboratories that measured and reported dioxin-like PCB concentrations in Mozzarella cheese were between 72 and 75. The concentrations ranged from 0.42 pg/g fresh weight for CB-81 to 222 pg/g fresh weight for CB-118. The dioxin-like PCBs contribute to about 29% of the total TEQ in the sample with CB-126 as the main contributor (29%). The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 27% ranging from 21% for CB-153 to 50% for CB-77.

#### Eggs

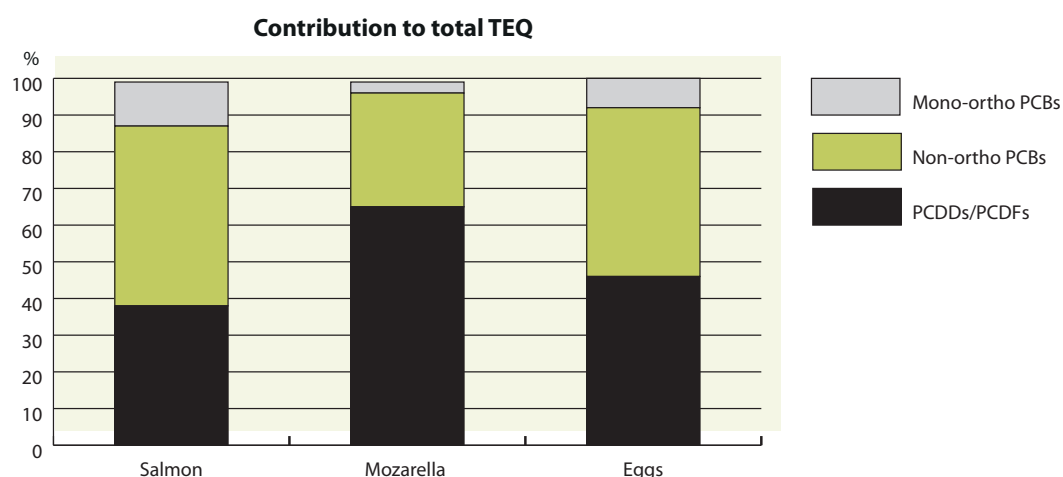
Dioxin-like PCBs were reported by 73 to 75 laboratories. Levels were ranging from 0.24 pg/g fresh weight for

CB-81 to 124 pg/g fresh weight for CB-118. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 24% ranging from 19% for CB-189 to 35% for CB-123. The contribution of the dioxin-like PCBs to the total TEQ was about 54% with CB-126 as the main contributor (48%).

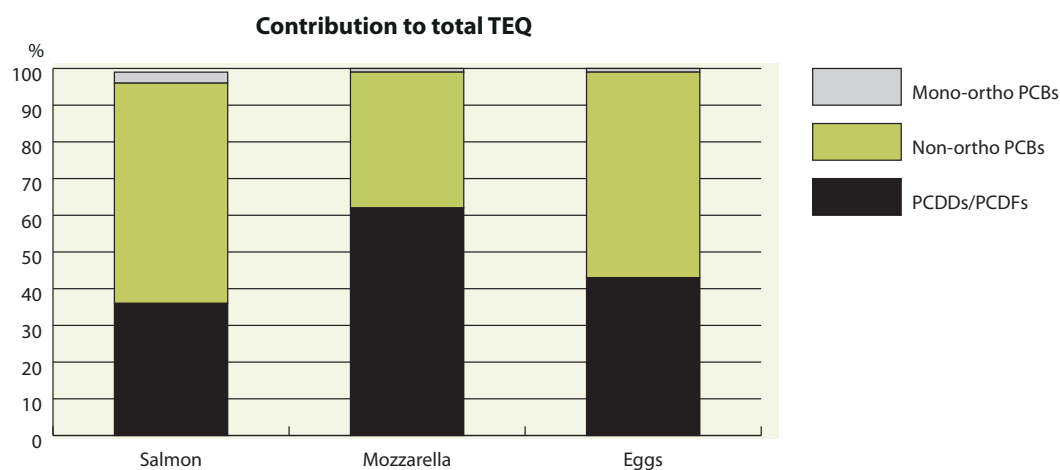
#### Total TEQ

In Figure 1 and 2 the contribution of the three groups of dioxin-like compounds is depicted based on WHO TEF1998 and WHO TEF2005, respectively. For salmon filet and eggs, dioxin-like PCBs contributed to 50% or more of the total TEQs (using WHO TEF1998), demonstrating the importance of PCBs for the determination of the total 2,3,7,8-TCDD related toxic potency of food samples.

The RSD for total TEQ on fresh weight basis calculated from the RSD of individual congeners was 13% for salmon filet, 11% for Mozzarella cheese and 12% for eggs.



**Figure 1.** The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using the WHO1998 TEFs, in the three food samples.



**Figure 2.** The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using the WHO<sub>2005</sub> TEFs, in the three food samples.

### *Indicator PCBs*

#### Analyte solution

Sixty-five laboratories reported Indicator PCBs in the analyte solution. The average RSD was 10% ranging from 9.5-11%.

#### Salmon filet

For the salmon filet sample Indicator PCB results were received from 68 laboratories. The concentrations were varying between 0.67 ng/g fresh weight (CB-28) and 12.1 ng/g fresh weight (CB-153). The RSDs were ranging from 21-32% with an average of 26%. The consensus median for the sum of Indicator PCBs was 32.3 ng/g fresh weight.

#### Mozzarella cheese

Within the deadline, 55-56 laboratories reported results of Indicator PCBs in the Mozzarella cheese sample. The concentrations ranged from 22 pg/g fresh weight (CB-28) to 363 pg/g fresh weight (CB-153) with a consensus median for the sum of Indicator PCBs of 922 pg/g fresh weight. The average RSD was 37% ranging from 17-60%.

#### Eggs

Results were obtained from 56-57 laboratories. The concentrations of Indicator PCBs in the eggs sample were ranging from 6 pg/g fresh weight (CB-52) to 567 pg/g fresh weight (CB-153) and the consensus median for the sum was 241 pg/g fresh weight. The average RSD was 33% ranging from 17-59%.

### *PBDEs*

#### Analyte solution

The tri- to heptaBDE standard solution was analyzed by 41 to 42 laboratories and 29 laboratories reported values for BDE-209. The RSDs were between 8.1-11% for all congeners.

#### Salmon filet

PBDE concentrations were reported by 40 to 41 laboratories, except for BDE-209 for which 27 results were received. The consensus concentrations were in the range 2.7 pg/g fresh weight for BDE-183 and 12.5 ng/g fresh weight for BDE-47. The consensus concentration for BDE-209 was 42 pg/g fresh weight. The sum of tri- to heptaBDEs was 21.3 ng/g fresh weight. The range of RSDs on fresh weight was 21-48% with an average of 31% including BDE-209.

#### Mozzarella cheese

Within the deadline, 34 laboratories had reported results for tri- to heptaBDEs and 25 laboratories reported results for BDE-209. The concentrations varied between 0.84 pg/g fresh weight (BDE-28) and 91 pg/g fresh weight (BDE-47/99). The concentration for BDE-209 was 28 pg/g fresh weight. The sum of tri- to heptaBDEs was 220 pg/g fresh weight. The RSD calculated from the concentrations on fresh weight ranged from 19-67% with an average of 36% for PBDEs including BDE-209.

#### Eggs

Between 31 and 32 laboratories reported results for tri- to heptaBDEs and 22 reported results for BDE-209. The concentrations varied between 0.54 pg/g fresh weight (BDE-28) and 145 pg/g fresh weight (BDE-183). The concentration for BDE-209 was 111 pg/g fresh weight. The sum of tri- to heptaBDEs was 258 pg/g fresh weight. The RSDs for the individual congeners were ranging from 19 to 65% with an average of 32% including BDE-209.

### *HBCD*

Also in this round of the study, total HBCD and the isomers  $\alpha$ -,  $\beta$ - and  $\gamma$ -HBCD could be determined and reported. A total of 15 laboratories reported  $\alpha$ -HBCD in the standard solution and 12-15 laboratories reported all three isomers in the food samples. The consensus concentrations for the sum of individual HBCD isomers were 2.1 ng/g fresh weight for salmon, and 151 and 111 pg/g fresh weight for Mozzarella cheese and eggs, respectively. Since only few laboratories reported HBCD, these values are regarded as indicative. For salmon, the sum of individual isomers determined by LC-MS agreed well with the total amount of HBCD determined by GC-MS.  $\alpha$ -HBCD was the dominating (94%) isomer in this sample. For the other food samples, the discrepancy between the sum of individual isomers and the total HBCD was quite large.

### *Lipid content*

The mean and RSDs (in parentheses) for the lipid contents of the food samples were calculated to be 8.6% (14%) for salmon filet, 26.7% (6%) for Mozzarella cheese and 9.8% (11%) for eggs.

# Acknowledgements

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## **Appendix B:**

Study announcement and  
instructions for participants



## Announcement for Interlaboratory Comparison on POPs in Food 2011

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### Introduction

We hereby announce the 12th round of the interlaboratory comparison on the determination of dioxins, PCBs, PBDEs and HBCD in food. The study is open for academic, regulatory as well as commercial laboratories world-wide. The organizer of this study is the Department of Analytical Chemistry at the Norwegian Institute of Public Health in Oslo, Norway. The study is scheduled to take place from January to April 2011. A draft report will be available prior to the evaluation meeting which will take place at the Dioxin 2011 Symposium in August, Brussels, Belgium. The final report will be available to the participants by December 2011 together with a certificate for participation.

### Objectives

The objectives of this exercise are to assess the interlaboratory consistency in results from analyses of dioxins, PCBs, PBDEs and HBCD in regular foods known to contribute to the intake in the general population and to assess the world-wide readiness and capacity in analysing dioxins and other halogenated persistent pollutants in food. The study also serves as a quality assurance instrument for the participating laboratories.

### Participants

We encourage all laboratories world-wide working in this field to participate and assess their analytical performance. Participants are requested to completely fill out the Registration Form and mark for the desired sample types and what analytes they intend to determine.

### Analytical requirements

In this interlaboratory comparison, all the seventeen 2, 3, 7, 8-substituted PCDDs and PCDFs, the four non-ortho PCBs, CB-77, 81, 126 and 169 as well as the eight mono-ortho PCBs, CB-105, 114, 118, 123, 156, 157, 167, and 189 will be assessed. In addition, you are invited to determine six marker PCBs, eight PBDEs and HBCD. The concentration of the following congeners can be reported: CB-28, 52, 101, 138, 153 and 180 and BDE-28, 47, 99, 100, 153, 154, 183 and 209. The concentration of  $\alpha$ -HBCD,  $\beta$ -HBCD and  $\gamma$ -HBCD as well as the total of these isomers will also be assessed. The test materials consist of three fresh food homogenates. You can choose to analyse one, two or all three of the food items. We encourage you to determine as many analytes as possible. You are further requested to determine and report the lipid content of the foods.

We also include standard solutions of all analytes that should be analysed as solutions of known concentration, which may be used to check your own calibration solutions.

### Test material

The test materials consist of three unfortified natural food product homogenates, Salmon filet (labelled S) ~115 g, Mozzarella cheese (labelled M) ~50 g, and Eggs (labelled E) ~70 g, and will be distributed by an international courier service to the participating laboratories.

**Please note:**

**In order to avoid delay at customs, please inform us if there are import restrictions for any of these samples in your country.**

**Instructions for analysis and reporting**

Further detailed instructions and reporting forms will be sent out simultaneously with the dispatch of the samples in January.

In short, laboratories should:

- use their own standard operation procedures for extraction clean-up and instrumental determination
- use their own reference standards for identification and quantification
- report a single concentration for each analyte in each food matrix determined on fresh weight basis
- report limits of detection for all measured analytes in each food item
- report the lipid content

**Time schedule**

Announcement	<b>December 2010</b>
Return of registration form	<b>December 17, 2010</b>
Shipment of test material	<b>January 10, 2011</b>
Confirmation of receipt of test material by participant	<b>Within 7 days</b>
Reporting of test results <sup>a)</sup>	<b>April 15, 2011</b>
Publication of draft report on web-site	<b>August 2011</b>
Evaluation meeting at Dioxin 2011 Brussels, Belgium	<b>August 2011</b>
Final report available to all participants	<b>November 2011</b>

- a) Please be sure that your results are reported on time as there will be **no extension of the deadline.**

**Participation fee**

To all laboratories that have received the test materials, a corresponding invoice will be sent. The participation fee for any combination of the analytes in one food item is 9000 NOK, for two food items 11200 NOK, and for the complete set of all three food items the fee is 13400 NOK.

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## Interlaboratory Comparison on Dioxins in Food 2011

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### Instructions for participants

January 2011

#### 1. Introduction

This is the 12th round of the interlaboratory comparison exercise on the determination of dioxins, PCBs, PBDEs and HBCD in food organised by the Department of Analytical Chemistry, Norwegian Institute of Public Health, Oslo, Norway. The objective of this exercise is to assess the interlaboratory comparability of the results from analyses of all dioxins and dioxin-like PCBs included in the WHO<sub>98</sub>-TEF scheme in regular foods. Participants may also determine and report concentrations of six marker PCBs, eight polybrominated diphenylethers (PBDEs) and hexabromocyclododecane (HBCD). The exercise serves as a quality assurance instrument for the participating laboratories. A further objective is to assess the world-wide readiness and capacity for the determination of dioxin-like compounds, marker PCBs, PBDEs and HBCD in food. Instructions for the analysis and submission of results are given below.

**Please read these instructions carefully before starting the experimental work.**

The participating laboratories will collaboratively assess the interlaboratory comparability in the analytical performance for determination of:

- dioxins and furans: all seventeen 2,3,7,8-substituted PCDDs and PCDFs
- non-ortho PCBs: CB-77, 81, 126 and 169
- mono-ortho PCBs: CB-105, 114, 118, 123, 156, 157, 167 and 189.
- marker PCBs: CB-28, 52, 101, 138, 153 and 180
- PBDEs: BDE-28, 47, 99, 100, 153, 154, 183 and 209
- HBCD:  $\alpha$ -HBCD,  $\beta$ -HBCD,  $\gamma$ -HBCD and total HBCD

In Eggs (E), Mozzarella Cheese (M), and Salmon (S). The mentioned analytes should also be determined in the respective six standard solutions.

In this round of the Interlaboratory comparison study, the concentration of  $\alpha$ -HBCD,  $\beta$ -HBCD and  $\gamma$ -HBCD as well as the total of these isomers will be assessed. Both results from GC-MS and LC-MS or LC-MS/MS are welcome.

#### 2. Participants

A list of participants is attached. 90 laboratories have announced their participation in the study.

#### 3. Design of the study



### 3.1 Test materials

#### Samples

One standard solution of each:

- EDF-5008-50 with PCDDs/PCDFs at concentrations 2:5:10 pg/μl for tetra:penta-hexa-hepta:octa chlorinated dibenzo-p-dioxins/-dibenzo furans respectively
- EC-4986/1000 with non-ortho PCBs at concentration 10 pg/μl
- EC-4987/100 with mono-ortho PCBs at concentration 100 pg/μl
- EC-5179/50 with marker PCBs at concentration 100 pg/μl
- EO-5103/100 with PBDEs at concentration 25 pg/μl, except BDE-209 at 100 pg/μl
- ULM-4834-S/100 with α-HBCD at a concentration 500 pg/μl

One sample of each

- ca. 70 g eggs, lipid content about 10%
- ca. 50 g mozzarella cheese, lipid content about 20%
- ca. 115 g salmon, lipid content about 10%

#### Fortification

The samples are prepared from regular market foods. There is no fortification or spiking of the PCDD, PCDF, PCB, PBDE or HBCD analytes in the food samples.

#### Shipment

The samples are fresh frozen food homogenates. They are distributed by DHL and should reach the receiving laboratory in good condition within a few days. The airwaybill numbers will be made available for the participants to trace the shipment at <http://www.dhl.com>.

### 3.2 Coding

#### Coding of laboratories

Upon arrival of the samples in the participant's laboratory, the Microsoft excel file named "Participant confirmation", shall be filled in and **immediately** returned to the co-ordinators by e-mail or telefax. The code of the laboratory will then be given by the co-ordinators. The laboratory codes will not be revealed to the other participants or to third parties.

#### Coding of samples

Egg samples	E
Mozzarella samples	M
Salmon samples	S

The above sample coding is marked on the sample bottles.

### 3.3 Analytical procedure

#### Methods to be used

Laboratories shall use

- their own methods for sample preparation and instrumental analysis
- their own internal- and quantification standards
- their own lipid determination procedure

### Standard solutions

The standard solutions should be analysed using the laboratory's own quantification standards and methods and the results shall be reported.

### General

Beware of the high risk of background contamination and positive blank values when analysing food samples with levels of dioxins, PCBs, PBDEs and HBCD in the low ppt range.

Use sample size according to expected levels of dioxins for the determinations in order to achieve a detection level that leaves as few as possible analytes as non-detected. The sample amount dispatched is not meant for replicate analyses.

The samples might become inhomogeneous during freezing and transport. Re-homogenise all received material of each food item before any portion is taken out for analysis.

## **4. Reporting**

### 4.1 Results to be reported

Laboratories are recommended to report as many as possible of the congeners mentioned in chapter 1.

The reports must include the determined lipid percent for all three matrixes. Also, the actual sample amount (g) for each determination must be reported.

The analytical report must include concentrations for all the congeners in all the samples on fresh weight basis, see Report forms B, C, D for PCDD/PCDF and dioxin-like PCBs and Report form 2, 3, 4 for marker PCBs, PBDEs and HBCD.

Laboratories must report one concentration on fresh weight basis for each congener which is detected ( $S/N \geq 3$ ), as well as the limit of determination (LOD,  $S/N = 3$ ) for each sample. Non-detected congeners ( $S/N < 3$ ) must be marked ND in the Comments column of the Report form. **Please note that the LOD will be used as concentration of non-detected congeners.**

### 4.2 Checklist

Please use the attached checklist before returning the Report forms with your results.

### 4.3 Submitting results

Three Microsoft Excel files are provided to each participant comprising:

#### **Participants confirmation**

- confirmation of receiving test materials

#### **Report form dioxins and dioxinlike PCBs**

- analytical data, Report forms A, B, C and D

#### **Report form marker PCBs, PBDEs and HBCD**

- analytical data, Report forms 1, 2, 3 and 4

Participants are requested to submit their reports electronically to avoid possible transcription errors.

**Please, do not alter rows or columns in the original Report forms!**

The electronic report shall be sent to [dioxin@fhi.no](mailto:dioxin@fhi.no) within the deadline.

If necessary, a hard copy of the Report forms can be provided. Please contact one of the co-ordinators. If a hard copy report is used, it shall either be faxed to: + 47 21 07 66 86 or mailed to:

Norwegian Institute of Public Health  
att. Veronica Horpestad Liane  
P.O. Box 4403 Nydalen  
N-0403 Oslo, Norway

**Deadline**

**The reports must be in our hands no later than April 15th, 2011** to enable us to prepare the draft report for the Dioxin 2011 Symposium in Brussels, Belgium. There will be no extension of this deadline. A confirmation for receiving your results will be sent to you by e-mail within a week.

**5. Statistical evaluations**

Prior to the final report, a draft version will be prepared based on the data reported by April 16th. The co-ordinators will calculate mean, median and between-laboratory standard deviations for each congener. Outliers will be removed, and consensus values will be calculated. In case of extreme deviation from normal distribution, appropriate procedures will be used to get a best available estimate of the true value. For the dioxin-like compounds, TEQ values will be calculated for each laboratory and a consensus TEQ value based on the consensus of the congeners. Z-scores will be calculated for laboratories' results for PCDD/PCDF TEQs and PCB TEQs.

Statistical results based on the reported data as well as other important information from the evaluation of the data, will be discussed during a consultation meeting in August at the Dioxin 2011 Symposium in Brussels, Belgium.

**6. Final report**

The final report will be prepared by the co-ordinators. All participants will be presented by their laboratory code. A draft will be published on the Internet in July/August. The results will be discussed during the Dioxin 2011 Symposium in Brussels, Belgium. The final report will be available by November 2011. The report will be available in an electronic version on <http://www.fhi.no>. Certificates of participation in the study will be given to all laboratories submitting results.

## 7. Fee

To all laboratories that have received the materials, an invoice will be sent. The participation fee for any combination of the 29 dioxin-like congeners, six marker PCBs, 8 PBDEs and HBCD is

- NOK 9000 for one food item
- NOK 11200 for two food items
- NOK 13400 for the complete set of all three food items.

Up to six standard solutions will be distributed free of charge to all participants, dependent on which analytes the participating laboratories intend to determine.

Invoices will be sent out after we have received the Participant confirmation from the participants.

## 8. Time schedule

Announcement	<b>December 2010</b>
Return of registration form	<b>December 17, 2010</b>
Shipment of test material	<b>January 10, 2011</b>
Confirmation of receipt of test material by participant	<b>Within 7 days</b>
Reporting of test results <sup>a)</sup>	<b>April 15, 2011</b>
Publication of draft report on web-site	<b>August 2011</b>
Evaluation meeting at Dioxin 2011 Brussels, Belgium	<b>August 2011</b>
Final report available to all participants	<b>November 2011</b>

- a) Please be sure that your results are reported in time as there will be **no extension of the deadline.**

## 9. Co-ordinators of the study

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## Interlaboratory Comparison on Dioxins in Food 2010

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### Checklist

In order to avoid possible misunderstandings and errors when reporting your results, we here give a list of possible pitfalls. Please, check this list and your Report forms before reporting your results.

- Are the results for each congener filled out in the correct order? Be especially aware of 2,3,4,6,7,8- and 1,2,3,7,8,9-HxCDF, and PCB 81.
- Are all congener results reported in pg/ $\mu$ l for standards and pg/g for samples?
- Are both concentration and LOD reported for each congener?
- Are sample amount and measured lipid content filled in?
- Are not detected congeners marked with ND in the Comments column?



## **Appendix C:**

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### Summary results

Consensus of congener concentrations

Consensus of TEQ values

Consensus statistics

Laboratories' reported TEQs

Lipid determination

Laboratories' Z-scores

Z-score plots





## Consensus of congener concentrations

	Salmon		Mozzarella Cheese		Egg	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
<b>2,3,7,8-TCDD</b>	0.28	3.2	0.091	0.34	0.020	0.21
<b>1,2,3,7,8-PeCDD</b>	0.50	5.7	0.24	0.90	0.082	0.84
<b>1,2,3,4,7,8-HxCDD</b>	0.029	0.34	0.079	0.29	0.056	0.58
<b>1,2,3,6,7,8-HxCDD</b>	0.21	2.4	0.31	1.2	0.17	1.8
<b>1,2,3,7,8,9-HxCDD</b>	0.022	0.25	0.089	0.33	0.067	0.69
<b>1,2,3,4,6,7,8-HpCDD</b>	0.051	0.59	0.19	0.71	0.31	3.2
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.23	2.6	0.14	0.52	0.62	6.4
<b>2,3,7,8-TCDF</b>	4.9	56	0.028	0.10	0.42	4.3
<b>1,2,3,7,8-PeCDF</b>	0.64	7.4	0.049	0.18	0.20	2.0
<b>2,3,4,7,8-PeCDF</b>	3.4	39	0.50	1.9	0.25	2.6
<b>1,2,3,4,7,8-HxCDF</b>	0.089	1.0	0.44	1.7	0.11	1.2
<b>1,2,3,6,7,8-HxCDF</b>	0.13	1.5	0.39	1.4	0.094	0.97
<b>2,3,4,6,7,8-HxCDF</b>	0.11	1.3	0.32	1.2	0.092	0.95
<b>1,2,3,7,8,9-HxCDF</b>	0.0074	0.085	0.012	0.046	0.014	0.15
<b>1,2,3,4,6,7,8-HpCDF</b>	0.022	0.26	0.23	0.86	0.14	1.4
<b>1,2,3,4,7,8,9-HpCDF</b>	0.0089	0.10	0.022	0.082	0.014	0.14
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.036	0.42	0.041	0.15	0.060	0.62
<b>PCB 77</b>	100	1145	0.60	2.2	2.8	29
<b>PCB 126</b>	38	436	3.4	13	3.6	37
<b>PCB 169</b>	8.2	94	1.2	4.5	0.50	5.1
<b>PCB 81</b>	2.2	25	0.42	1.6	0.24	2.4
<b>PCB 105</b>	1700	19545	68	254	43	441
<b>PCB 114</b>	100	1149	8.3	31	2.2	23
<b>PCB 118</b>	4816	55356	222	826	124	1274
<b>PCB 123</b>	49	568	3.8	14	2.0	20
<b>PCB 156</b>	725	8330	31	115	45	463
<b>PCB 157</b>	165	1901	8.2	30	7.9	81
<b>PCB 167</b>	368	4234	14	51	25	253
<b>PCB 189</b>	71	821	5.3	20	6.9	71

fw. - Fresh weight

lw. - Lipid weight

## Consensus of congener concentrations

	Salmon		Mozzarella Cheese		Egg	
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
<b>CB 28</b>	674	7741	22	82	31	321
<b>CB 52</b>	1381	15877	31	117	6.0	62
<b>CB 101</b>	5359	61601	42	157	8.9	92
<b>CB 138</b>	9195	105694	306	1142	474	4869
<b>CB 153</b>	12073	138768	363	1354	567	5825
<b>CB 180</b>	3586	41219	158	589	358	3679
<b>BDE 28</b>	47	541	0.84	3.1	0.54	5.5
<b>BDE 47</b>	1250	14368	91	339	16	161
<b>BDE 99</b>	291	3343	91	340	22	228
<b>BDE 100</b>	302	3466	15	56	8.6	89
<b>BDE 153</b>	67	773	11	41	51	520
<b>BDE 154</b>	170	1956	7.7	29	16	164
<b>BDE 183</b>	2.7	31	3.1	12	145	1487
<b>BDE 209</b>	42	482	28	104	111	1141
<b><math>\alpha</math>-HBCD</b>	1970	22644	30	112	270	2775
<b><math>\beta</math>-HBCD</b>	41	471				
<b><math>\gamma</math>-HBCD</b>	94	1080	24	89	21	217
<b>Tot HBCD</b>	2103	24172	27	101	288	2958
<b>Sum PCB</b>	32268	370900	922	3441	1445	14848
<b>Sum BDE wo./ 209</b>	2129	24477	220	820	258	2654
<b>Sum BDE</b>	2171	24958	248	924	369	3795

fw. - Fresh weight

lw. - Lipid weight

wo.-without

## Consensus of TEQs

TEF1998	Salmon		Mozzarella Cheese		Egg	
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
<b>2,3,7,8-TCDD</b>	0.28	3.2	0.091	0.34	0.020	0.21
<b>1,2,3,7,8-PeCDD</b>	0.50	5.7	0.24	0.90	0.082	0.84
<b>1,2,3,4,7,8-HxCDD</b>	0.0029	0.034	0.0079	0.029	0.0056	0.058
<b>1,2,3,6,7,8-HxCDD</b>	0.021	0.24	0.031	0.12	0.017	0.18
<b>1,2,3,7,8,9-HxCDD</b>	0.0022	0.025	0.0089	0.033	0.0067	0.069
<b>1,2,3,4,6,7,8-HpCDD</b>	0.00051	0.0059	0.0019	0.0071	0.0031	0.032
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.000023	0.00026	0.000014	0.000052	0.000062	0.00064
<b>2,3,7,8-TCDF</b>	0.49	5.6	0.0028	0.010	0.042	0.43
<b>1,2,3,7,8-PeCDF</b>	0.032	0.37	0.0025	0.0092	0.010	0.10
<b>2,3,4,7,8-PeCDF</b>	1.7	20	0.25	0.93	0.13	1.3
<b>1,2,3,4,7,8-HxCDF</b>	0.0089	0.10	0.044	0.17	0.011	0.12
<b>1,2,3,6,7,8-HxCDF</b>	0.013	0.15	0.039	0.14	0.0094	0.097
<b>2,3,4,6,7,8-HxCDF</b>	0.011	0.13	0.032	0.12	0.0092	0.095
<b>1,2,3,7,8,9-HxCDF</b>	0.00074	0.0085	0.0012	0.0046	0.0014	0.015
<b>1,2,3,4,6,7,8-HpCDF</b>	0.00022	0.0026	0.0023	0.0086	0.0014	0.014
<b>1,2,3,4,7,8,9-HpCDF</b>	0.000089	0.0010	0.00022	0.00082	0.00014	0.0014
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.0000036	0.000042	0.0000041	0.000015	0.0000060	0.000062
<b>PCB 77</b>	0.010	0.11	0.000060	0.00022	0.00028	0.0029
<b>PCB 126</b>	3.8	44	0.34	1.3	0.36	3.7
<b>PCB 169</b>	0.082	0.94	0.012	0.045	0.0050	0.051
<b>PCB 81</b>	0.00022	0.0025	0.000042	0.00016	0.000024	0.00024
<b>PCB 105</b>	0.17	2.0	0.0068	0.025	0.0043	0.044
<b>PCB 114</b>	0.050	0.57	0.0042	0.015	0.0011	0.011
<b>PCB 118</b>	0.48	5.5	0.022	0.083	0.012	0.13
<b>PCB 123</b>	0.0049	0.057	0.00038	0.0014	0.00020	0.0020
<b>PCB 156</b>	0.36	4.2	0.015	0.057	0.023	0.23
<b>PCB 157</b>	0.083	0.95	0.0041	0.015	0.0039	0.040
<b>PCB 167</b>	0.0037	0.042	0.00014	0.00051	0.00025	0.0025
<b>PCB 189</b>	0.0071	0.082	0.00053	0.0020	0.00069	0.0071
<b>PCDDs/PCDFs</b>	3.1	35	0.76	2.8	0.35	3.6
<b>Non-ortho PCBs</b>	3.9	45	0.35	1.3	0.37	3.8
<b>Mono-ortho PCBs</b>	1.2	13	0.054	0.20	0.045	0.47
<b>Total TEQ</b>	<b>8.1</b>	<b>93</b>	<b>1.2</b>	<b>4.3</b>	<b>0.76</b>	<b>7.8</b>

fw. - Fresh weight

lw. - Lipid weight

## Consensus of TEQs

TEF2005	Salmon		Mozzarella Cheese		Egg	
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
<b>2,3,7,8-TCDD</b>	0.28	3.2	0.091	0.34	0.020	0.21
<b>1,2,3,7,8-PeCDD</b>	0.50	5.7	0.24	0.90	0.082	0.84
<b>1,2,3,4,7,8-HxCDD</b>	0.0029	0.034	0.0079	0.029	0.0056	0.058
<b>1,2,3,6,7,8-HxCDD</b>	0.021	0.24	0.031	0.12	0.017	0.18
<b>1,2,3,7,8,9-HxCDD</b>	0.0022	0.025	0.0089	0.033	0.0067	0.069
<b>1,2,3,4,6,7,8-HpCDD</b>	0.00051	0.0059	0.0019	0.0071	0.0031	0.032
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.000068	0.00079	0.000042	0.00016	0.00019	0.0019
<b>2,3,7,8-TCDF</b>	0.49	5.6	0.0028	0.010	0.042	0.43
<b>1,2,3,7,8-PeCDF</b>	0.019	0.22	0.0015	0.0055	0.0060	0.061
<b>2,3,4,7,8-PeCDF</b>	1.0	12	0.15	0.56	0.076	0.78
<b>1,2,3,4,7,8-HxCDF</b>	0.0089	0.10	0.044	0.17	0.011	0.12
<b>1,2,3,6,7,8-HxCDF</b>	0.013	0.15	0.039	0.14	0.0094	0.097
<b>2,3,4,6,7,8-HxCDF</b>	0.011	0.13	0.032	0.12	0.0092	0.095
<b>1,2,3,7,8,9-HxCDF</b>	0.00074	0.0085	0.0012	0.0046	0.0014	0.015
<b>1,2,3,4,6,7,8-HpCDF</b>	0.00022	0.0026	0.0023	0.0086	0.0014	0.014
<b>1,2,3,4,7,8,9-HpCDF</b>	0.000089	0.0010	0.00022	0.00082	0.00014	0.0014
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.000011	0.00013	0.000012	0.000046	0.000018	0.00018
<b>PCB 77</b>	0.010	0.11	0.000060	0.00022	0.00028	0.0029
<b>PCB 126</b>	3.8	44	0.34	1.3	0.36	3.7
<b>PCB 169</b>	0.25	2.8	0.036	0.13	0.015	0.15
<b>PCB 81</b>	0.00065	0.0075	0.00013	0.00047	0.000071	0.00072
<b>PCB 105</b>	0.051	0.59	0.0020	0.0076	0.0013	0.013
<b>PCB 114</b>	0.0030	0.034	0.00025	0.00093	0.000066	0.00068
<b>PCB 118</b>	0.14	1.7	0.0066	0.025	0.0037	0.038
<b>PCB 123</b>	0.0015	0.017	0.00011	0.00042	0.000059	0.00061
<b>PCB 156</b>	0.022	0.25	0.00092	0.0034	0.0014	0.014
<b>PCB 157</b>	0.0050	0.057	0.00025	0.00091	0.00024	0.0024
<b>PCB 167</b>	0.011	0.13	0.00041	0.0015	0.00074	0.0076
<b>PCB 189</b>	0.0021	0.025	0.00016	0.00059	0.00021	0.0021
<b>PCDDs/PCDFs</b>	2.4	27	0.66	2.4	0.29	3.0
<b>Non-ortho PCBs</b>	4.0	46	0.38	1.4	0.38	3.9
<b>Mono-ortho PCBs</b>	0.24	2.8	0.011	0.040	0.0077	0.079
<b>Total TEQ</b>	<b>6.7</b>	<b>77</b>	<b>1.0</b>	<b>3.9</b>	<b>0.67</b>	<b>6.9</b>

fw. - Fresh weight

lw. - Lipid weight

## Consensus statistics

### Analyte solution

	Target value pg/μl	Consensus median, pg/μl	Median all values pg/μl	Consensus mean, pg/μl	Standard deviation, pg/μl	Relative standard deviation, %	No. of values reported	No. of values removed
2,3,7,8-TCDD	2.0	2.0	2.0	2.0	0.21	11	86	0
1,2,3,7,8-PeCDD	5.0	4.8	4.8	4.8	0.35	7.3	86	1
1,2,3,4,7,8-HxCDD	5.0	4.9	4.9	4.9	0.52	11	86	0
1,2,3,6,7,8-HxCDD	5.0	4.8	4.8	4.8	0.41	8.5	86	0
1,2,3,7,8,9-HxCDD	5.0	5.1	5.1	5.1	0.49	9.6	86	0
1,2,3,4,6,7,8-HpCDD	5.0	5.0	5.0	5.0	0.43	8.6	86	0
1,2,3,4,6,7,8,9-OCDD	10	9.9	9.9	9.9	0.93	9.4	86	0
2,3,7,8-TCDF	2.0	1.9	1.9	1.9	0.19	10	86	0
1,2,3,7,8-PeCDF	5.0	5.0	5.0	5.0	0.46	9.2	86	1
2,3,4,7,8-PeCDF	5.0	4.8	4.8	4.8	0.41	8.5	86	1
1,2,3,4,7,8-HxCDF	5.0	4.9	4.9	4.9	0.42	8.6	86	0
1,2,3,6,7,8-HxCDF	5.0	5.0	5.0	5.1	0.44	8.7	86	0
2,3,4,6,7,8-HxCDF	5.0	5.0	5.0	5.0	0.43	8.6	86	0
1,2,3,7,8,9-HxCDF	5.0	5.0	5.0	5.0	0.46	9.1	86	0
1,2,3,4,6,7,8-HpCDF	5.0	4.9	4.9	5.0	0.44	8.7	86	0
1,2,3,4,7,8,9-HpCDF	5.0	5.0	5.0	5.1	0.47	9.3	86	0
1,2,3,4,6,7,8,9-OCDF	10	9.9	9.9	10	1.2	12	86	0
PCB 77	10	10	10	10	1.0	10	83	3
PCB 126	10	10	10	10	1.0	10	83	4
PCB 169	10	10	10	10	0.93	9.2	83	3
PCB 81	10	10	10	10	1.1	11	82	3
PCB 105	100	102	102	102	8.7	8.6	85	2
PCB 114	100	102	102	102	10	9.9	85	2
PCB 118	100	101	101	101	9.9	9.8	86	2
PCB 123	100	103	103	102	8.8	8.6	84	2
PCB 156	100	104	104	103	9.1	8.8	85	2
PCB 157	100	104	104	103	8.4	8.2	84	1
PCB 167	100	103	103	103	8.7	8.4	84	2
PCB 189	100	101	101	102	9.0	8.8	84	2

## Consensus statistics

### Salmon, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
<b>2,3,7,8-TCDD</b>	0.28	0.28	0.27	0.075	27	88	2	5
<b>1,2,3,7,8-PeCDD</b>	0.50	0.50	0.48	0.11	23	88	4	5
<b>1,2,3,4,7,8-HxCDD</b>	0.029	0.030	0.029	0.0086	30	88	12	18
<b>1,2,3,6,7,8-HxCDD</b>	0.21	0.21	0.21	0.048	23	88	2	5
<b>1,2,3,7,8,9-HxCDD</b>	0.022	0.023	0.021	0.0081	38	88	16	23
<b>1,2,3,4,6,7,8-HpCDD</b>	0.051	0.056	0.058	0.023	40	88	9	18
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.23	0.24	0.23	0.096	41	88	11	10
<b>2,3,7,8-TCDF</b>	4.9	4.9	4.7	1.1	24	88	2	1
<b>1,2,3,7,8-PeCDF</b>	0.64	0.64	0.64	0.15	24	88	3	0
<b>2,3,4,7,8-PeCDF</b>	3.4	3.4	3.3	0.78	24	88	1	1
<b>1,2,3,4,7,8-HxCDF</b>	0.089	0.090	0.091	0.027	30	88	5	5
<b>1,2,3,6,7,8-HxCDF</b>	0.13	0.13	0.13	0.032	24	88	5	2
<b>2,3,4,6,7,8-HxCDF</b>	0.11	0.11	0.11	0.032	30	88	7	7
<b>1,2,3,7,8,9-HxCDF</b>	0.0074	0.010	0.0082	0.0049	60	88	28	51
<b>1,2,3,4,6,7,8-HpCDF</b>	0.022	0.027	0.025	0.011	44	88	24	17
<b>1,2,3,4,7,8,9-HpCDF</b>	0.0089	0.010	0.0085	0.0046	54	88	27	53
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.036	0.045	0.040	0.018	46	88	18	26
<b>PCB 77</b>	100	100	98	23	23	87	1	1
<b>PCB 126</b>	38	38	37	9.5	26	87	1	1
<b>PCB 169</b>	8.2	8.2	8.0	2.0	25	87	3	2
<b>PCB 81</b>	2.2	2.3	2.1	0.63	30	86	16	7
<b>PCB 105</b>	1700	1701	1700	376	22	89	1	0
<b>PCB 114</b>	100	100	101	30	30	89	2	1
<b>PCB 118</b>	4816	4830	4801	1147	24	90	1	0
<b>PCB 123</b>	49	55	47	23	48	88	20	7
<b>PCB 156</b>	725	725	732	170	23	89	1	0
<b>PCB 157</b>	165	166	163	37	23	88	2	0
<b>PCB 167</b>	368	378	377	86	23	88	3	0
<b>PCB 189</b>	71	72	71	17	24	88	1	0

## Consensus statistics

### Mozzarella Cheese, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
<b>2,3,7,8-TCDD</b>	0.091	0.093	0.086	0.023	27	73	6	6
<b>1,2,3,7,8-PeCDD</b>	0.24	0.24	0.24	0.060	25	73	4	5
<b>1,2,3,4,7,8-HxCDD</b>	0.079	0.080	0.081	0.026	32	73	5	7
<b>1,2,3,6,7,8-HxCDD</b>	0.31	0.31	0.31	0.084	27	73	2	4
<b>1,2,3,7,8,9-HxCDD</b>	0.089	0.092	0.085	0.026	31	73	6	9
<b>1,2,3,4,6,7,8-HpCDD</b>	0.19	0.19	0.19	0.058	30	73	7	7
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.14	0.20	0.16	0.087	53	73	17	12
<b>2,3,7,8-TCDF</b>	0.028	0.035	0.030	0.015	50	73	18	10
<b>1,2,3,7,8-PeCDF</b>	0.049	0.050	0.050	0.017	35	73	7	10
<b>2,3,4,7,8-PeCDF</b>	0.50	0.50	0.48	0.11	23	73	2	2
<b>1,2,3,4,7,8-HxCDF</b>	0.44	0.44	0.43	0.12	27	73	2	2
<b>1,2,3,6,7,8-HxCDF</b>	0.39	0.39	0.37	0.080	22	73	3	1
<b>2,3,4,6,7,8-HxCDF</b>	0.32	0.32	0.30	0.086	29	73	3	5
<b>1,2,3,7,8,9-HxCDF</b>	0.012	0.019	0.015	0.010	70	73	17	44
<b>1,2,3,4,6,7,8-HpCDF</b>	0.23	0.23	0.24	0.079	33	73	6	5
<b>1,2,3,4,7,8,9-HpCDF</b>	0.022	0.028	0.026	0.012	46	73	15	24
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.041	0.054	0.047	0.027	57	73	20	24
<b>PCB 77</b>	0.60	0.81	0.66	0.33	50	72	22	10
<b>PCB 126</b>	3.4	3.4	3.2	0.88	27	72	4	3
<b>PCB 169</b>	1.2	1.2	1.2	0.26	22	72	6	8
<b>PCB 81</b>	0.42	0.43	0.41	0.12	30	72	11	9
<b>PCB 105</b>	68	70	69	15	22	74	5	0
<b>PCB 114</b>	8.3	8.3	8.3	2.0	25	74	5	5
<b>PCB 118</b>	222	226	231	59	25	75	4	0
<b>PCB 123</b>	3.8	3.9	3.6	0.93	26	74	9	11
<b>PCB 156</b>	31	31	31	6.4	21	74	7	0
<b>PCB 157</b>	8.2	8.3	8.2	2.0	25	73	6	3
<b>PCB 167</b>	14	14	14	2.8	20	74	7	2
<b>PCB 189</b>	5.3	5.3	5.3	1.4	26	74	5	6

## Consensus statistics

### Egg, fresh weight

	Consensus median, pg/g	Median all values pg/g	Consensus mean, pg/g	Standard deviation, pg/g	Relative standard deviation, %	No. of values reported	No. of values removed	No. of reported non-detects
<b>2,3,7,8-TCDD</b>	0.020	0.021	0.020	0.0066	33	74	7	8
<b>1,2,3,7,8-PeCDD</b>	0.082	0.084	0.084	0.021	26	74	6	5
<b>1,2,3,4,7,8-HxCDD</b>	0.056	0.057	0.058	0.016	28	74	5	8
<b>1,2,3,6,7,8-HxCDD</b>	0.17	0.17	0.17	0.045	26	74	1	6
<b>1,2,3,7,8,9-HxCDD</b>	0.067	0.068	0.066	0.020	31	74	7	8
<b>1,2,3,4,6,7,8-HpCDD</b>	0.31	0.32	0.31	0.091	29	74	4	5
<b>1,2,3,4,6,7,8,9-OCDD</b>	0.62	0.64	0.63	0.21	34	74	5	2
<b>2,3,7,8-TCDF</b>	0.42	0.42	0.42	0.088	21	74	1	1
<b>1,2,3,7,8-PeCDF</b>	0.20	0.20	0.20	0.037	19	74	2	2
<b>2,3,4,7,8-PeCDF</b>	0.25	0.25	0.26	0.047	18	74	1	2
<b>1,2,3,4,7,8-HxCDF</b>	0.11	0.11	0.12	0.036	31	74	5	5
<b>1,2,3,6,7,8-HxCDF</b>	0.094	0.096	0.093	0.026	28	74	5	5
<b>2,3,4,6,7,8-HxCDF</b>	0.092	0.093	0.088	0.028	32	74	4	8
<b>1,2,3,7,8,9-HxCDF</b>	0.014	0.016	0.015	0.0060	40	74	14	27
<b>1,2,3,4,6,7,8-HpCDF</b>	0.14	0.14	0.15	0.045	30	74	3	3
<b>1,2,3,4,7,8,9-HpCDF</b>	0.014	0.016	0.016	0.0078	50	74	17	28
<b>1,2,3,4,6,7,8,9-OCDF</b>	0.060	0.064	0.062	0.026	43	74	12	13
<b>PCB 77</b>	2.8	2.9	2.9	0.84	29	73	8	4
<b>PCB 126</b>	3.6	3.6	3.6	0.82	23	73	3	3
<b>PCB 169</b>	0.50	0.52	0.50	0.11	22	73	10	9
<b>PCB 81</b>	0.24	0.24	0.23	0.068	29	73	12	9
<b>PCB 105</b>	43	43	44	9.3	21	74	4	0
<b>PCB 114</b>	2.2	2.3	2.3	0.70	30	74	13	10
<b>PCB 118</b>	124	124	128	26	20	75	6	0
<b>PCB 123</b>	2.0	2.1	2.1	0.73	35	74	13	12
<b>PCB 156</b>	45	45	47	10	22	74	2	0
<b>PCB 157</b>	7.9	7.9	8.1	1.7	21	73	4	3
<b>PCB 167</b>	25	25	25	4.7	19	74	4	0
<b>PCB 189</b>	6.9	6.9	7.1	1.4	19	73	2	4



## Consensus statistics

### Analyte solution

	Target value pg/µl	Median, pg/µl all values	Median, pg/µl outliers removed	Mean, pg/µl all values	Mean, pg/µl outliers removed
CB 28	100	103	103	102	102
CB 52	100	103	103	102	102
CB 101	100	99	99	98	99
CB 138	100	104	104	103	102
CB 153	100	103	103	101	102
CB 180	100	104	104	103	103
BDE 28	25	24	24	24	24
BDE 47	25	24	24	24	24
BDE 99	25	24	24	24	24
BDE 100	25	24	24	24	24
BDE 153	25	24	24	24	24
BDE 154	25	24	24	24	24
BDE 183	25	24	24	24	24
BDE 209	100	100	100	99	99
α-HBCD *	500	494	494	496	496

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Number of reported values	Number of reported outliers
CB 28	17	11	65	2
CB 52	17	10	65	3
CB 101	16	9	65	3
CB 138	21	12	65	2
CB 153	17	10	65	3
CB 180	17	10	65	2
BDE 28	11	11	42	0
BDE 47	8.8	8.8	42	0
BDE 99	8.7	8.7	42	0
BDE 100	8.1	8.1	42	0
BDE 153	11	11	42	0
BDE 154	10	10	42	0
BDE 183	11	11	41	0
BDE 209	10	10	29	0
α-HBCD *	7.0	7.0	15	0

NDs: Non-detects

\* : Indicative value due to few reported values

## Consensus statistics

### Salmon, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
CB 28	690	674	674	809	739	739
CB 52	1383	1381	1381	2841	1379	1379
CB 101	5380	5359	5359	5475	5377	5377
CB 138	9195	9195	9195	9566	9566	9566
CB 153	12073	12073	12073	12104	12104	12104
CB 180	3611	3586	3586	3830	3645	3645
BDE 28	47	47	47	48	48	48
BDE 47	1250	1250	1250	1224	1224	1224
BDE 99	292	292	291	291	291	286
BDE 100	302	302	302	293	293	293
BDE 153	67	67	67	68	68	68
BDE 154	170	170	170	177	177	177
BDE 183	3.1	2.9	2.7	4.8	2.9	2.8
BDE 209	64	42	42	249	50	48
$\alpha$ -HBCD *	1970	1970	1970	1993	1993	1993
$\beta$ -HBCD *	50	40	41	66	42	43
$\gamma$ -HBCD *	110	94	94	162	97	97
Tot HBCD *	2103	2103	2103	2300	2300	2300

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	Number of reported values	Number of outliers	Number of reported NDs
CB 28	48	32	32	68	4	0
CB 52	417	21	21	68	2	0
CB 101	30	27	27	68	1	0
CB 138	26	26	26	68	0	0
CB 153	28	28	28	68	0	0
CB 180	35	22	22	68	2	0
BDE 28	33	33	33	41	0	0
BDE 47	26	26	26	41	0	0
BDE 99	24	24	22	41	0	1
BDE 100	21	21	21	41	0	0
BDE 153	24	24	24	41	0	0
BDE 154	30	30	30	41	0	0
BDE 183	155	50	43	40	5	15
BDE 209	382	54	48	27	4	6
$\alpha$ -HBCD *	27	27	27	15	0	0
$\beta$ -HBCD *	144	45	45	15	1	5
$\gamma$ -HBCD *	75	35	35	15	4	1
Tot HBCD *	22	22	22	12	0	0

NDs: Non-detects

\* : Indicative value due to few reported values

**Consensus statistics**  
**Mozzarella Cheese, fresh weight**

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
CB 28	37	21	22	87	25	25
CB 52	39	31	31	95	36	36
CB 101	58	43	42	111	48	47
CB 138	318	306	306	400	319	319
CB 153	363	363	363	447	375	375
CB 180	160	158	158	218	160	160
BDE 28	1.5	1.0	0.84	5.8	1.3	1.0
BDE 47	92	91	91	206	94	94
BDE 99	92	91	91	135	97	97
BDE 100	15	15	15	43	16	16
BDE 153	11	11	11	23	11	11
BDE 154	8.0	7.6	7.7	24	7.4	7.5
BDE 183	3.6	3.2	3.1	26	3.5	3.4
BDE 209	44	28	28	292	35	37
$\alpha$ -HBCD *	30	30	30	28	28	26
$\beta$ -HBCD *	17	15		20	12	
$\gamma$ -HBCD *	22	20	24	29	19	24
Tot HBCD *	31	27	27	47	29	28

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	Number of reported values	Number of outliers	Number of reported NDs
CB 28	252	59	60	55	18	3
CB 52	227	52	52	55	15	2
CB 101	136	54	53	55	13	2
CB 138	112	22	22	56	3	0
CB 153	90	19	19	56	2	0
CB 180	161	17	17	56	3	0
BDE 28	352	64	67	34	5	9
BDE 47	270	27	27	34	2	0
BDE 99	119	31	31	34	2	0
BDE 100	307	19	19	34	3	0
BDE 153	184	24	22	34	4	1
BDE 154	302	22	20	34	5	2
BDE 183	459	40	42	34	6	8
BDE 209	339	64	62	25	7	6
$\alpha$ -HBCD *	32	32	32	12	0	5
$\beta$ -HBCD *	96	65		12	2	12
$\gamma$ -HBCD *	71	68	119	12	3	10
Tot HBCD *	70	29	20	11	3	4

NDs: Non-detects

\* : Indicative value due to few reported values

## Consensus statistics

### Egg, fresh weight

	Median, pg/g all values	Median, pg/g outliers removed	Median, pg/g outliers and NDs removed	Mean, pg/g all values	Mean, pg/g outliers removed	Mean, pg/g outliers and NDs removed
CB 28	34	31	31	69	35	34
CB 52	10	6.0	6.0	52	7.0	6.7
CB 101	14	9.1	8.9	56	11	11
CB 138	485	474	474	564	490	498
CB 153	570	567	567	646	551	561
CB 180	360	354	358	405	363	369
BDE 28	0.94	0.63	0.54	1.5	0.68	0.62
BDE 47	16	16	16	39	17	17
BDE 99	22	22	22	40	23	24
BDE 100	8.7	8.6	8.6	13	9.2	9.1
BDE 153	51	51	51	53	53	53
BDE 154	16	16	16	19	17	17
BDE 183	145	145	145	150	150	150
BDE 209	123	114	111	454	114	112
$\alpha$ -HBCD *	285	285	270	243	243	238
$\beta$ -HBCD *	18	18		18	18	
$\gamma$ -HBCD *	18	18	21	17	17	21
Tot HBCD *	306	306	288	256	256	247

	Relative standard deviation, % all values	Relative standard deviation, % outliers removed	Relative standard deviation, % outliers and NDs removed	Number of reported values	Number of outliers	Number of reported NDs
CB 28	179	28	28	56	10	2
CB 52	227	65	59	56	20	6
CB 101	263	52	53	56	16	5
CB 138	57	25	22	57	4	1
CB 153	61	21	17	57	4	1
CB 180	51	23	19	57	3	1
BDE 28	146	64	65	31	5	12
BDE 47	221	31	31	31	6	1
BDE 99	213	29	29	31	2	2
BDE 100	162	26	26	31	2	1
BDE 153	19	19	19	32	0	0
BDE 154	78	20	20	32	1	1
BDE 183	30	30	30	31	0	0
BDE 209	238	36	36	22	4	2
$\alpha$ -HBCD *	38	38	40	12	0	1
$\beta$ -HBCD *	54	54		12	0	12
$\gamma$ -HBCD *	39	39	61	12	0	10
Tot HBCD *	38	38	40	11	0	1

NDs: Non-detects

\* : Indicative value due to few reported values

## Laboratories' reported TEQs, sum indicator PCB and sum BDE without BDE 209

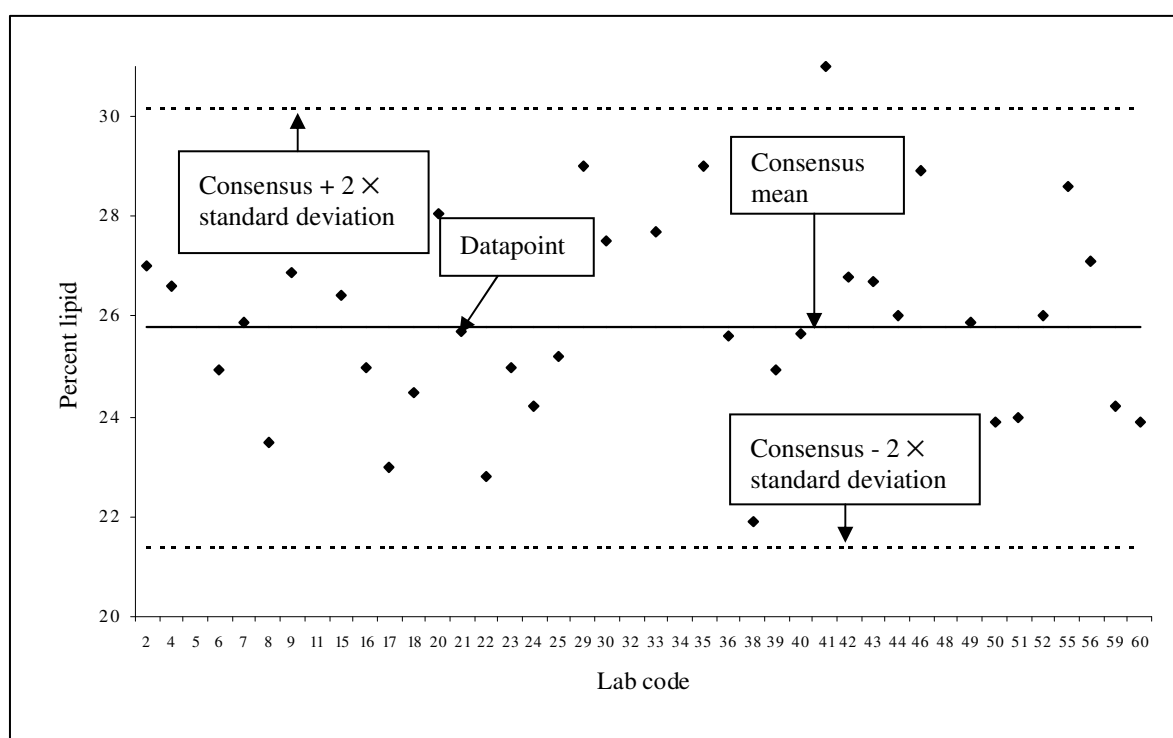
	Median	Mean	SD	RSD	Min	Max	Reporting
	pg/g	pg/g	pg/g	%	pg/g	pg/g	laboratories
<b>Salmon fresh weight</b>							
PCDD/PCDF TEQ	3.1	3.6	4.1	112	0.17	37	88
Non-ortho PCB TEQ	3.9	4.2	4.0	94	0.34	40	87
Mono-ortho PCB TEQ	1.2	1.3	1.3	101	0.14	13	90
Total TEQ	8.1	8.7	9.0	104	0.47	91	94
Sum indicator PCB	33125	34625	13394	39	6652	124058	68
Sum BDE without BDE 209	2167	2106	471	22	71	3088	41
<b>Mozarella cheese fresh weight</b>							
PCDD/PCDF TEQ	0.76	0.84	0.44	53	0.089	3.3	73
Non-ortho PCB TEQ	0.35	0.38	0.20	54	0.041	1.3	72
Mono-ortho PCB TEQ	0.055	0.065	0.038	59	0.017	0.21	75
Total TEQ	1.2	1.2	0.66	54	0.026	4.8	78
Sum indicator PCB	982	1353	1481	110	516	9954	56
Sum BDE without BDE 209	218	463	968	209	143	5677	34
<b>Egg fresh weight</b>							
PCDD/PCDF TEQ	0.35	0.45	0.52	115	0.18	4.2	74
Non-ortho PCB TEQ	0.37	0.44	0.37	86	0.036	3.2	73
Mono-ortho PCB TEQ	0.046	0.058	0.051	89	0.015	0.43	75
Total TEQ	0.76	0.88	0.87	99	0.015	7.8	80
Sum indicator PCB	1518	1788	1156	65	288	8559	57
Sum BDE without BDE 209	269	310	215	69	84	1425	32

## Presentation of results for lipid determination

Removal of outliers and calculation of consensus were done by the following procedure:

1. The mean was calculated from all the reported data.
2. Values outside a range of  $\pm 2 \times$  the standard deviation of this mean, were defined as outliers and removed from the data set.
3. Mean, standard deviation and median were re-calculated from the remaining data. This mean was called consensus.

The diagram shows the reported data with consensus and consensus  $\pm$  the new standard deviation  $\times 2$ .



### Z-Scores of lipid content

Z-scores of lipid content were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

Where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

### Lipid determination for Salmon

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
1	9.0		48	9.2		99	8.9	
2	9.9		49	9.2		100	8.6	
3	9.2		50	8.8		102	6.2	
4	9.1		51	9.2				
5	16	outlier	52	8.6				
6	8.6		53	9.0				
7	8.1		54	8.6				
8	8.6		55	8.1				
9	8.6		56	8.2				
10	4.5		57	8.7				
11	8.6		58	10				
12	9.6		59	5.2				
13	8.4		60	8.9				
15	9.0		61	9.2				
16	8.8		62	8.7				
17	8.7		63	8.9				
18	8.9		64	8.8				
19	12		65	7.1				
20	8.8		66	8.7				
21	9.0		67	8.7				
22	8.5		68	8.3				
23	8.4		69	8.2				
24	9.2		71	8.7				
25	8.9		72	8.8				
26	8.3	73	7.6					
27	7.6	75	7.9					
28	8.6	76	8.9					
29	9.4	77	9.6					
30	9.3	78	8.8					
31	7.7	79	8.1					
32	9.3	80	9.4					
33	8.7	81	6.0					
34	8.0	83	8.5					
35	8.9	84	5.6					
36	8.4	85	8.8					
37	7.4	86	12					
38	9.4	87	8.8					
39	6.2	88	8.9					
40	10	90	9.9					
41	8.3	92	9.8					
42	8.5	93	9.0					
43	31	outlier	94	9.3				
44	3.6		95	8.2				
45	8.3		96	8.3				
46	8.4		97	8.0				
47	9.0		98	9.3				

Mean	Standard deviation	Relative standard deviation	Median
8.6	1.2	14	8.7

### Lipid determination for Mozzarella Cheese

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
1	27.7		62	25.1				
3	26.9		63	25.3				
4	27.4		65	26.8				
5	25.2		66	26.7				
6	25.3		67	19.0	outlier			
7	26.3		68	26.9				
8	24.1		70	30.6				
11	27.2		71	27.2				
12	27.3		72	26.8				
15	28.7		74	26.2				
17	29.7		75	24.4				
18	26.4		76	26.8				
19	19.5	outlier	77	25.6				
21	22.0		78	26.0				
22	27.6		80	26.7				
23	26.1		83	27.5				
24	26.0		84	22.7				
25	28.0		85	27.1				
26	25.5		86	26.4				
27	18.9	outlier	87	25.7				
29	27.2		90	27.8				
30	26.4		92	27.5				
31	25.7		93	28.3				
32	26.9		94	31.2				
33	25.8		95	26.0				
34	25.3		96	22.4				
35	27.2		97	26.7				
36	26.2		98	24.9				
39	25.5		100	24.8				
40	30.8		101	28.0				
43	29.8		102	24.6				
44	26.9							
47	26.9							
48	26.2							
49	28.3							
50	26.8							
51	14.1	outlier						
53	28.8							
54	30.6							
55	27.3							
56	25.8							
57	27.7							
58	27.6							
59	27.8							
60	27.0							
61	27.6							

Mean	Standard deviation	Relative standard deviation	Median
26.7	1.73	6.5	26.8

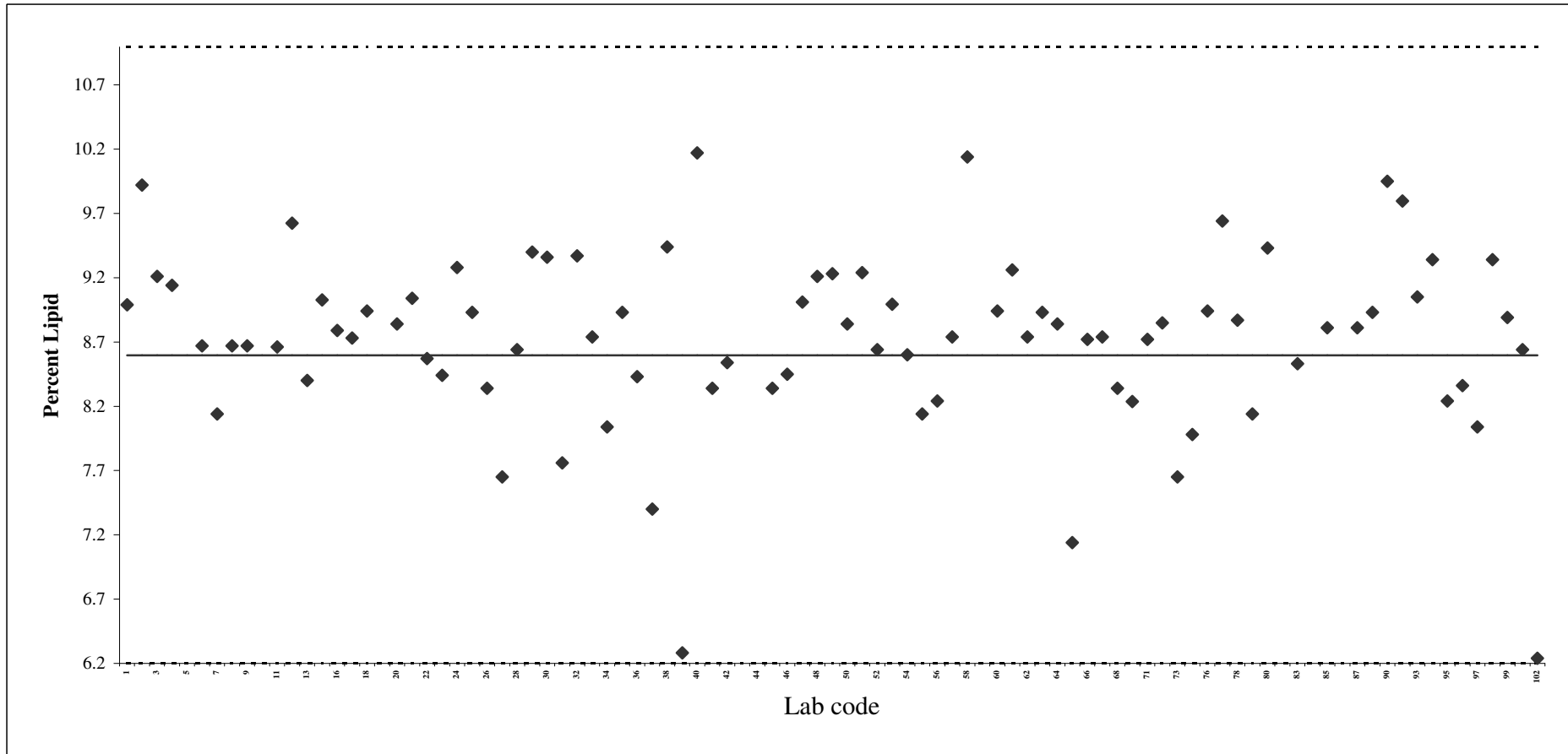


### Lipid determination for Egg

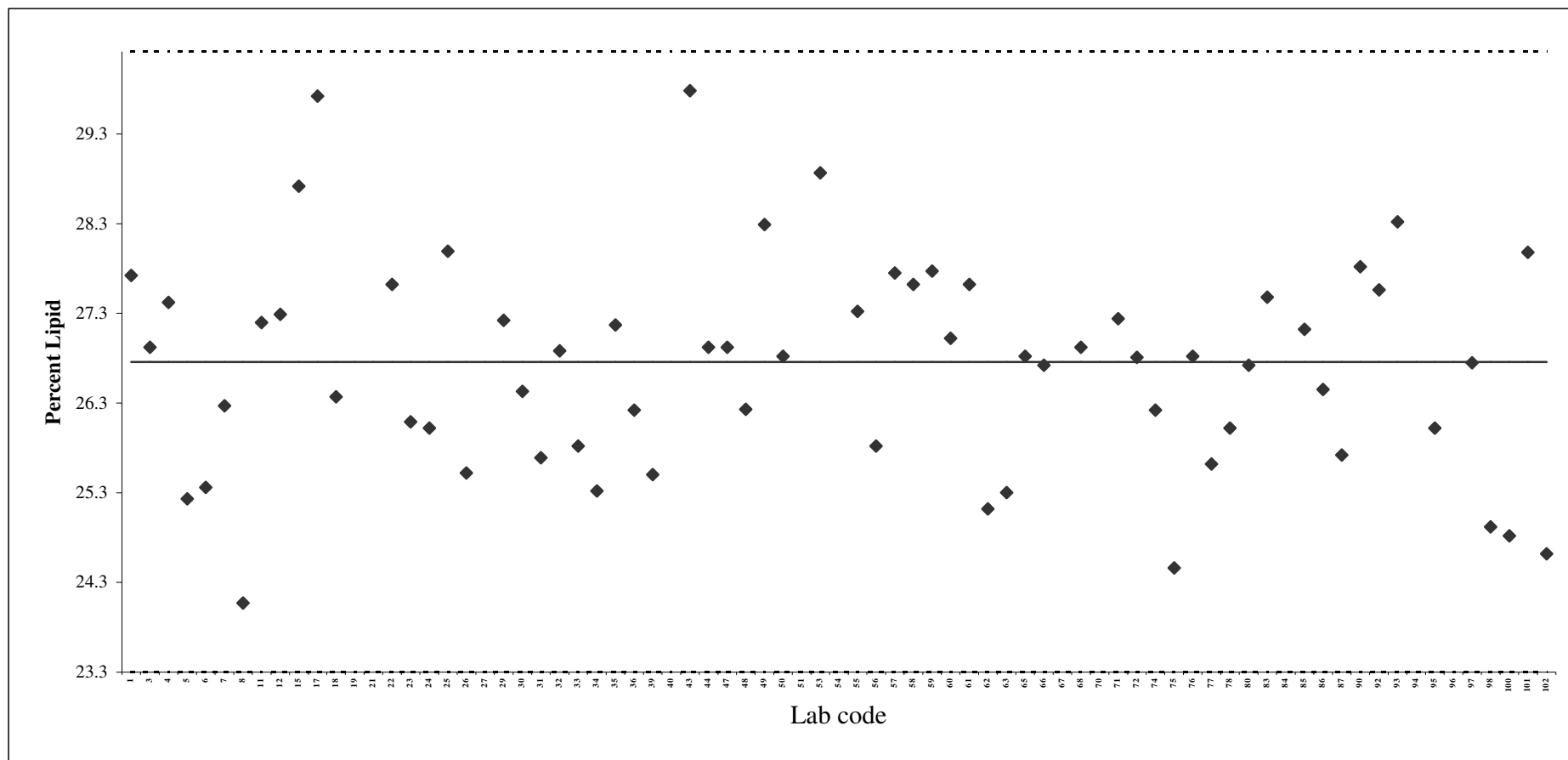
Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
1	8.5		59	9.7				
2	12		60	9.2				
3	10		61	9.7				
4	11		62	9.7				
5	11		63	10				
6	10		65	13				
7	9.5		66	10				
8	9.9		67	9.4				
11	9.0		68	8.5				
12	10		70	11				
15	11		71	9.6				
16	9.9		72	9.3				
17	10		73	8.5				
18	11		75	8.4				
19	10		76	10				
21	11		77	9.5				
22	8.6		78	4.8	outlier			
23	9.0		82	9.6				
24	11		83	10				
25	9.3		84	7.5				
26	8.5		85	9.2				
27	8.5		86	8.8				
28	10		90	9.4				
29	12		92	14	outlier			
30	9.3		93	10				
31	11		94	11				
32	9.7		95	9.6				
33	9.7		96	7.4				
34	7.8		97	9.6				
35	11		98	10				
36	10		100	9.0				
39	8.4		101	11				
40	12		102	8.8				
43	20	outlier	103	10				
44	7.6							
47	10							
48	10							
49	10							
50	9.6							
51	4.9	outlier						
52	11							
53	7.4							
54	10							
56	8.9							
57	8.5							
58	11							

Mean	Standard deviation	Relative standard deviation	Median
9.8	1.1	11	9.7

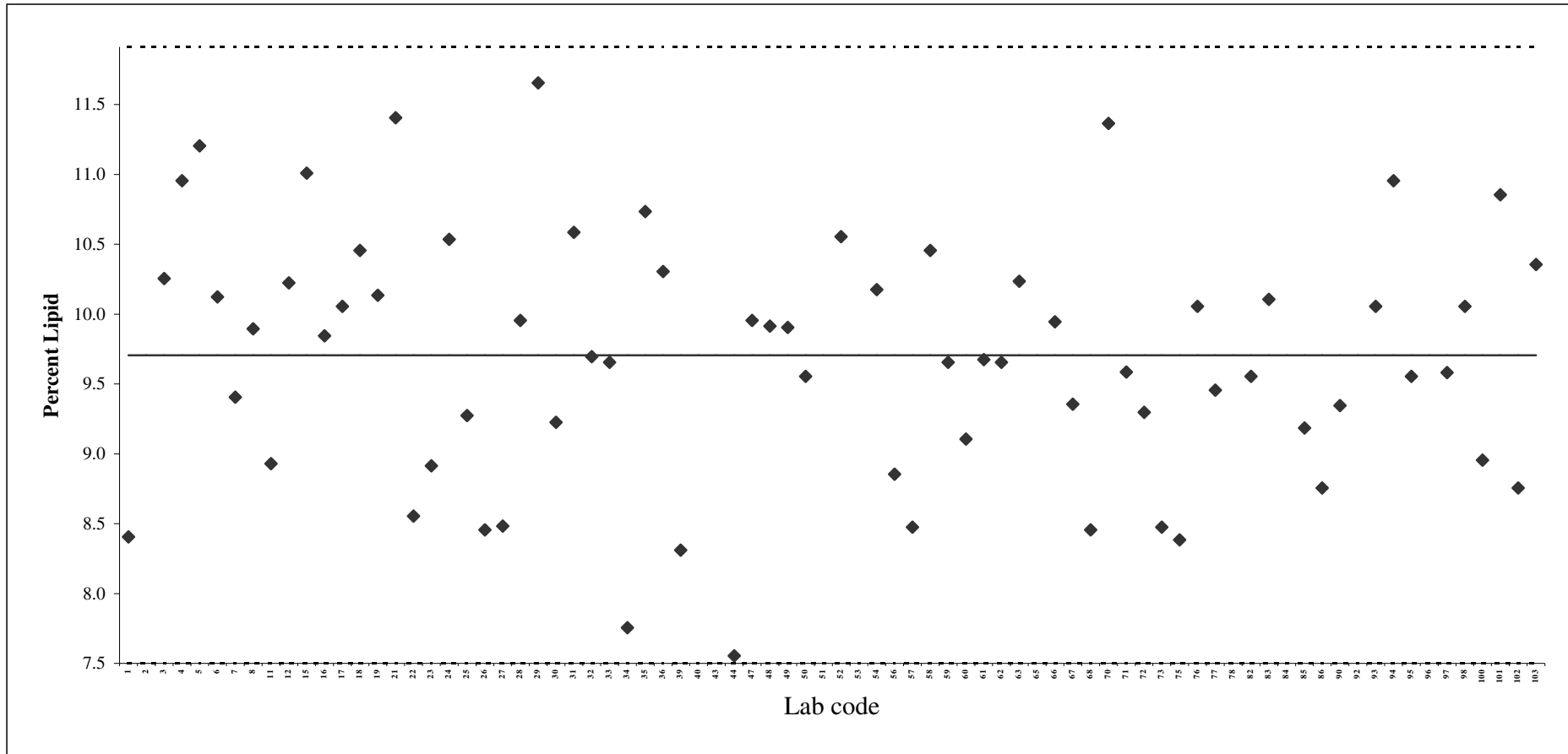
# Lipid determination; Salmon



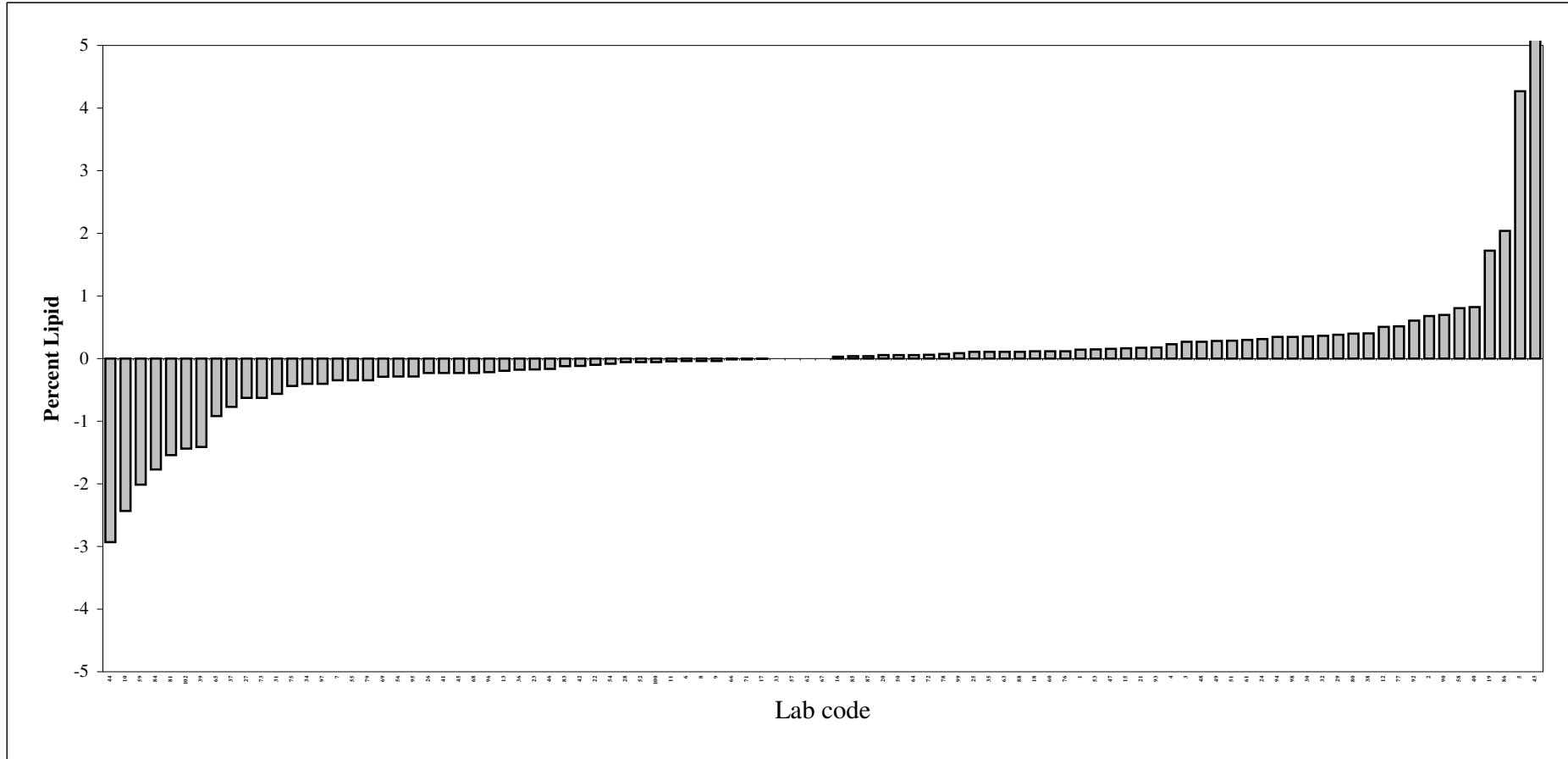
## Lipid determination; Mozzarella Cheese



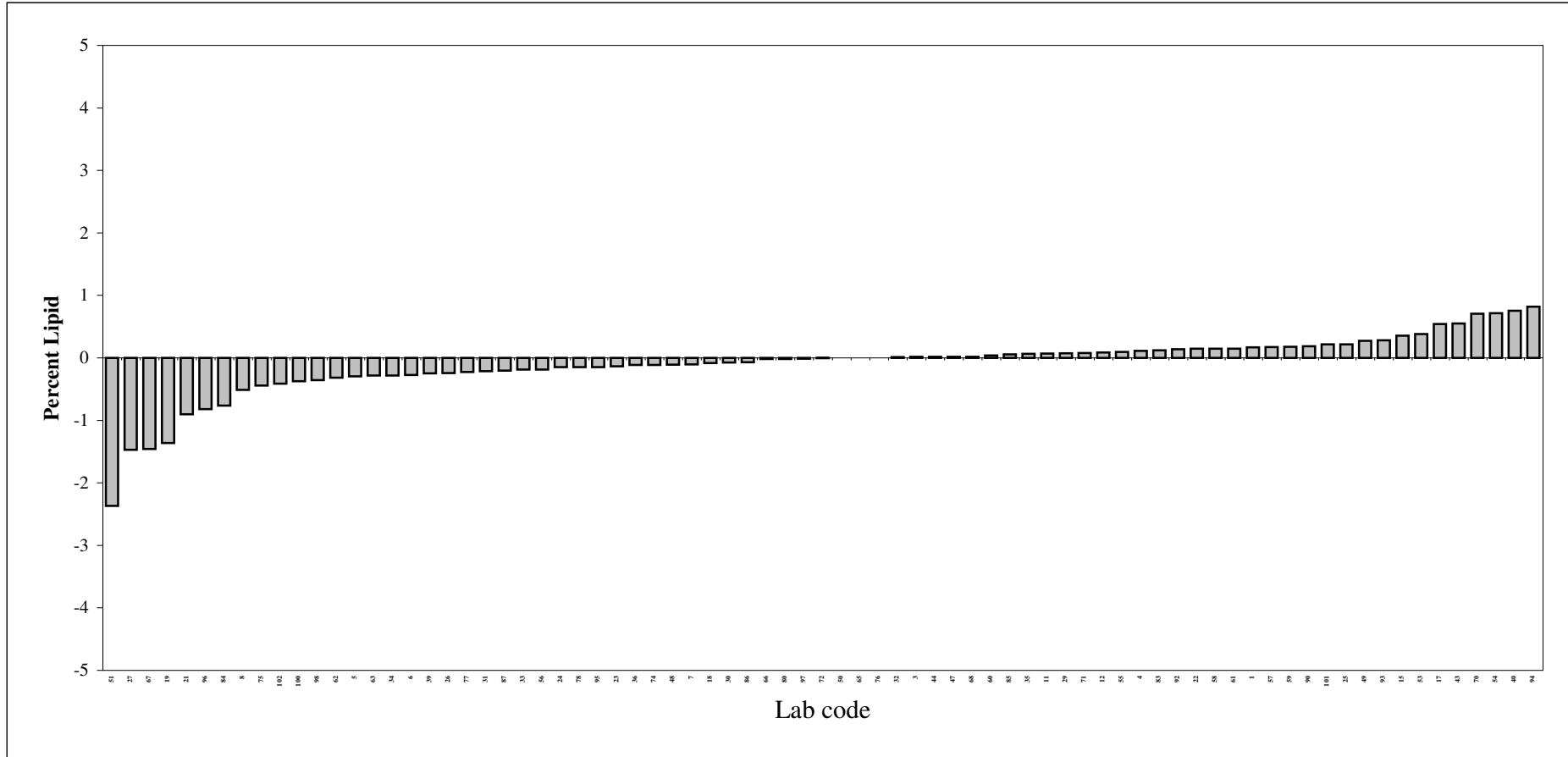
# Lipid determination; Egg



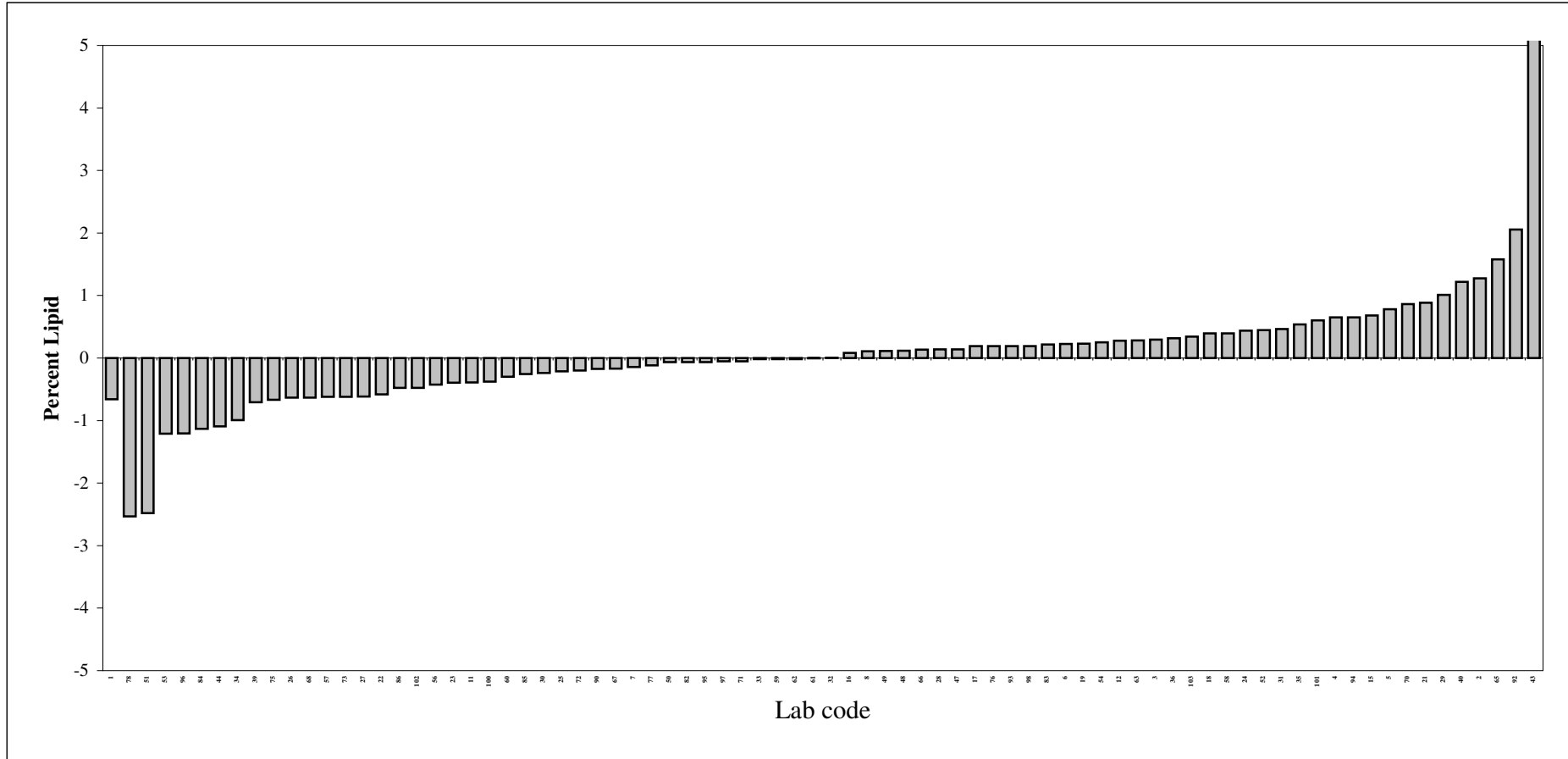
### Z-score lipid determination; Salmon



## Z-score lipid determination; Mozzarella Cheese



# Z-score lipid determination; Egg



Laboratories Z-scores: Analyte solution

LABCODE	Sum TE total	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum u/209	Sum m/209
1	-4.9*			0.12	0.19	-0.26	-2.0
2	-0.047	-0.048	-0.078	0.25			
3	0.40	0.31	1.3	0.80	1.1		
4	-0.67	-0.64	-0.97	-1.3	-0.41	-0.49	-2.2
5	0.25	0.28	-0.13	0.16	-0.52		
6	-0.52	-0.53	-0.37	-0.014	-0.73	-0.48	-0.70
8	-0.27	-0.31	0.19	0.23	-0.10	-0.14	-0.36
9	-0.15	-0.074					
10	-0.070	-0.13	0.64	-0.065	-0.047	-0.20	-0.084
11	-0.23	-0.30	0.58	0.31	0.18	0.15	0.14
12	-0.080	-0.11	0.21	0.50	-0.066	0.23	0.31
13	-0.073	-0.063	-0.16	-0.30	0.031	-0.47	-2.1
15	-0.062	-0.057	-0.14	0.042			
16	-0.38	-0.38	-0.33	-0.88	-0.14		
17	-0.32	-0.45	1.2	0.41	-0.043		
19	-0.37	-0.36	-0.66	-0.046	-0.19		
21	-0.24	-0.25	-0.052	0.020	0.24		
22	0.19	0.16	0.59	0.48	0.50	-0.37	-2.1
23	0.14	0.11	0.36	0.45	0.30	0.094	0.56
24	-0.69	-0.75	-0.061	0.039			
25	-0.11	-0.14	0.14	0.34	0.13		
26	0.49	0.49	0.54	0.55	0.45	0.68	-1.4
27	0.083	0.11	-0.20	0.034	0.33	0.21	0.23
28	0.070	0.010	0.73	0.52	0.50	0.25	-1.7
29	-0.054	-0.051	-0.082	-0.13	-0.37		
30	-0.023	-0.033	0.051	0.28	0.025	0.33	0.23
31	-0.21	-0.23	-0.15	0.40			
32	-0.15	-0.13	-0.51	-0.11	-0.60		
33	0.044	0.0041	0.41	0.75	0.52	0.10	0.13
34	-0.093	-0.11	0.15	-0.31	-0.26		
35	-5.0*			-4.7	0.066		
36	-0.24	-0.28	0.33	-0.088	-0.075		
37	-1.1*	-0.68					
38	-4.6*		-0.54	-0.21	-0.46		
39	-0.20	-0.24	0.14	0.46			
40	-0.27	-0.31	0.23	-0.0039	-0.30		
41	-0.016	-0.028	0.11	0.12	-0.0056		
42						-0.11	0.14
43	3.1	0.29	38	0.11	0.61		
44	-1.2	-1.3	0.045	-0.73	-1.0		
45	-0.055	-0.076	0.16	0.17	-0.022		
47	-0.12	-0.17	0.57	-0.46	0.0090		
48	-0.18	-0.21	0.064	0.31	0.43	0.065	-1.8
49	-0.058	-0.075	0.089	0.31		0.18	0.043
50	0.31	0.28	0.69	0.18			
51	0.48	0.48	0.53	-0.058	0.043	-0.56	-0.70
52	-0.10	-0.10	-0.055	0.16			
53	-0.57	-0.55	-0.79	-0.65			
54	-0.63*	-0.21					
55	-0.26	-0.29	-0.046	0.29	-0.27	-0.35	-0.23
56	-0.025	-0.11	0.86	0.74	0.36	0.19	0.30
57	-0.13	-0.13	-0.23	0.77	-0.43	1.4	0.84
58	-0.013	-0.015	-0.051	0.38	-0.16	-0.053	-0.029
59	-0.010	0.015	-0.40	0.47	-0.21	0.72	-1.4
60	-0.57*	-0.14					
61	-0.038	-0.019	-0.38	0.54	0.28	-0.42	-0.36
62	0.15	0.14	0.28	0.40	-0.11		
63	-0.078	-0.10	0.18	-0.17			
64	-0.40*	-0.44	0.050	-0.57	0.13	-0.68	-2.3
65	0.17	0.15	0.45	0.33	0.27		
66	-0.10	-0.12	0.10	0.34	0.46	-0.11	-1.9
67	0.25	0.35	-1.2	0.85	-1.4	-0.0039	-1.9
69	-0.12	-0.12	-0.17	0.081	0.0034	0.32	0.23
70	-0.12	0.27	-5.0	-0.10			
71	0.20	0.24	-0.26	-0.054		0.13	0.076
72	-4.9*			0.23	0.18	-0.077	-0.12
73	0.074	0.078	0.014	0.066	-0.26		
74	-0.064	-0.11	0.44	0.62		0.36	0.21
75	-0.65	-0.62	-0.96	-0.95	-0.64		
76	-0.17	-0.19	-0.041	0.38	0.080		
77	-0.61	-0.69	0.25	0.071	-2.5		
78	0.80	0.74	1.6	0.71	0.24		
79	0.24	0.23	0.35	0.28		0.036	-1.8
80	0.011	0.017	-0.049	-0.042			
81	1.1	1.4	-1.3	-0.86		-0.62	-2.2
82	-0.79*	-0.39					
83	-0.11	-0.10	-0.35	-0.023	0.27	-0.22	-0.24
84	0.055	0.011	0.50	0.67	0.12		
85	-0.27	-0.29	-0.023	0.084		-0.36	-0.41
86	-0.065	-0.082	0.12	0.13			
87	0.43	0.45	0.20	0.41	-0.60	0.46	0.34
88	-0.14	-0.14	-0.12	0.081			
90	-0.0067	0.0010	-0.090	-0.074			
91	-0.56	-0.59	-0.39	0.25			
93	0.023	0.018	0.064	0.076	0.15	0.19	-0.031
94	0.15	0.13	0.48	-0.06	0.14	-0.26	0.045
95	-0.43	-0.20	-3.0	-1.6	-3.1	-0.82	-0.68
96	-0.19	-0.73	5.3	6.2	4.2		
97	-0.085	-0.10	-0.10	1.0	-0.22	-0.011	-0.0068
98	-0.42	-0.46	0.049	-0.29	-0.20	-0.14	-0.047
100	0.092	0.12	-0.20	0.093	-0.32		
103	-1.7	-1.8	0.25	0.32	-0.21		



Laboratories Z-scores: Salmon

LABCODE:	Sum TE total	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum u/209	Sum m/209
1	-4.3*			0.0040	0.54	0.15	0.053
2	0.41	0.16	0.92	-0.61			
3	0.51	0.25	0.79	0.30	0.078		
4	-1.0	-1.2	-0.90	-1.2	-0.028	-4.8	-4.8
5	-4.1	-4.1	-4.2	-4.1	-4.0		
6	-0.54	-0.38	-0.83	-0.010	0.52	-0.72	-0.46
7	-0.44	-0.38	-0.58	-0.14	1.4		
8	-0.085	0.34	-0.42	-0.11	-0.70	0.15	0.23
9	2.2						
10	0.64	1.7	0.024	-0.013	0.27	1.8	1.9
11	0.48	0.38	0.50	0.68	0.97	0.91	0.86
12	0.16	0.029	0.15	0.55	-0.044	0.73	0.77
13	1.9	4.8	0.25	0.0074	1.8	-0.20	-0.30
15	-0.54	-0.49	-0.63	-0.40			
16	-0.24	0.27	-0.42	-0.95	0.19		
17	0.23	-0.086	0.56	-0.018	0.20		
18	11	24	2.9	3.3			
19	-0.36	0.77	-1.4	0.29	0.055		
20	-0.088	-0.35	0.18	-0.28			
21	-0.23	0.023	-0.41	-0.28	-0.45		
22	0.027	0.086	-0.0051	-0.022	-0.48	-1.3	-1.4
23	-0.25	0.087	-0.50	-0.33	-0.045	0.19	0.26
24	-0.29	-0.72	-0.14	0.36			
25	0.13	0.046	0.37	-0.47	0.23		
26	-1.0	-1.2	-1.0	-0.80	-0.13	-0.19	-0.29
27	0.012	0.52	-0.37	-0.066	0.66	-0.013	-0.049
28	0.31	0.11	0.61	-0.17	0.18	-0.021	-0.12
29	0.085	0.063	0.15	-0.071	-0.74		
30	-0.42	-0.35	-0.52	-0.31	-0.35	-0.015	-0.054
31	51	56	46	53			
32	-0.22	-0.055	-0.59	0.58	0.10		
33	-0.16	-0.064	-0.21	-0.22	-0.38	0.031	0.030
34	-0.23	-0.26	0.0036	-0.96	-0.78		
35	-4.7*			-3.0	-0.30		
36	0.56	0.35	0.69	0.69	1.3		
37	-3.8*	-1.7					
38	-1.7*		0.30	0.26	-0.26		
39	-1.2	-1.3	-1.2	-1.2			
40	0.69	0.73	0.47	1.3	-1.1		
41	-0.47	-1.1	0.018	-0.37	-0.10		
42						-0.86	-0.89
43	-4.6	-4.7	-4.6	-4.4	-3.7		
44	-3.0	-2.4	-3.5	-2.8	-2.3		
45	-0.94	-1.8	-0.36	-0.70	-0.26		
46	1.4	4.9	-0.88	-0.047	14		
47	0.38	0.45	0.65	-0.75	4.0		
48	0.12	0.10	0.045	0.40	0.95	0.31	0.21
49	0.93	0.73	0.91	1.5		0.61	0.68
50	0.27	-0.26	0.74	0.15			
51	0.34	0.39	0.44	-0.13	0.12	0.36	0.41
52	-0.57	-0.38	-0.75	-0.44			
53	-0.14	0.10	-0.28	-0.30			
54	-2.9*	0.50					
55	0.14	-0.063	0.26	0.26	-0.16	-0.37	-0.39
56	0.41	0.035	0.78	0.20	0.22	0.10	0.067
57	0.18	0.040	0.053	0.97	1.0	2.3	2.2
58	-0.10	0.015	-0.13	-0.33	-0.45	-0.14	-0.23
59	-0.40	-0.047	-0.71	-0.29	0.73	-0.84	-0.92
60	0.085	-0.051	0.012	0.69			
61	-0.42	0.0044	-0.93	0.17	-0.42	-0.36	-0.27
62	1.0	1.6	0.69	0.82	0.32		
63	0.51	-0.021	0.98	0.32			
64	0.79	0.78	1.1	-0.045	0.24	0.94	0.83
65	0.90	0.54	1.0	1.4	2.0		
66	-0.21	-0.37	-0.20	0.20	1.4	0.055	-0.042
67	-1.8	-3.1	-2.1	2.5	0.97	-1.8	-1.8
68	0.014	-0.10	0.034	0.26	-0.88		
69	0.39	0.48	0.29	0.44	0.57	0.62	0.95
71	-0.15	0.21	-0.37	-0.41		0.16	0.64
72	-4.2*			0.77	0.92	0.97	1.0
73	-0.10	0.45	-0.47	-0.36	-0.79		
75	0.15	0.42	-0.038	0.057	-0.68		
76	0.18	0.13	-0.0070	0.91	0.16		
77	-0.89	-1.1	-0.79	-0.59	3.2		
78	-0.13	-0.20	-0.23	0.36	0.88		
79	-1.0	-0.86	-1.3	-0.72	0.26	-1.9	-1.9
80	0.65	4.4	-3.4	4.2			
81	-0.15	0.20	-0.21	-0.88		0.087	-0.011
83	0.58	0.66	0.66	0.11	0.54	0.57	0.58
84	2.7	1.1	4.4	1.3	1.2		
85	0.25	0.54	0.16	-0.18		-0.017	-0.11
86	0.23	0.27	0.11	0.51			
87	0.33	-0.079	0.66	0.27	-0.31	0.11	0.069
88	0.36	0.23	0.48	0.25			
90	0.37	0.34	0.39	0.41			
92	0.24	0.15	-0.27	2.2			
93	-0.033	-0.52	0.21	0.44	0.81	0.32	0.28
94	-0.39	-0.17	-0.77	0.28	0.020	-0.87	-0.85
95	2.4	0.76	2.7	5.7	2.3	0.63	12
96	-0.56	-0.87	-0.28	-0.68	-0.61		
97	0.76	-0.28	1.8	0.14		0.81	0.85
98	0.53	-0.021	1.2	-0.32	-0.43	-0.63	-0.50
99	-0.62	-0.39	-0.77	-0.74			
100	-0.39	-0.057	-0.85	0.26	0.0061		
102	-3.6						

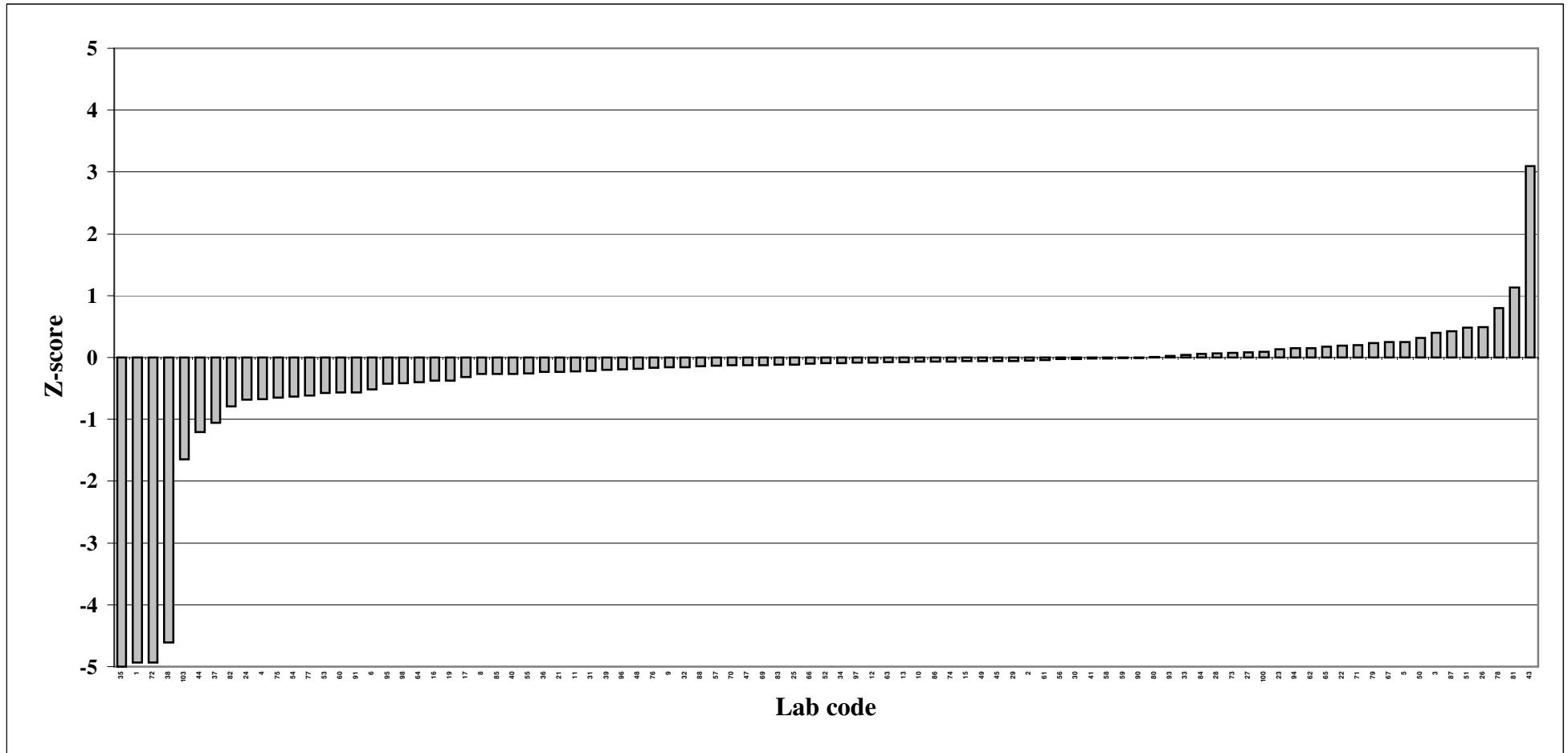
### Laboratories Z-scores: Mozzarella cheese

LABCODE:	Sum TE total	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209	Sum m/209
1	-4,8*			0.013	-0.31	4.0	3.0
3	0.68	0.69	0.73	0.22	-0.11		
4	-1.4	-1.2	-1.8	-1.2	0.37	124	110
5	0.18	0.22	0.16	-0.27	-0.30		
6	-0.45	-0.33	-0.71	-0.44	-1.1	0.46	5.9
7	-0.28	-0.18	-0.48	-0.39	0.54		
8	-0.10	0.13	-0.61	-0.11	-0.16	1.4	1.8
11	0.13	-0.025	0.40	0.57	0.74	-0.021	-0.26
12	0.42	0.41	0.47	0.24	-0.41	0.26	3.3
15	-0.50	-0.32	-0.85	-0.74			
17	0.081	-0.18	0.65	0.12	1.0		
18	7.7	11	2.1	0.046			
19	-1.8	-1.6	-2.4	-1.2	-2.2		
21	0.0078	-0.023	-0.056	0.86	2.7		
22	0.38	0.51	0.13	0.14	0.17	-1.7	-2.1
23	0.0074	0.012	0.029	-0.20	0.32	-0.18	1.5
24	-0.48	-0.34	-0.92	0.38			
25	0.13	-0.12	0.65	0.19	3.6		
26	-0.14	-0.082	-0.27	-0.13	3.0	22	19
27	-0.69	-0.34	-1.4	-1.1	-0.29	-1.1	-0.68
29	0.19	0.12	0.31	0.28	2.7		
30	0.43	0.69	-0.19	0.81	3.5	1.6	1.6
31	16	17	14	14			
32	-0.49	-0.72	-1.7	11	9.1		
33	-0.12	0.028	-0.41	-0.33	-0.84	-0.41	0.058
34	0.13	-0.064	0.72	-0.96	-0.62		
35	-4,9*			-2.6	-0.18		
36	0.47	0.16	1.1	0.46	0.17		
39	-0.17	-0.29	0.022	0.18			
40	2.9	1.8	4.2	9.3	8.1		
43	2.3	-1.9	9.5	14	34		
44	-1.5	-0.35	-4.4	0.53	1.2		
47	-0.23	0.83	-4.4	12	49		
48	0.12	0.13	0.092	0.14	0.042	2.1	1.3
49	0.39	0.36	0.37	0.91		0.33	7.3
50	0.43	0.52	0.30	-0.022			
51	0.29	0.41	0.21	-0.92	-0.50	-0.15	0.82
53	1.1	1.8	-0.30	-0.28			
54	-2,5*	-1.1					
55	-0.10	-0.21	0.16	-0.27	-0.61	-0.81	-0.88
56	0.095	0.11	0.072	0.051	-0.22	-0.063	-0.32
57	0.59	1.3	-1.0	0.55	-0.092	2.1	1.6
58	0.18	0.24	0.14	-0.36	-0.46	-0.43	-0.94
59	-0.19	-0.13	-0.37	0.12	-0.31	-0.19	-0.74
60	-0.11	-0.23	0.063	0.39			
61	-0.57	-0.44	-0.95	0.22	1.4	-0.66	6.9
62	0.26	0.43	-0.16	0.68	-0.82		
63	0.82	0.47	0.84	5.8			
65	0.55	0.69	0.14	1.3	0.98		
66	-0.34	-0.33	-0.40	-0.013	0.45	-0.56	-1.1
67	-2.0	-3.1	-0.011	0.53	0.42	2.2	1.4
68	0.56	0.15	1.3	1.8	5.8		
70	-2.5	-3.1	-1.0	-3.4			
71	-0.079	0.21	-0.64	-0.51		-0.037	5.4
72	-4,7*			1.7	2.1	3.2	3.0
74	0.26	0.20	0.16	1.8		1.6	1.4
75	-0.15	0.075	-0.57	-0.61	-0.75		
76	-0.22	-0.23	-0.30	0.52	0.55		
77	-0.83	-0.97	-0.65	-0.13	2.4		
78	-0.31	-0.33	-0.30	-0.14	-0.27		
80	-4.0	-4.4	-3.4	-2.8			
83	0.073	0.10	0.011	0.12	0.33	0.43	0.16
84	1.8	1.8	1.9	0.86	2.6		
85	0.043	0.13	-0.13	0.035		-1.7	-1.9
86	0.069	0.19	-0.23	0.31			
87	-0.12	-0.16	0.013	-0.29	-1.1	-0.54	-0.52
90	-0.72	-0.49	-1.1	-1.5			
91	11	11	12	13			
92	0.76	1.1	0.16	-0.31			
93	0.041	0.0031	0.10	0.19	-0.32	-0.52	-0.73
94	0.16	0.22	0.093	-0.18	0.23	-1.1	-0.94
95	6.4	4.8	9.9	5.3	2.6	33	130
96	2.5	3.8	-0.086	-0.042	0.41		
97	0.19	0.032	0.47	0.48	0.59	0.37	1.1
98	0.052	-0.19	0.65	-0.42	-0.45	-0.79	0.41
100	-1.1	-0.64	-2.3	0.33	1.8		
101	-1.9						
102	-1.5						

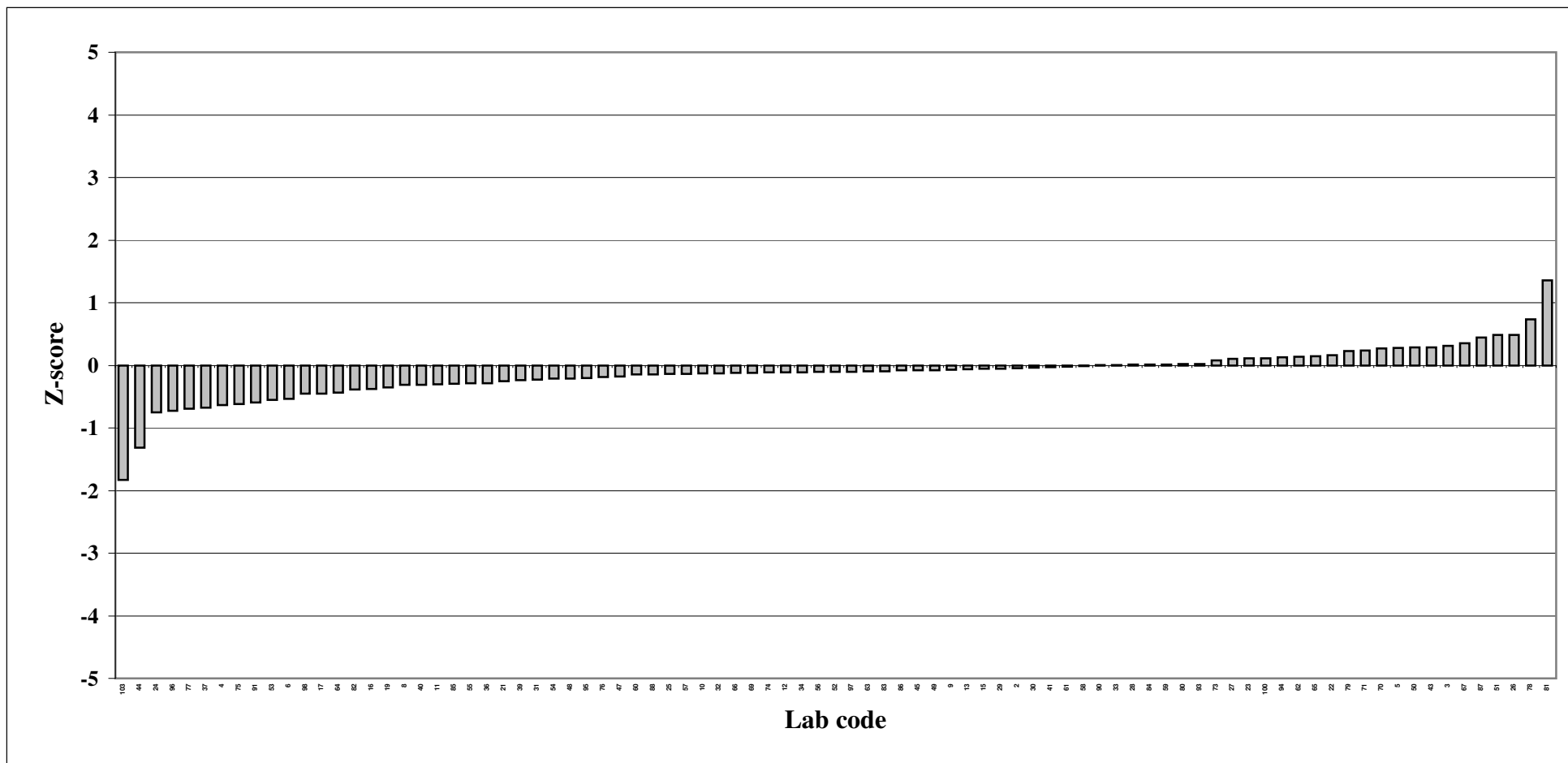
Laboratories Z-scores: Egg

LABCODE:	Sum TE total	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-ortho PCB	Sum Indicator PCB	Sum u/209	Sum m/209
1	-4.7*			-0.25	-0.034	0.17	-1.4
2	0.39	0.96	-0.014	-0.63			
3	0.66	0.56	0.83	0.086	-0.041		
4	-0.70	-0.65	-0.75	-0.62	-0.22	-0.34	-1.7
5	0.45	0.96	0.018	0.036	0.14		
6	-0.52	-0.34	-0.71	-0.37	-0.77	-2.3	-1.1
7	-0.55	-0.60	-0.52	-0.43	0.66		
8	0.52	1.6	-0.46	-0.050	0.35	0.58	0.54
11	0.38	0.13	0.59	0.50	0.54	0.11	0.27
12	0.38	0.23	0.53	0.31	-0.48	0.33	1.9
15	-0.22	0.29	-0.69	-0.32			
16	0.32	0.44	-0.20	3.6	11		
17	0.49	-0.17	1.1	0.40	0.68		
18	14	31	0.12	0.040			
19	-0.77	-0.24	-1.4	0.26	-1.1		
21	0.76	0.87	0.65	0.86	1.1		
22	-0.14	-0.14	-0.11	-0.40	-0.87	-3.4	-3.9
23	0.069	0.13	0.15	-0.17	-0.0059	-0.77	-1.2
24	-0.15	-0.86	0.42	0.71			
25	0.46	0.015	0.92	0.090	0.65		
26	0.062	0.26	-0.11	-0.084	2.5	2.7	0.37
27	0.22	0.71	-0.17	-0.38	-0.32	-0.25	0.030
28	0.21	-0.0056	0.41	0.31	-0.74	-0.011	-1.5
29	1.6	1.7	1.6	1.2	8.4		
30	-0.049	0.093	-0.31	0.94	1.5	1.5	0.67
31	47	56	38	42			
32	-2.0	0.068	-4.5	3.1	2.9		
33	-0.23	0.30	-0.71	-0.47	-0.61	0.13	0.40
34	-0.0027	-0.11	0.21	-0.91	-0.89		
35	-4.9*			-3.3	0.34		
36	0.56	-0.24	1.3	0.81	0.59		
39	-0.55	-0.83	-0.28	-0.63			
40	0.88	0.95	0.77	1.3	1.6		
43	8.6	-1.8	17	20	25		
44	3.0	3.7	2.9	-0.55	10		
47	1.0*	1.6	1.3				
48	0.10	-0.022	0.18	0.48	0.19	1.6	-0.36
49	0.16	-0.46	0.69	0.57		0.70	13
50	-0.49	-2.0	0.84	-0.035			
51	0.45	0.76	0.26	-0.44	-0.13	0.25	0.25
52	0.34	0.33	0.12	2.2			
53	0.22	1.2	-0.61	-0.70			
54	-1.3*	3.1					
56	-0.039	-0.076	-0.00000013	-0.074	0.067	1.9	1.5
57	0.65	1.9	-0.54	0.53	0.36	3.5	2.4
58	0.33	0.60	0.14	-0.23	-0.39	0.46	-1.2
59	-0.43	-0.21	-0.68	0.016	0.27	0.73	-1.0
60	-0.14	-0.57	0.20	0.40			
61	-0.69	-0.29	-1.2	0.21	-0.15	-0.25	-0.23
62	-0.72	-0.72	-0.71	-0.71	-1.5		
63	0.95	0.76	0.72	4.2			
65	2.0	2.0	1.8	3.7	2.6		
66	-0.65	-1.3	-0.28	1.0	0.84	-0.61	-1.9
67	-2.2*		0.14	0.15	0.17	2.7	0.36
68	0.77	-0.012	1.4	1.5	2.5		
70	-2.9	-2.4	-3.7	-0.33			
71	-0.32	0.0086	-0.62	-0.38		0.66	21
72	-4.6*			0.91	1.1	0.83	2.9
73	0.0069	0.49	-0.38	-0.55	-0.97		
75	-0.28	-0.078	-0.43	-0.70	-0.84		
76	-0.20	-0.17	-0.30	0.41	0.21		
77	1.7	-0.70	2.6	13	-4.0		
78	-0.26	-0.48	-0.090	0.16	0.27		
82	-2.6*	0.16					
83	0.16	0.37	-0.029	-0.024	0.48	0.065	-0.10
84	2.8	4.5	1.4	0.88	1.1		
85	0.88	1.2	0.53	0.98		1.2	0.34
86	-0.065	0.15	-0.27	-0.088			
90	-0.86	-0.63	-1.0	-1.5			
92	1.7	1.3	2.3	0.18			
93	-0.26	-0.54	-0.065	0.34	0.25	-0.072	-0.36
94	0.045	0.13	0.0042	-0.25	-0.45	-0.91	-0.91
95	9.7	10	9.6	6.8	2.4	23	82
96	0.75	0.84	0.67	0.65	1.1		
97	-0.12	-0.26	-0.0015	0.025	0.37	-0.92	-0.18
98	0.62	-0.17	1.5	-0.24	-0.23	-0.79	-1.3
100	-0.96	-0.48	-1.5	0.089	0.12		
101	-1.3*						
102	-1.1*						
103	-0.57	-0.44	-0.74	-0.21	0.13		

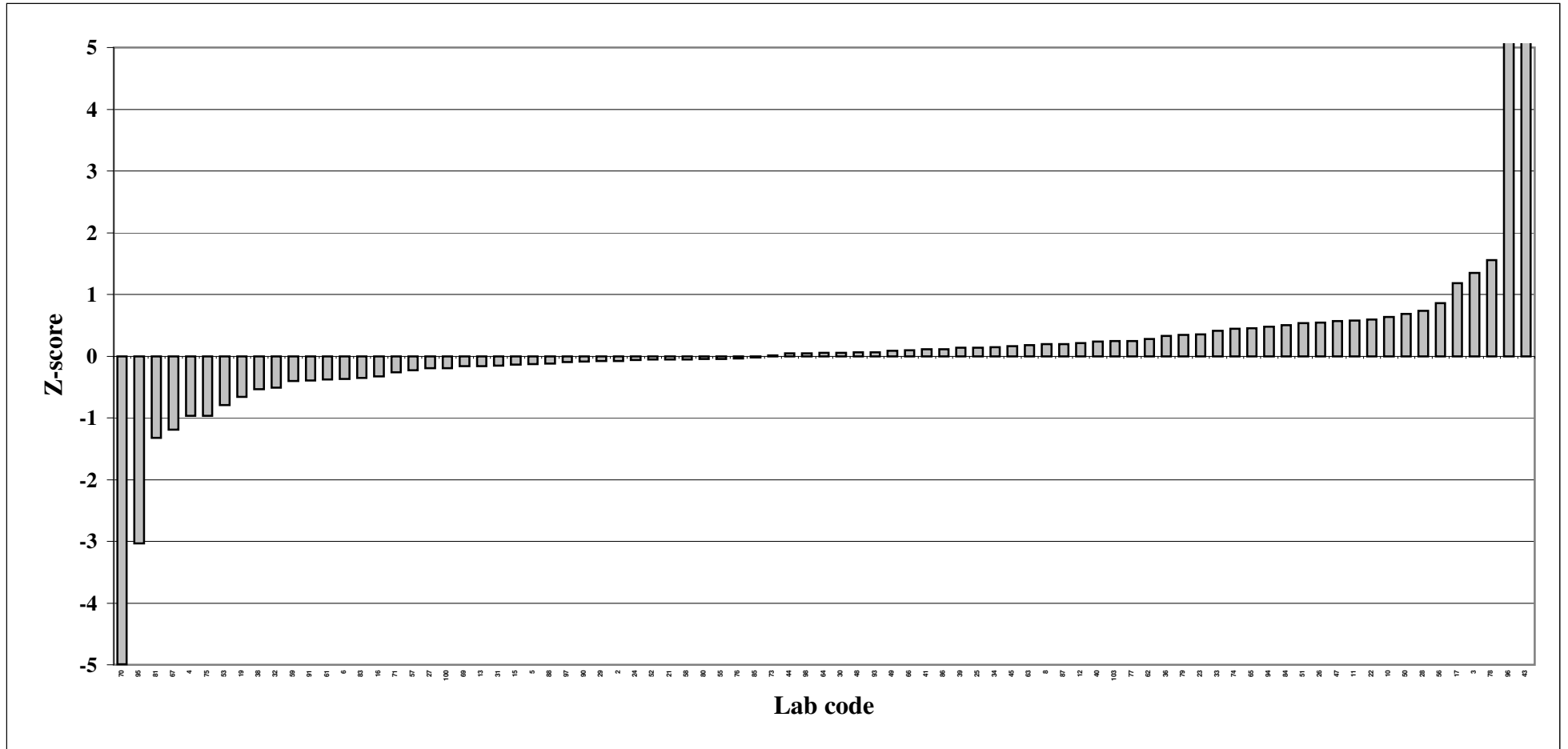
### Z-score analyte solution; total TEQ



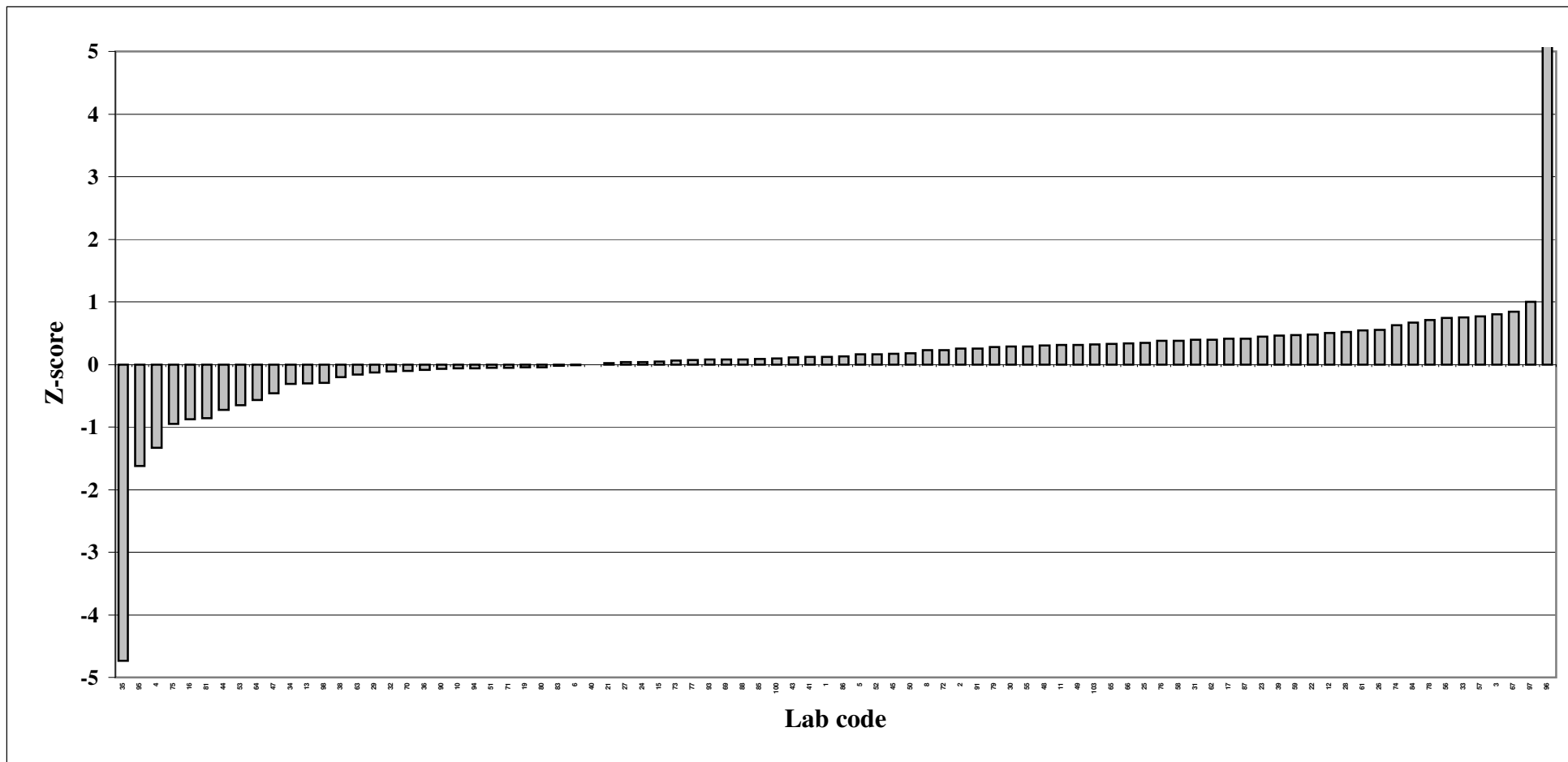
### Z-score analyte solution; PCDD/PCDF TEQ



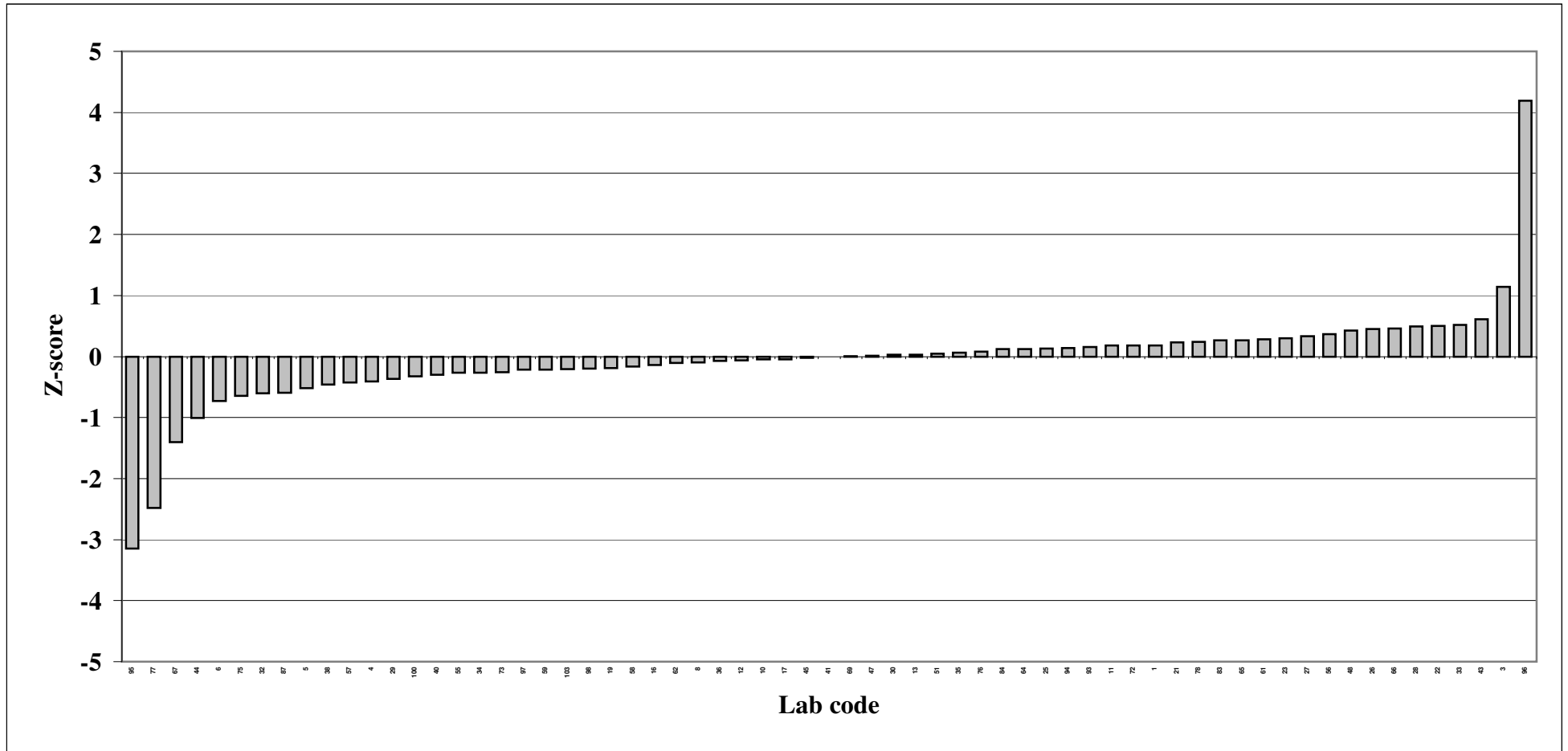
### Z-score analyte solution; non-ortho PCB TEQ



### Z-score analyte solution; mono-ortho PCB TEQ

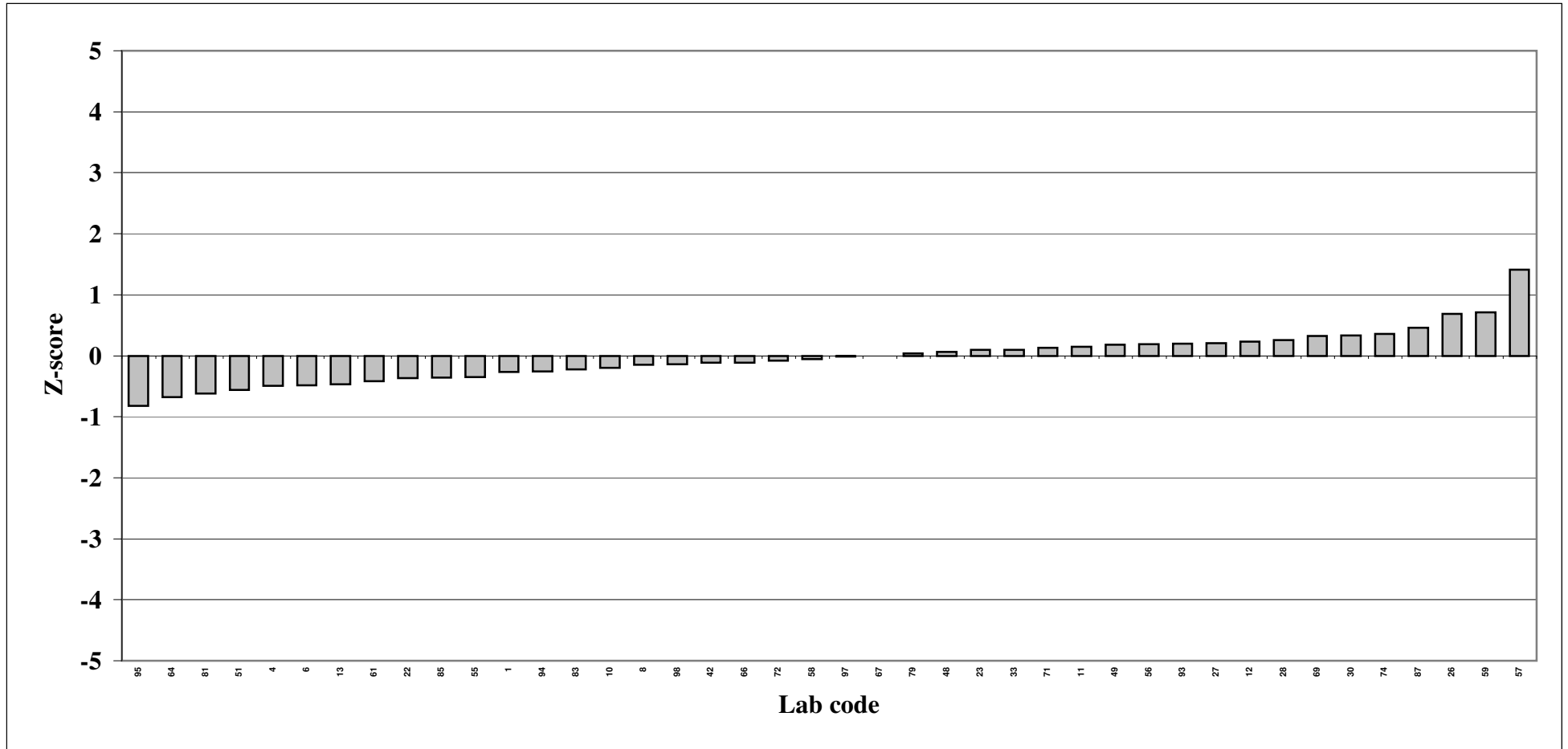


**Z-score analyte solution; sum indicator PCB**

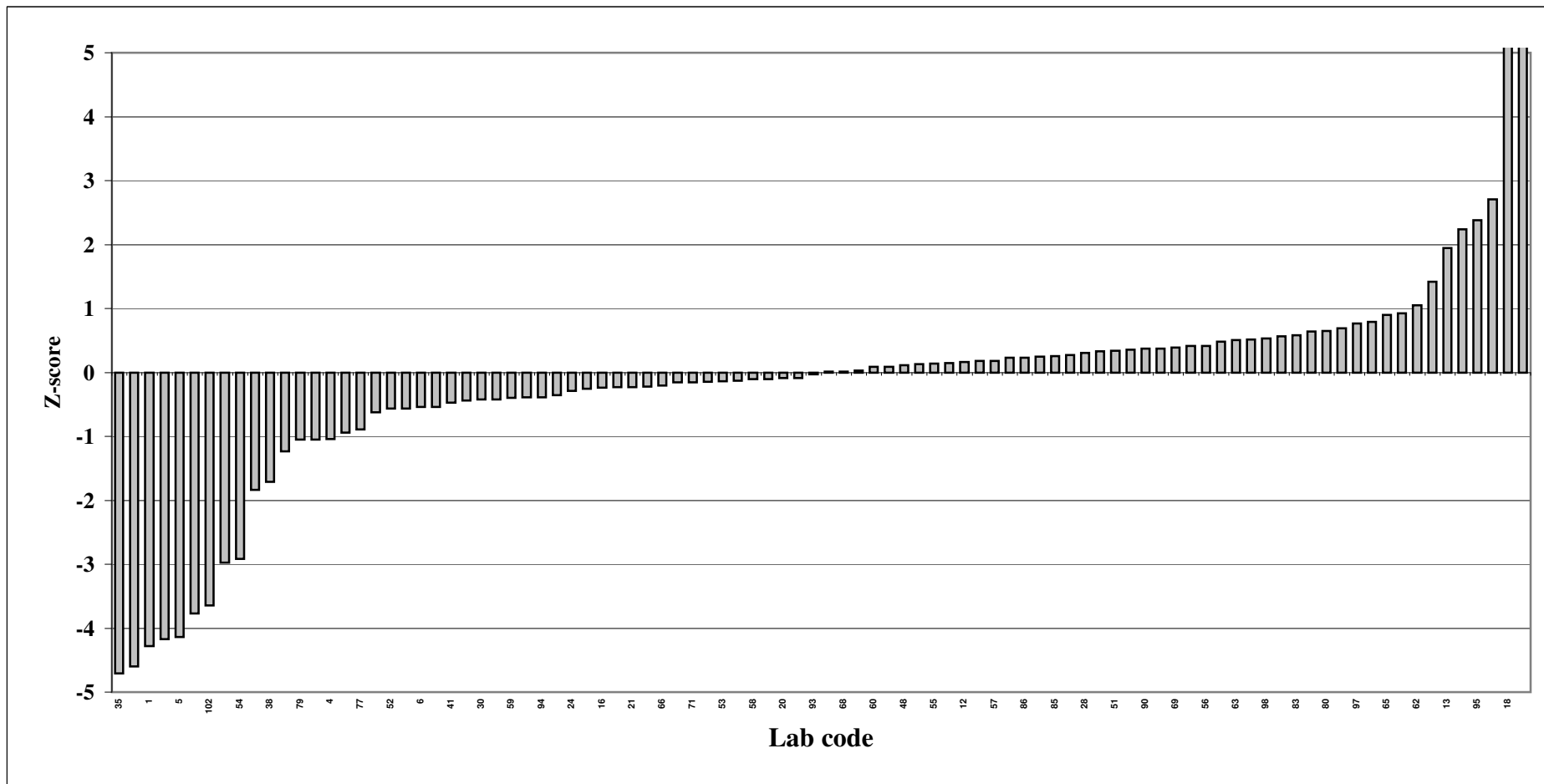




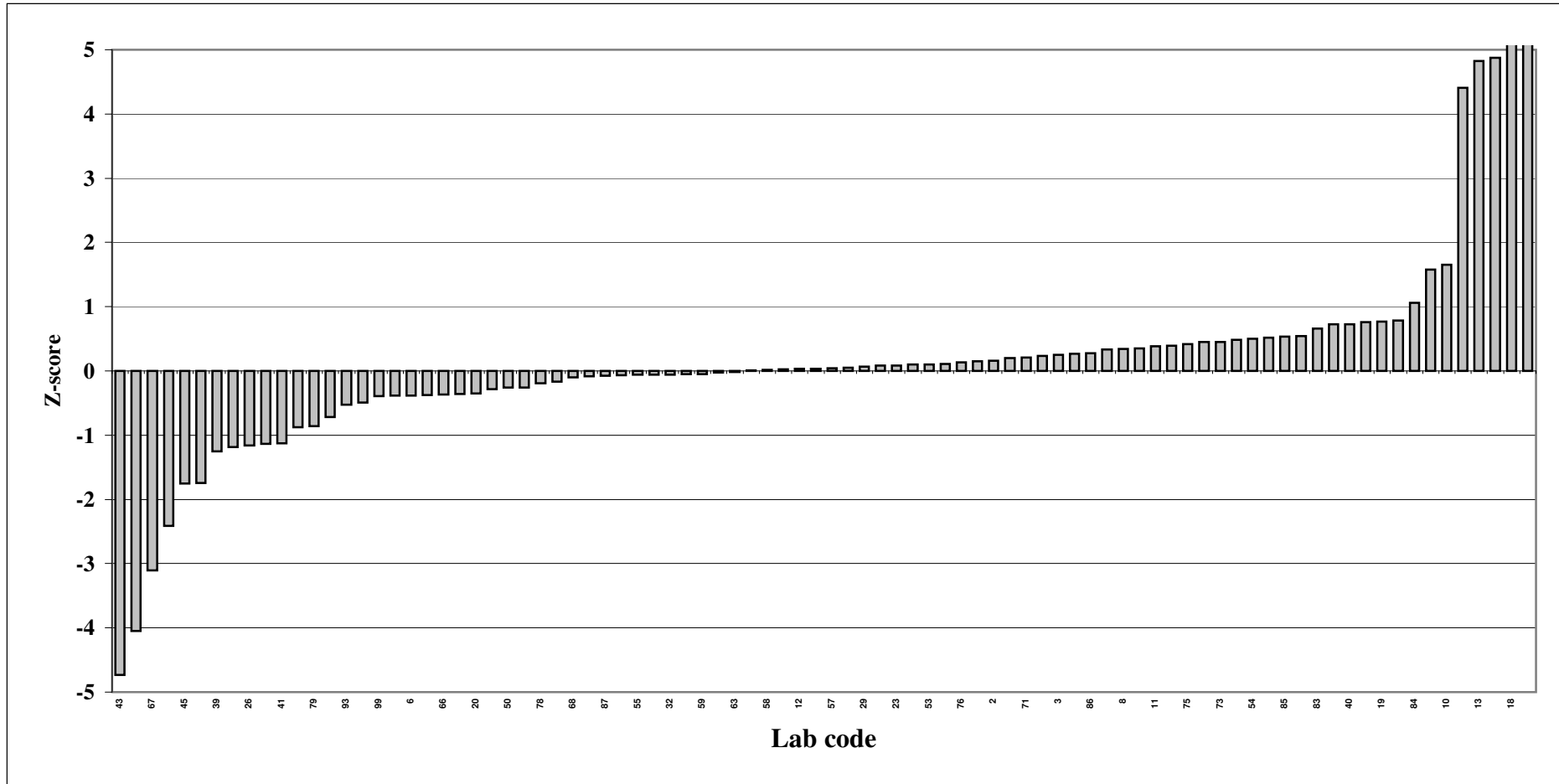
### Z-score analyte solution; sum PBDE without BDE-209



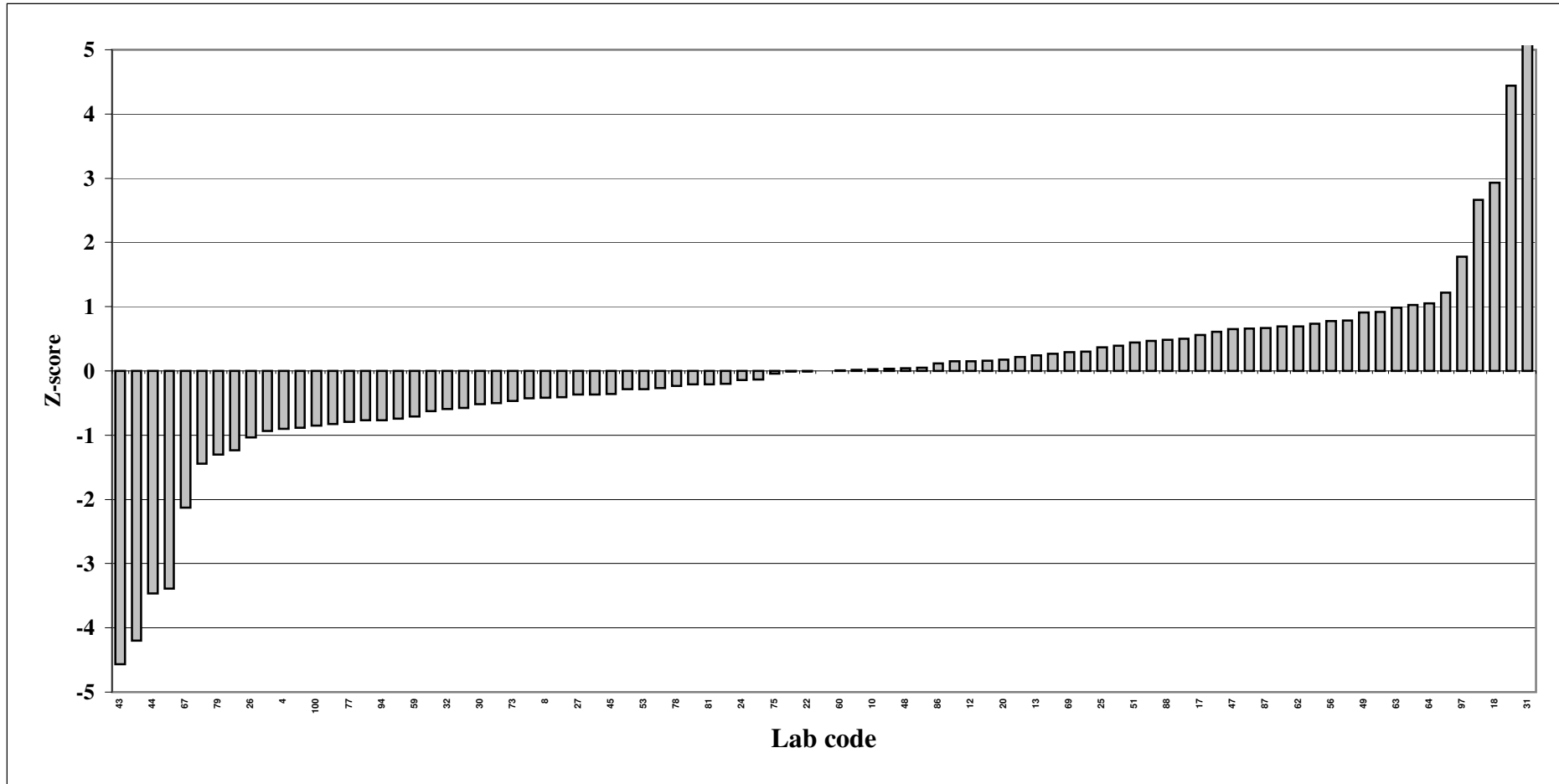
### Z-score Salmon; total TEQ



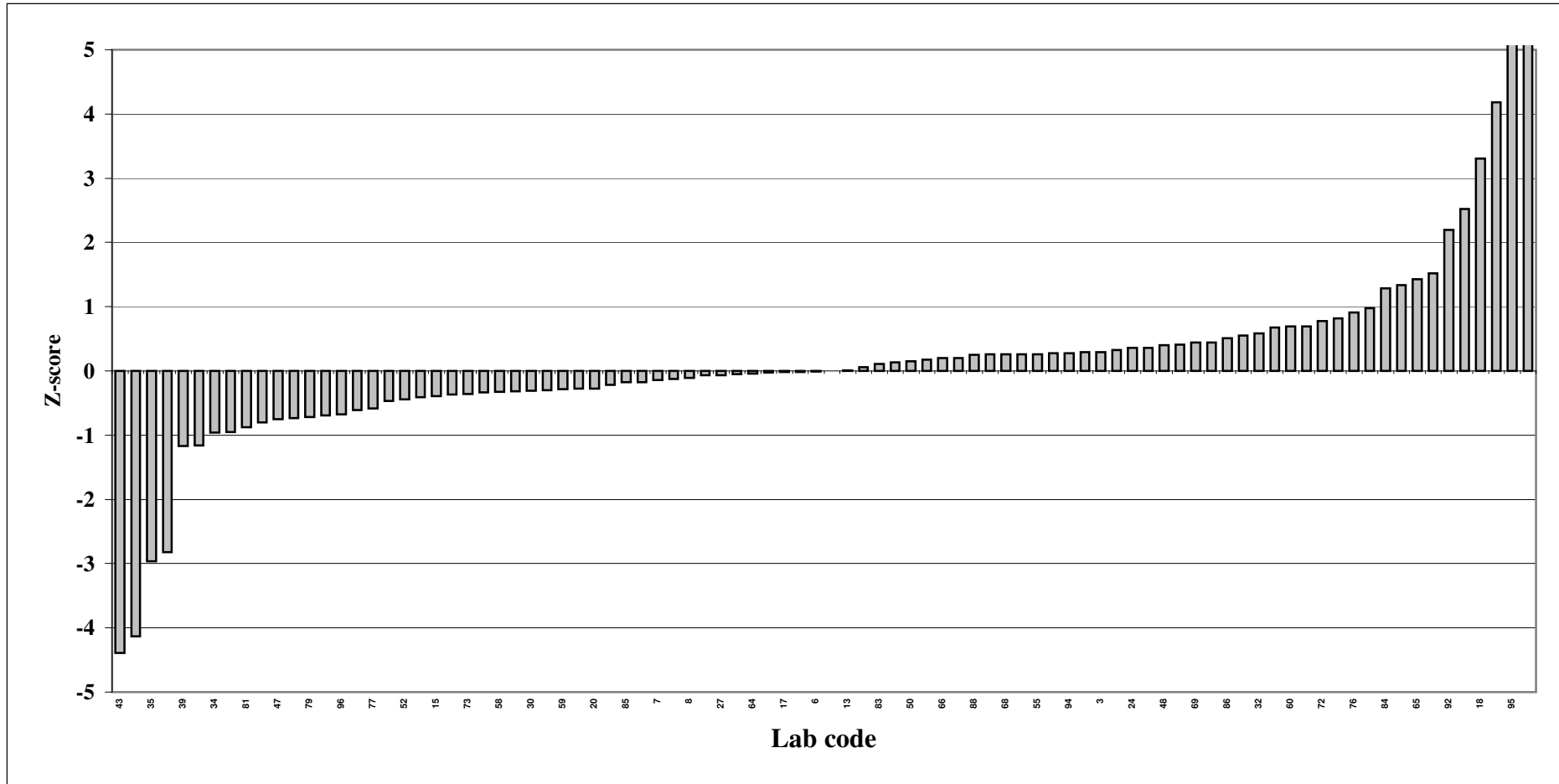
### Z-score Salmon; PCDD/PCDF TEQ



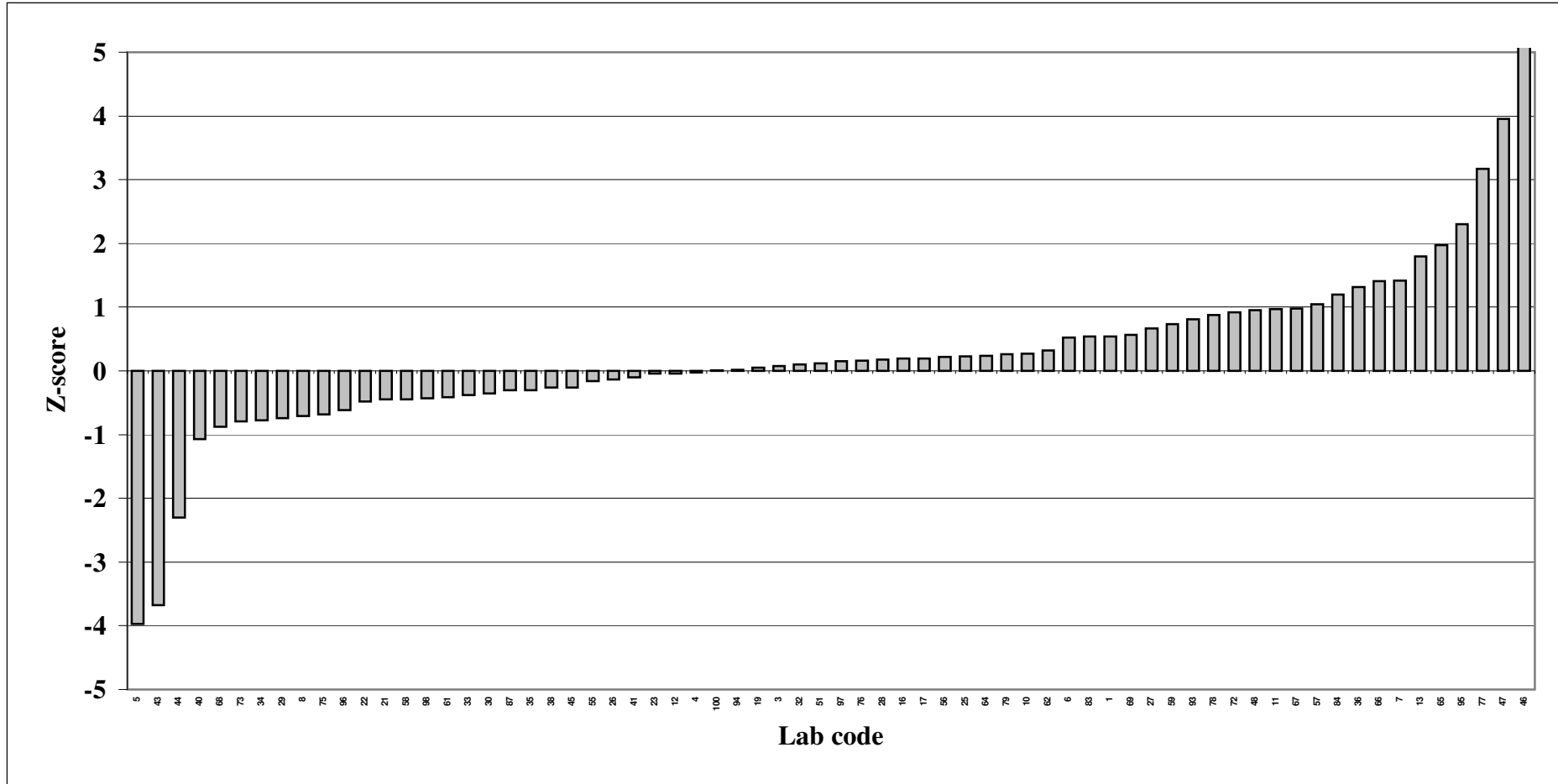
### Z-score Salmon; non-ortho PCB TEQ



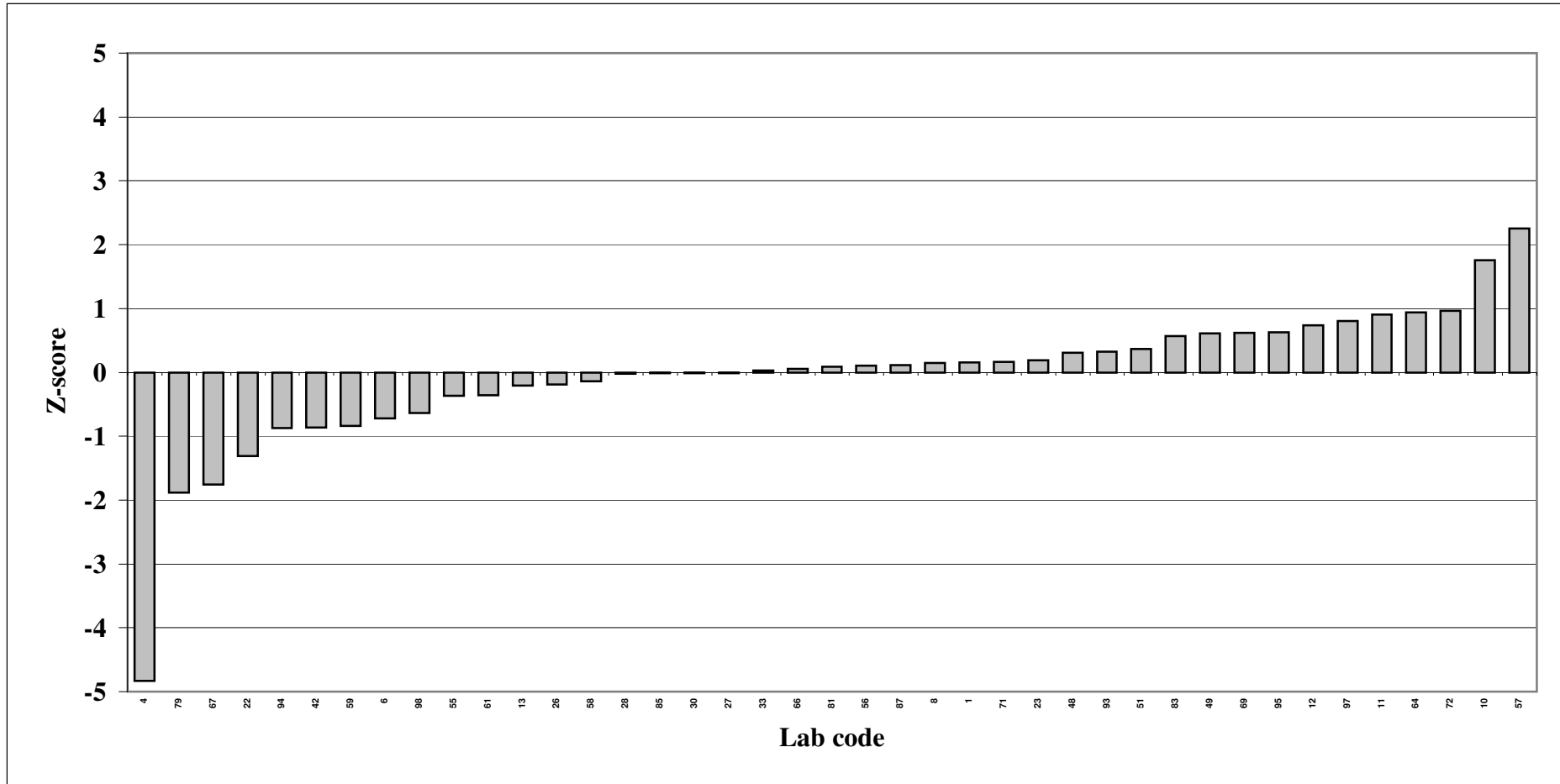
### Z-score Salmon; mono-ortho PCB TEQ



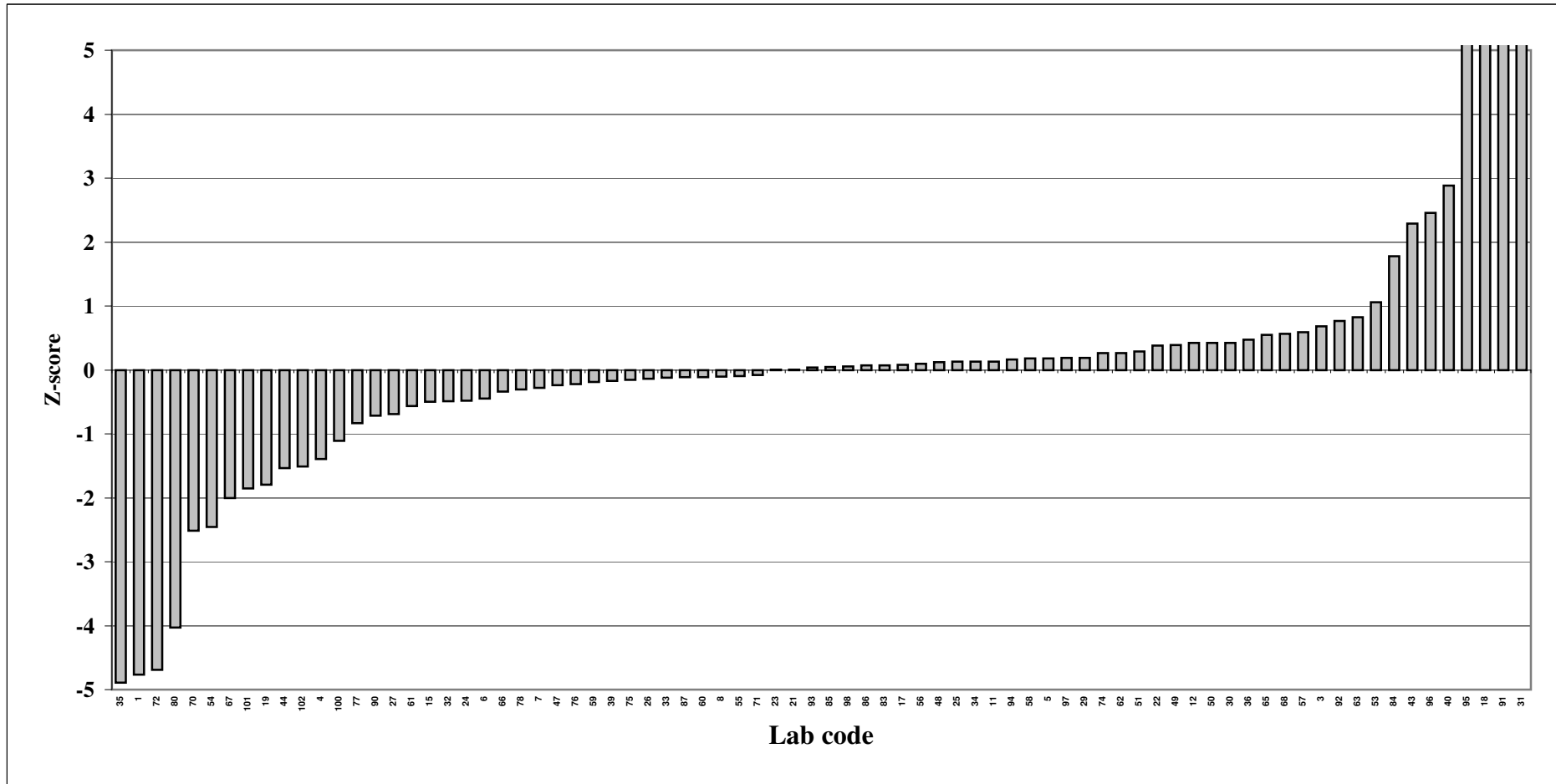
### Z-score Salmon; sum indicator PCB



### Z-score Salmon; sum PBDE without BDE-209

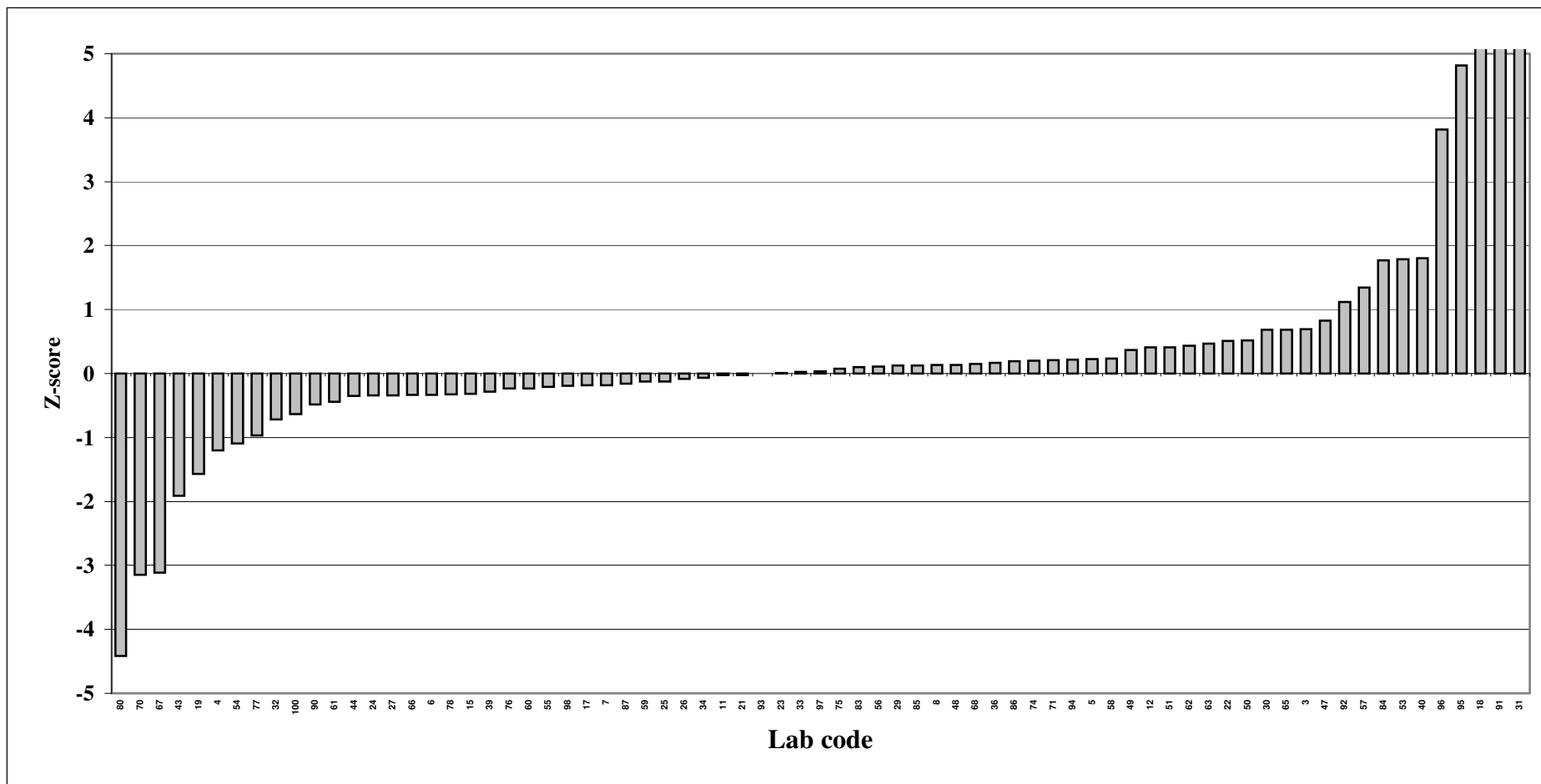


### Z-score Mozzarella Cheese; total TEQ

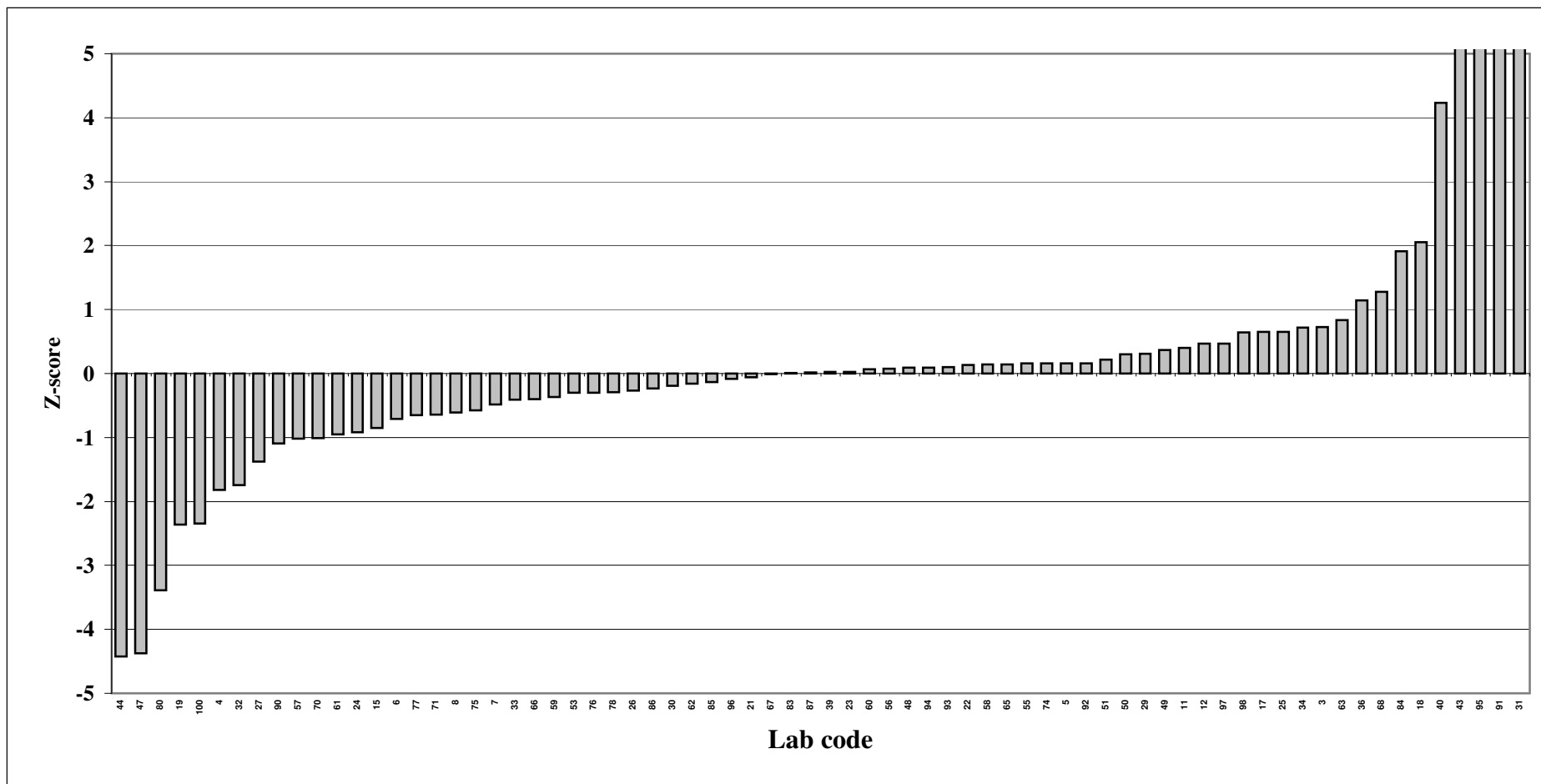




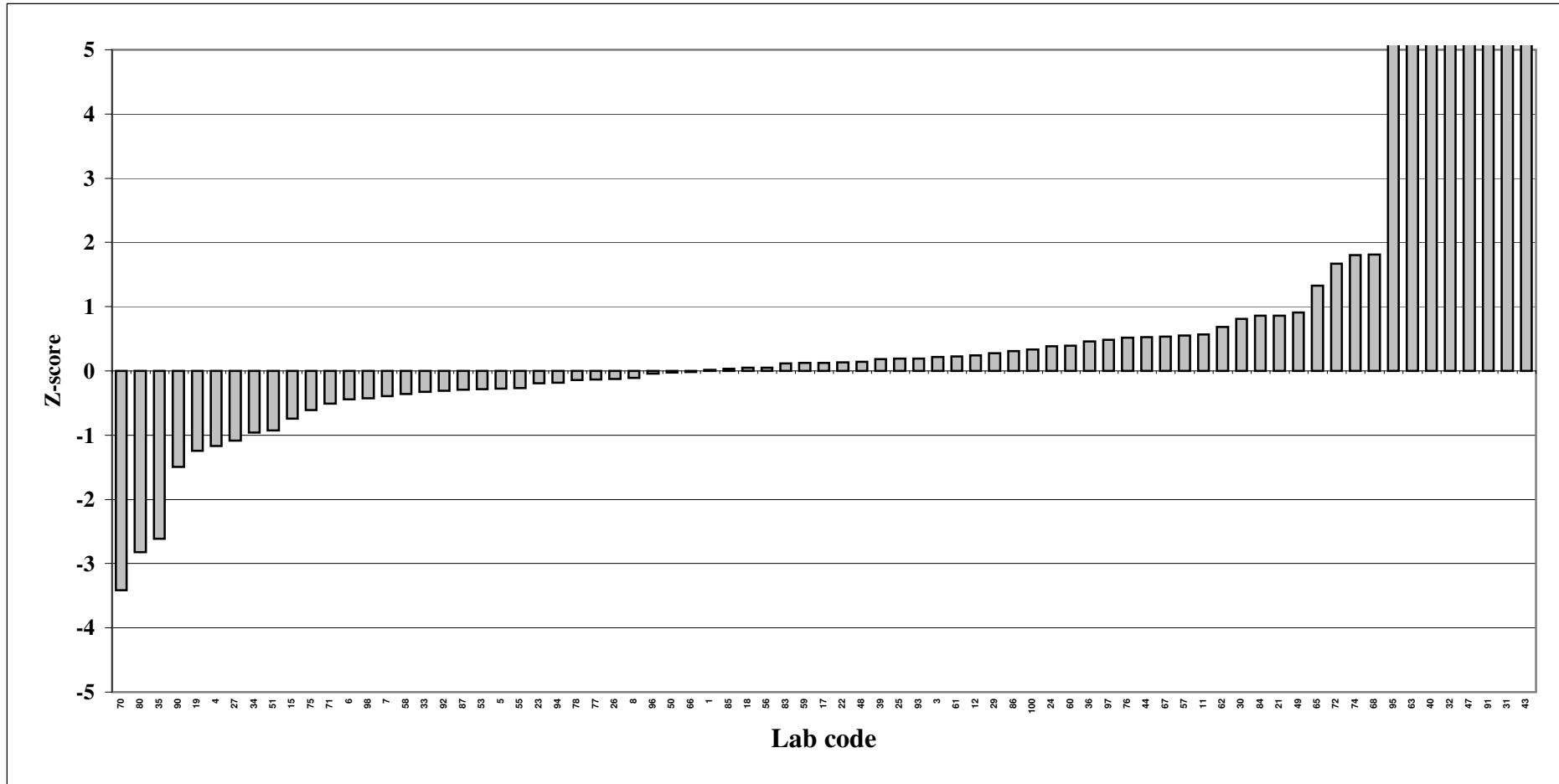
### Z-score Mozzarella Cheese; PCDD/PCDF TEQ



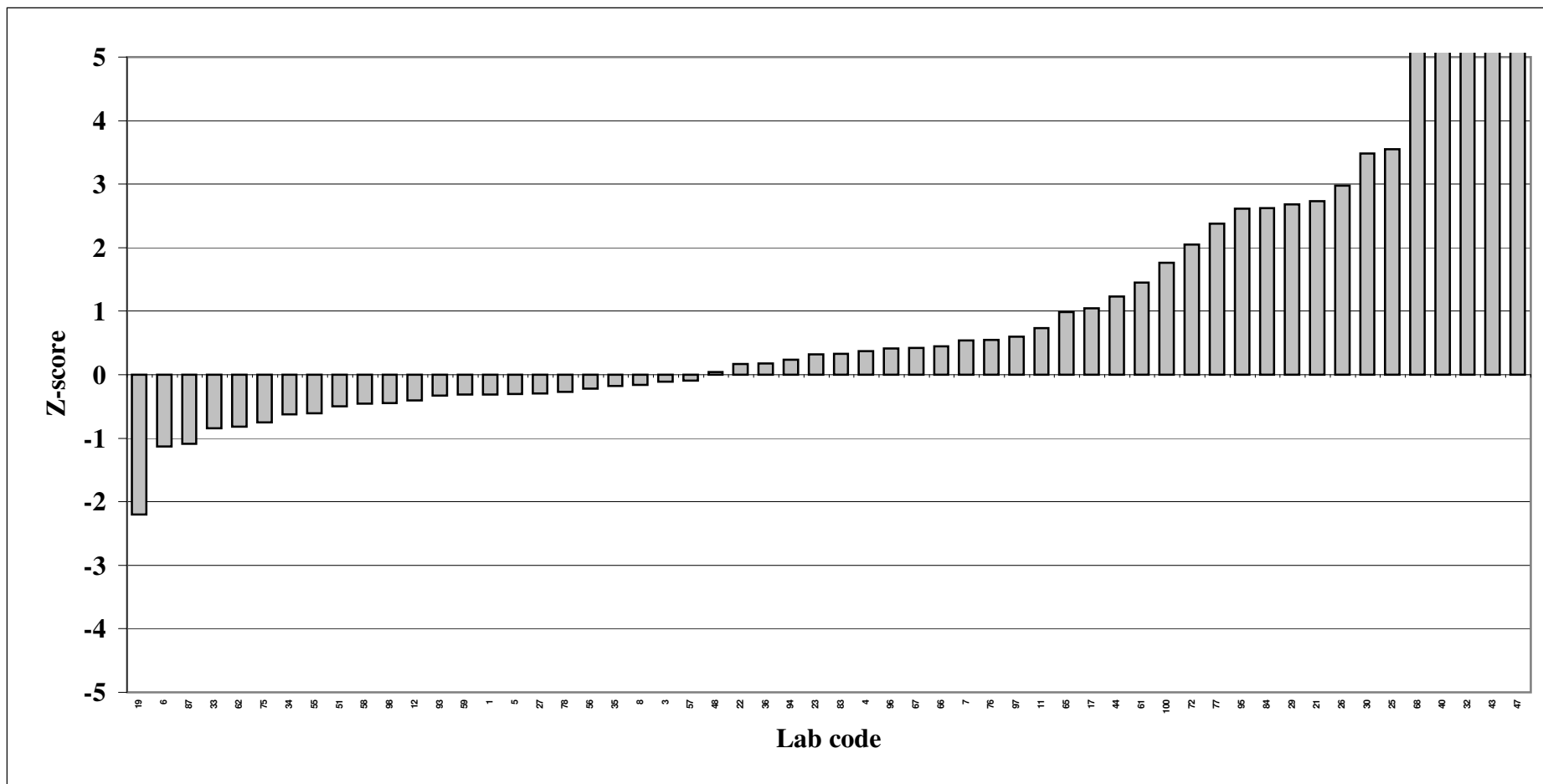
### Z-score Mozzarella Cheese; non-ortho PCB TEQ



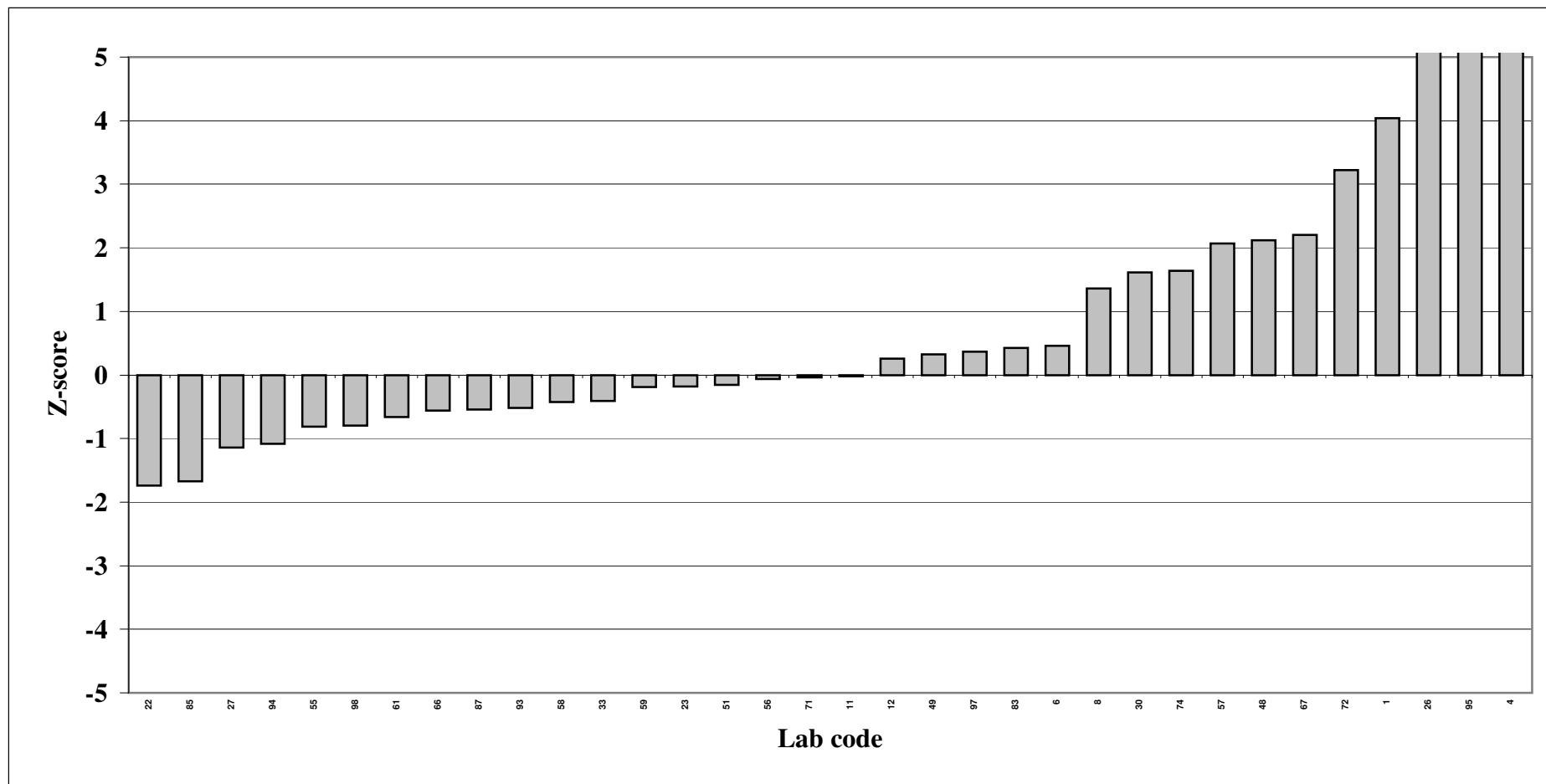
### Z-score Mozzarella Cheese; mono-ortho PCB TEQ



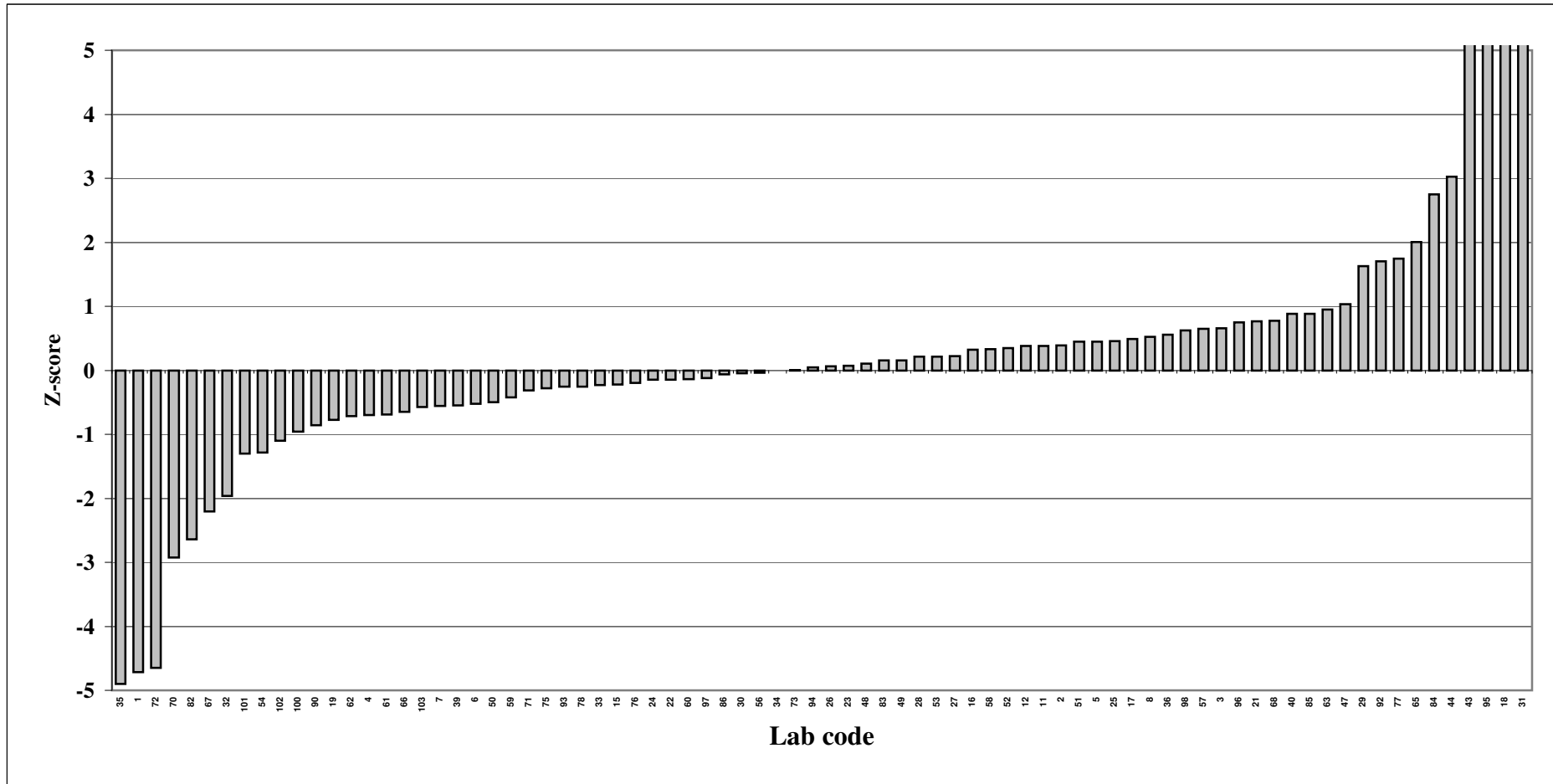
### Z-score Mozzarella Cheese; sum indicator PCB



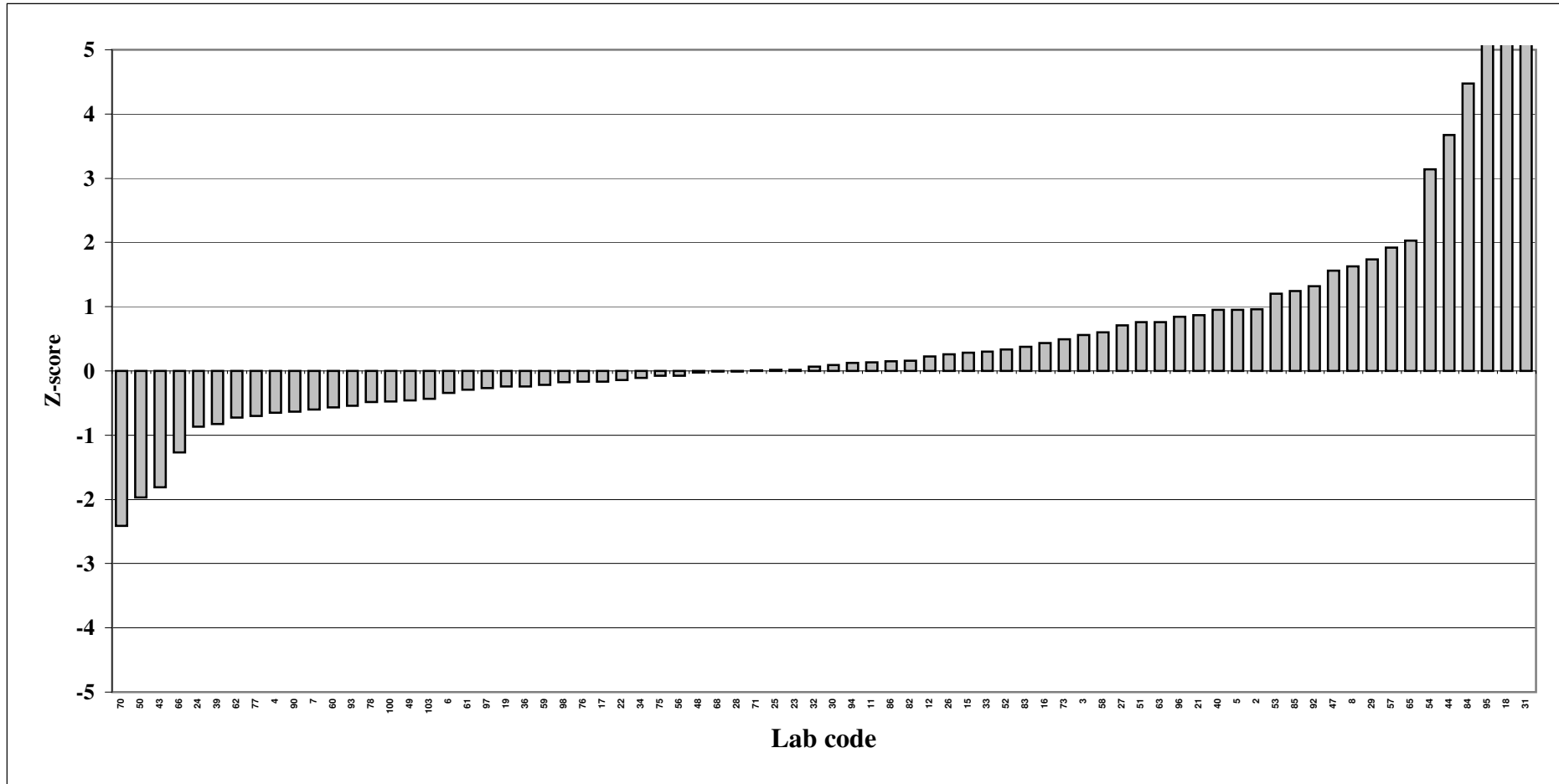
### Z-score Mozzarella Cheese; sum PBDE without BDE-209



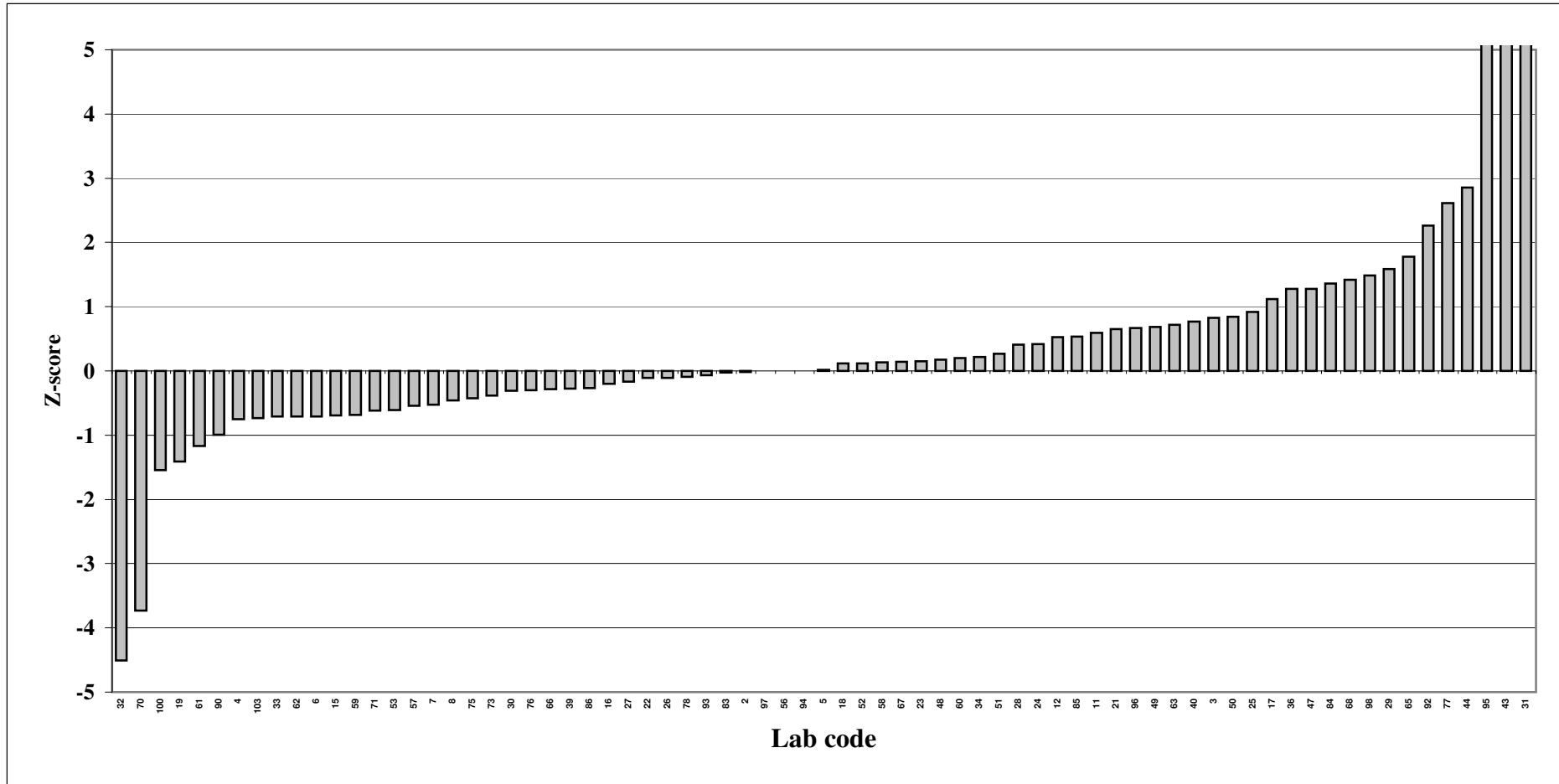
### Z-score Egg; total TEQ



### Z-score Egg; PCDD/PCDF TEQ

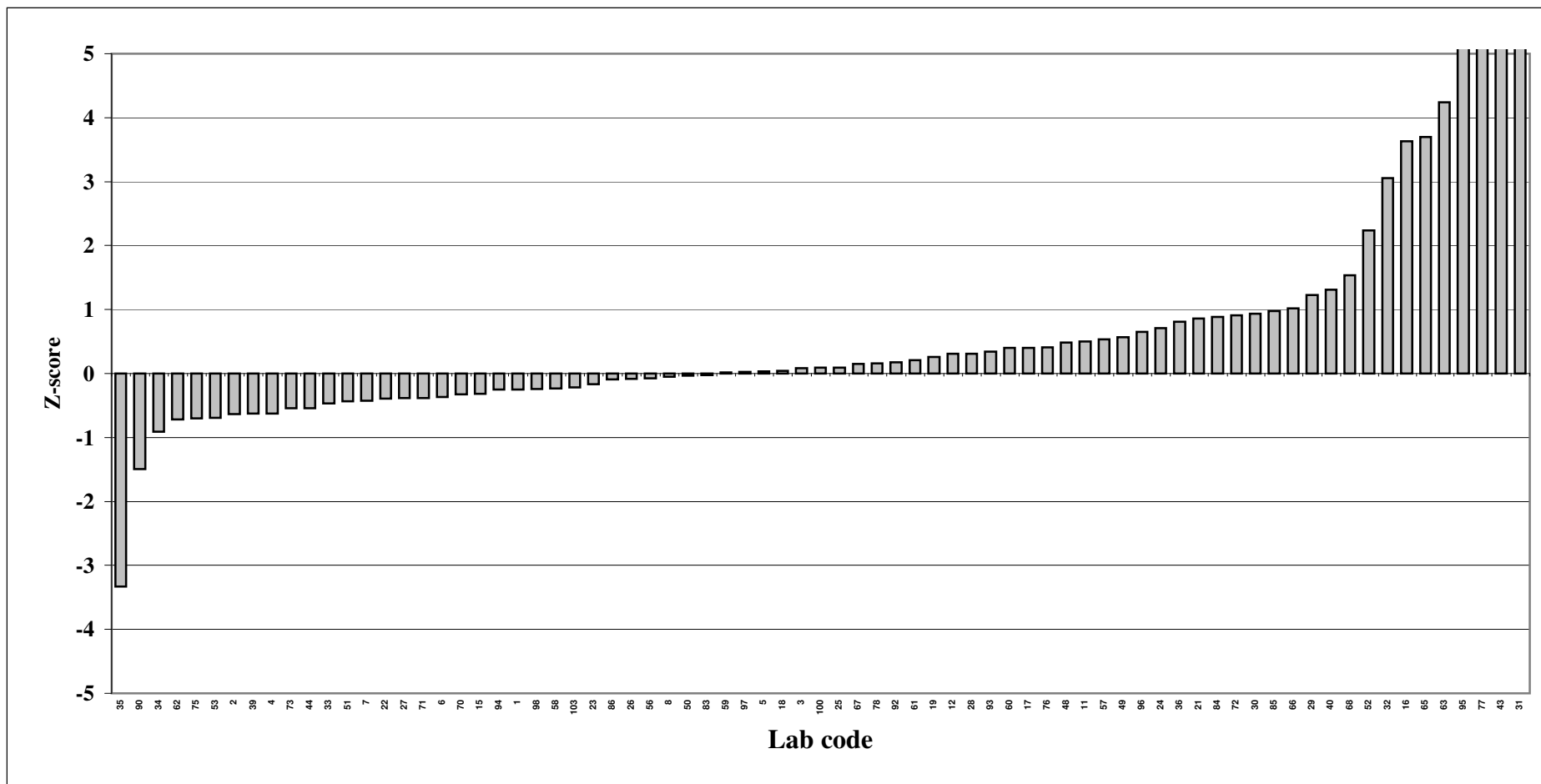


### Z-score Egg; non-ortho PCB TEQ

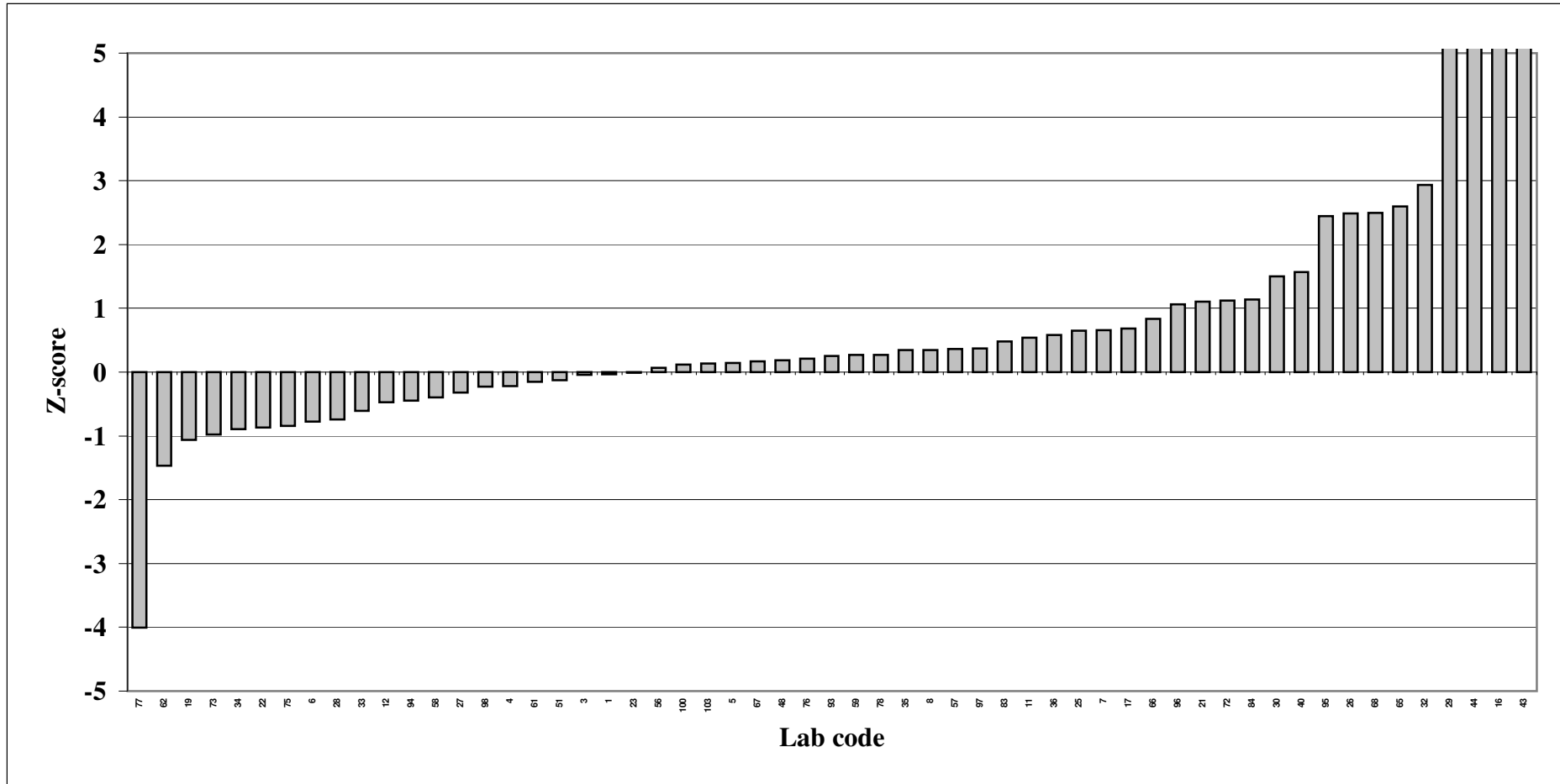




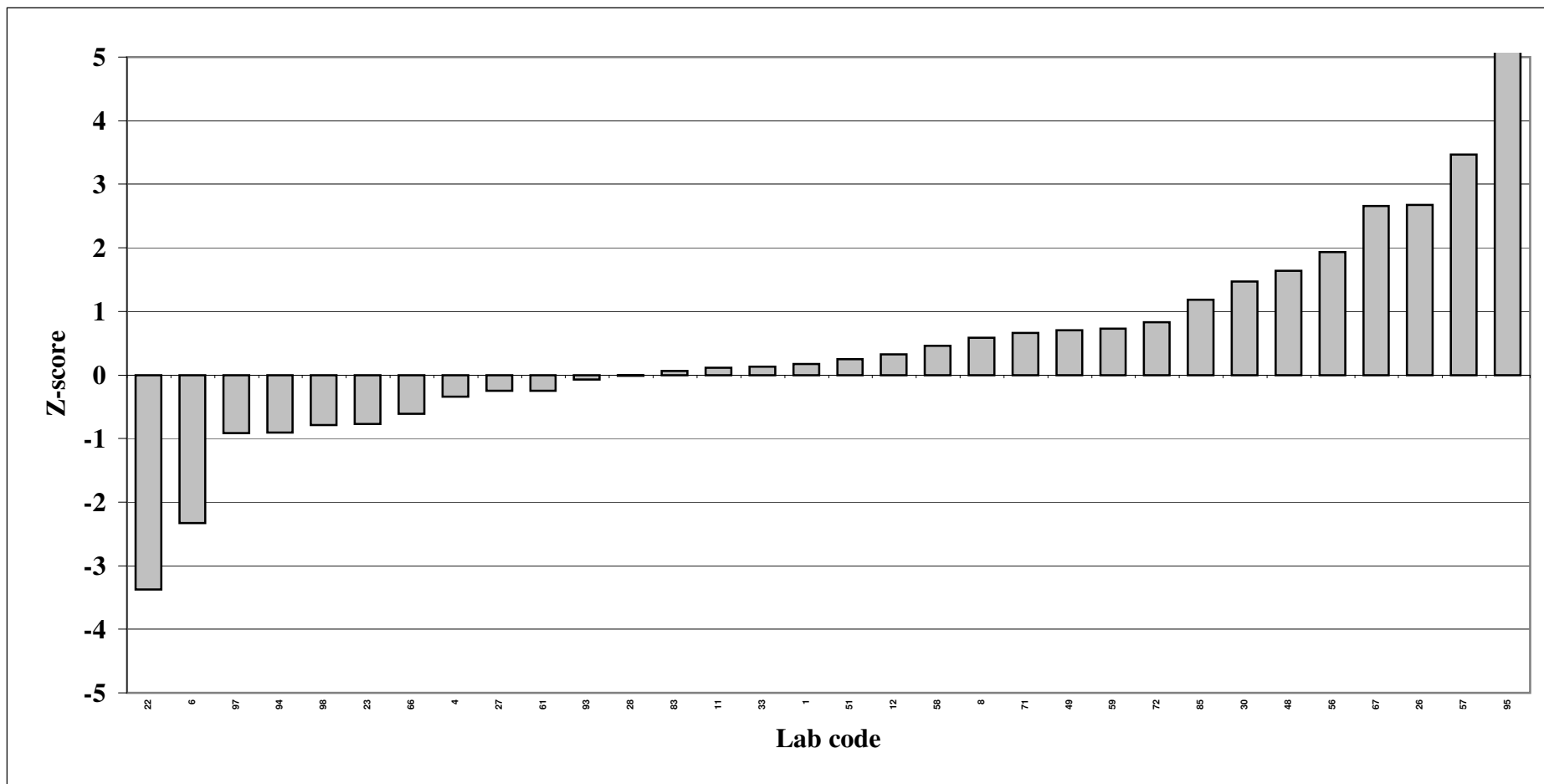
### Z-score Egg; mono-ortho PCB TEQ



### Z-score Egg; sum indicator PCB



### Z-score Egg; sum PBDE without BDE-209





## **Appendix D:**

WHO TEFs for human risk assessment



**WHO TEFs for human risk assessment based on the conclusions of the World Health**

**Organisation Meeting in Stockholm, Sweden, 15-18 June 1997 and International Programme on Chemical Safety expert meeting in Geneva, June 2005**

(M. van den Berg et al., Environ Health Perspect 1998;106:775-792; M. van den Berg et al., Toxicological sciences 93(2), 223-241 (2006))

Congener	TEF values (1998)	TEF values (2005)	Congener	TEF values (1998)	TEF values (2005)
"Dioxins"			"Dioxin-like" PCBs		
<i>Polychlorinated dibenzo-p-dioxins (PCDDs)</i>			<i>Non-ortho PCBs</i>		
2,3,7,8-TCDD	1	1	PCB 77	0.0001	0.0001
1,2,3,7,8-PeCDD	1	1	PCB 81	0.0001	0.0003
1,2,3,4,7,8-HxCDD	0.1	0.1	PCB 126	0.1	0.1
1,2,3,6,7,8-HxCDD	0.1	0.1	PCB 169	0.01	0.03
1,2,3,7,8,9-HxCDD	0.1	0.1			
1,2,3,4,6,7,8-HpCDD	0.01	0.01			
OCDD	0.0001	0.0003			
<i>Polychlorinated dibenzofurans (PCDFs)</i>			<i>Mono-ortho PCBs</i>		
2,3,7,8-TCDF	0.1	0.1	PCB 105	0.0001	0.0003
1,2,3,7,8-PeCDF	0.05	0.03	PCB 114	0.0005	0.0003
2,3,4,7,8-PeCDF	0.5	0.3	PCB 118	0.0001	0.0003
1,2,3,4,7,8-HxCDF	0.1	0.1	PCB 123	0.0001	0.0003
1,2,3,6,7,8-HxCDF	0.1	0.1	PCB 156	0.0005	0.0003
1,2,3,7,8,9-HxCDF	0.1	0.1	PCB 157	0.0005	0.0003
2,3,4,6,7,8-HxCDF	0.1	0.1	PCB 167	0.00001	0.0003
1,2,3,4,6,7,8-HpCDF	0.01	0.01	PCB 189	0.0001	0.0003
1,2,3,4,7,8,9-HpCDF	0.01	0.01			
OCDF	0.0001	0.0003			

Abbreviations used: "T" = tetra; "Pe" = penta; "Hx" = hexa; "Hp" = hepta; "O" = octa; "CDD" = chlorodibenzo-p-dioxin; "CDF" = chlorodibenzofuran; "CB" = chlorobiphenyl.





## **Appendix E:**

Homogeneity testing



# Homogeneity testing of test materials for “Interlaboratory Comparison on Dioxins in Food” organised by the Norwegian Institute of Public Health

## Introduction

The International Harmonized Protocol for the Proficiency Testing of Analytical Chemistry Laboratories (Pure Appl Chem 2006;78:145-96) states that “The bulk material prepared for the proficiency test must be sufficient homogeneous and stable, in respect of each analyte, to ensure that all laboratories receive distribution units that do not differ to any consequential degree in mean analyte concentration. The scheme provider must clearly state the procedure used to establish the homogeneity of the test material”.

The protocol requires that the variation in composition among the distributed units is negligible in relation to variation introduced by the measurements conducted by the participants of the proficiency test (PT). The estimated variation between the samples ( $s_{\text{sam}}$ ) should be less than 30% of the target standard deviation ( $\sigma_p$ ), i.e.,  $s_{\text{sam}} < 0.3 \sigma_p$ .

Further the protocol states that homogeneity testing is required to reassure the participants in proficiency testing schemes that the distributed units of the test material are sufficiently similar. The test specified calls for the selection of ten or more units at random after the putative homogenized material has been split and packaged into discrete samples for distribution. The material from each sample is then analyzed in duplicate, under randomized repeatability conditions (that is, all in one run) using a method with sufficient analytical precision. The value of  $\sigma_{\text{sam}}$  is then estimated from the mean squares after one-way analysis of variance (ANOVA).

Much depends on the quality of the analytical results of the homogeneity testing. If the analytical precision ( $\sigma_{\text{an}}$ ) of the homogeneity test is not small, important sampling variation may be obscured by analytical variation. We may get a non-significant result when testing for heterogeneity, not because it is not present, but the test has no power to detect it. It is recommended that the analytical (repeatability) precision of the method used in the homogeneity test should satisfy  $\sigma_{\text{an}} < 0.5 \sigma_p$

## Consequences for the Interlaboratory Comparison on Dioxins in Food

Below follows the consequences for the Interlaboratory Comparison on Dioxin in Food;

### 1.

The protocol recommends duplicate analysis of at least 10 distribution units. Due to limited amount of test material in each distribution unit and the requirement for sufficiently low analytical standard deviation, the test analysis has to be restricted to PCB, e.g., 6 indicator PCB or CB-153. It is, however, questionable whether analysis of indicator PCB also reflects the distribution of dioxins and other contaminants in the sample, as the test material is often prepared by mixing specifically contaminated material with background contaminated material in order to achieve a sufficient contamination level. Therefore, the distribution of PCBs in the sample might not be relevant for the distribution of dioxins in the sample. The analytical precision of the method used in the homogeneity test should be less than half of the target standard deviation, i.e.,  $\sigma_{\text{an}} < 0.5 \sigma_p$ . For determination of dioxins, the target standard deviation may be approximated by the requirement for trueness (Commission Regulation (EC) No 1883/2006) of  $\pm 20\%$  for total TEQ, i.e., the analytical precision should be less than 10%. This is unrealistic to achieve for the determination of dioxins.

## 2.

The homogeneity testing using, e.g., the determination of indicator PCBs, requires the analysis of at least 60 samples prior to shipment of the distribution units to the participants. This causes problems for the time schedule of the sample preparation and involves high costs.

## 3.

The laboratory conducting the homogeneity test on PT analytes would have access to the test material and knowledge of contamination levels prior to the start of the PT and would therefore not be qualified for participation in the PT.

### **Conclusion**

A valid testing of homogeneity of the test materials of the Interlaboratory Comparison (ILC) on Dioxins in Food with respect to the distribution of dioxins and dioxin-like PCBs is not guaranteed using indicator PCBs. It is doubtful that the analytical precision is small enough to detect a lack in sufficient homogeneity. Given the need for annually testing three different matrices for homogeneity, alternative, rapid and low cost homogeneity tests using surrogate should be applied.

### **Present approach for homogeneity testing for the ILC on Dioxins in Food**

The Harmonized Protocol states under Chapter Testing for sufficient homogeneity: “Tests for sufficient homogeneity are in practice never wholly satisfactory... However, given that sufficient homogeneity is a reasonable prior assumption (because proficiency testing scheme providers do their best to ensure it), and that the cost [and time-consumption] of testing for it is often high, it is sensible to make the main emphasis the avoidance of “Type 1 errors” (that is, false rejection of a satisfactory material).

Having this in mind and the facts that it is impossible to determine all analytes for homogeneity testing of food test material and that a single indicator analyte not necessarily reflects the distribution of the other analytes, we have developed an approach that ensures that the test material is thoroughly blended and evenly distributed among the individual test bottles. The homogeneity testing of solid samples is based on the principle of measuring electrolytic conductivity after addition of sodium chloride to a small portion of the coarsely blended test material. A demonstration of homogeneous distribution of the added salt in the sub samples would indicate our ability to evenly blend the food matrix, i.e., with this approach we ensure the efficiency of our blending procedure. This is especially of importance when blending highly contaminated food matrices with background contaminated food matrices.

When testing homogeneity of the food samples, sodium chloride was added to about 10% of the test material in such an amount that the conductivity was about doubled compared to the natural conductivity. This sub-sample was added to the total sample. For example, to 1 kg of homogenised chicken meat, 150 g NaCl were added resulting in an addition of 1% NaCl to the final test material of 15 kg. Conductivity measurements are performed as follows: boiling water is added to 10.0g of the test material, and the resulting dispersion is ultrasonicated. After centrifugation, the extract is filtered through folded paper filters and allowed to cool to room temperature. The electrolytic conductivity of the water extract is measured using a conductivity meter.

Homogeneity of the test material was demonstrated by comparing the conductivity in water extracts of 10 samples from the same bottle (variation within bottles), and in extracts from 10 different bottles (variation between bottles).

### **Example**

As an example, the relative standard deviation (RSD) of 10 conductivity measurements within a sample bottle containing chicken meat homogenate was 2%. The RSD for the measurement of samples from 10 different, randomly selected bottles was 3%. The contribution of the inhomogeneity to the total variation, calculated from  $RSD^2_{\text{inhomogeneity}} = RSD^2_{\text{between}} - RSD^2_{\text{within}}$ <sup>1</sup> was 2.2% and hence small and acceptable. The total uncertainty for the determination of PCDD/Fs is usually considerably larger, so the measured contribution of inhomogeneity to the total uncertainty can be neglected

<sup>1</sup>G. Becher, L.S. Haug, C. Thomsen, World-wide comparison on the quality of analytical determinations of PCDDs/PCDFs and dioxin-like PCBs in food, *Talanta* 63 (2004) 1115-1122.



## **Appendix 1:**

Presentation of results  
for analyte solution





# Appendix 1: Presentation of results: Analyte solution

## Statistic calculations for PCDDs, PCDFs, dioxin-like PCBs, indicator PCBs, PBDEs and $\alpha$ -HBCD

The analyte solution contained

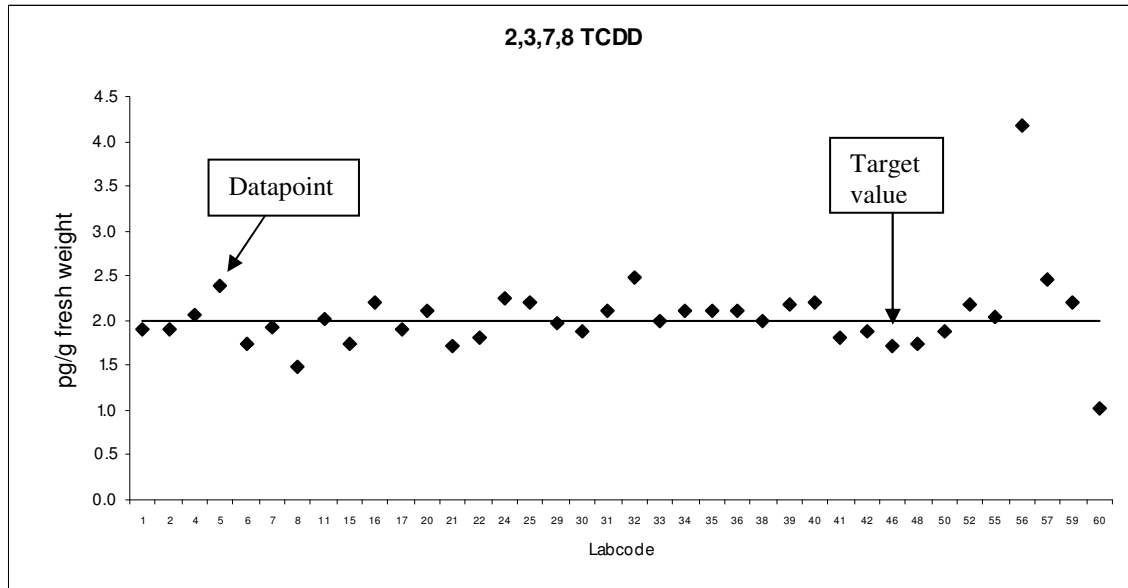
- PCDDs/PCDFs at concentrations of 2:5:10 pg/ $\mu$ l for tetra:penta-hexa-hepta:octa chlorinated dibenzodioxins/furans respectively.
- Non-ortho PCBs at concentration of 10 pg/ $\mu$ l.
- Mono-ortho PCBs and indicator PCBs at concentration of 100 pg/ $\mu$ l.
- PBDE at a concentration of 25 pg/ $\mu$ l, except BDE-209 at 100 pg/ $\mu$ l.
- $\alpha$ -HBCD at a concentration of 500 pg/ $\mu$ l.

These concentrations are called the congeners' target value.

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. The median was calculated from all the reported data.
2. Values outside a range of 50 % to 150 % of this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining data. This median and mean were called consensus median and mean.

The diagram shows the target value and the reported data. Values outside a range of 50 % to 150 % of “median of all values”, were defined as outliers and are not shown in the plot.



### Z-Scores of individual congeners

Z-scores of each congener were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

Where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

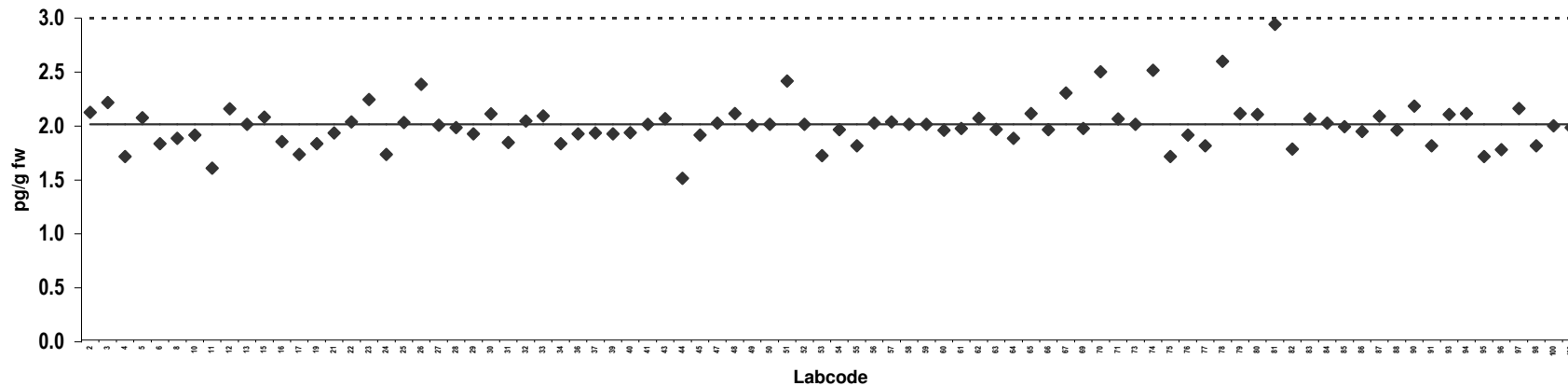
**Analyte solution**  
**Congener: 2,3,7,8 TCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	2.1		56	2.0	
3	2.2		57	2.0	
4	1.7		58	2.0	
5	2.1		59	2.0	
6	1.8		60	1.9	
8	1.9		61	2.0	
10	1.9		62	2.1	
11	1.6		63	2.0	
12	2.1		64	1.9	
13	2.0		65	2.1	
15	2.1		66	2.0	
16	1.8		67	2.3	
17	1.7		69	2.0	
19	1.8		70	2.5	
21	1.9		71	2.0	
22	2.0		73	2.0	
23	2.2		74	2.5	
24	1.7		75	1.7	
25	2.0		76	1.9	
26	2.4		77	1.8	
27	2.0		78	2.6	
28	2.0		79	2.1	
29	1.9		80	2.1	
30	2.1		81	2.9	
31	1.8		82	1.8	
32	2.0		83	2.0	
33	2.1		84	2.0	
34	1.8		85	2.0	
36	1.9		86	1.9	
37	1.9		87	2.1	
39	1.9		88	1.9	
40	1.9		90	2.2	
41	2.0		91	1.8	
43	2.1		93	2.1	
44	1.5		94	2.1	
45	1.9		95	1.7	
47	2.0		96	1.8	
48	2.1		97	2.1	
49	2.0		98	1.8	
50	2.0		100	2.0	
51	2.4		103	2.0	
52	2.0				
53	1.7				
54	1.9				
55	1.8				

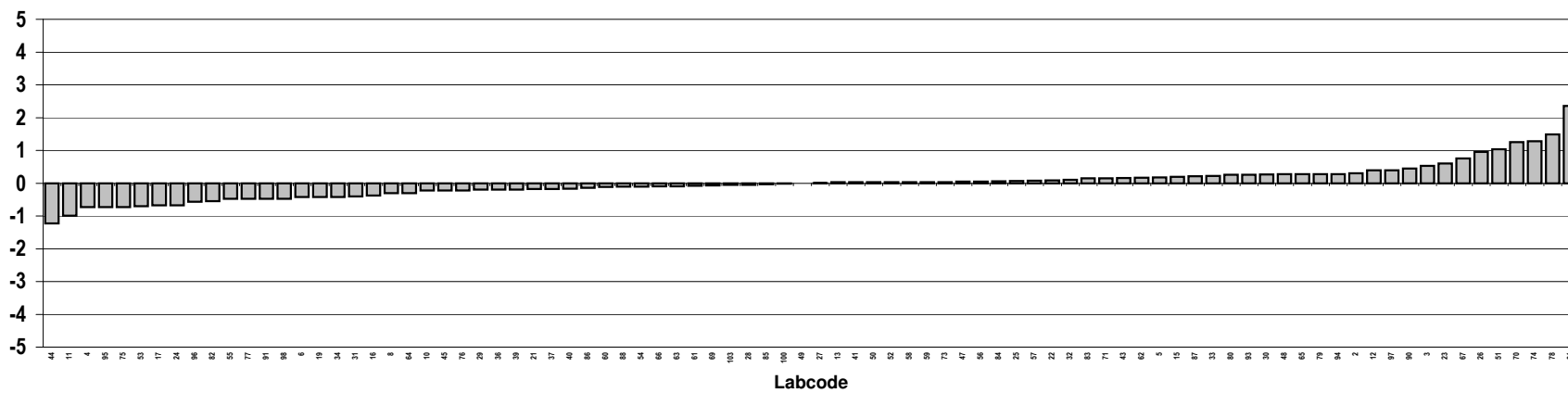
**Consensus statistics**

Consensus median, pg/g	2.0
Median all values pg/g	2.0
Consensus mean, pg/g	2.0
Standard deviation, pg/g	0.21
Relative standard deviation, %	11
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0

### 2,3,7,8 TCDD



### Z-score: 2,3,7,8 TCDD



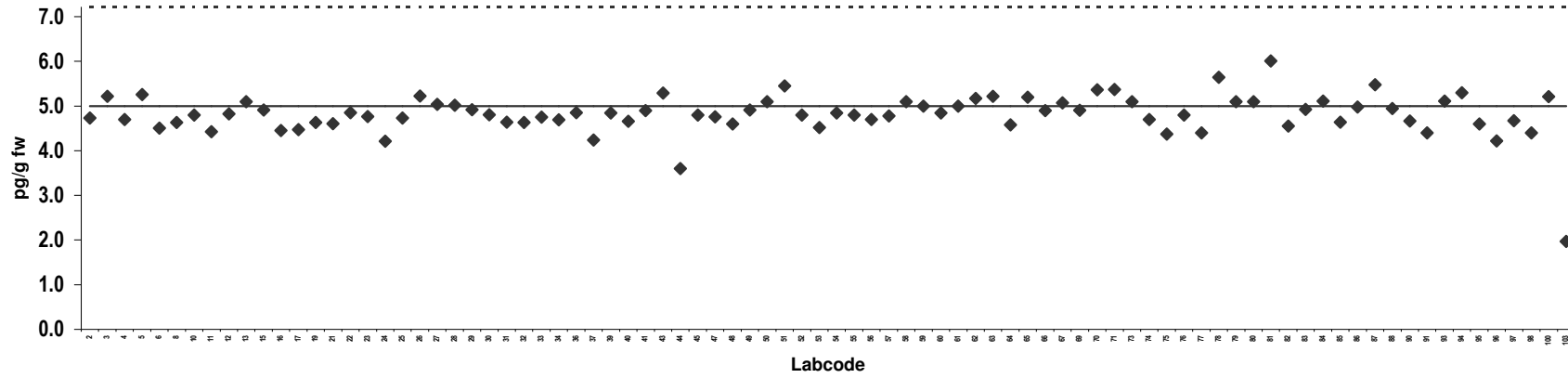
**Analyte solution**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4.7		56	4.7	
3	5.2		57	4.8	
4	4.7		58	5.1	
5	5.3		59	5.0	
6	4.5		60	4.8	
8	4.6		61	5.0	
10	4.8		62	5.2	
11	4.4		63	5.2	
12	4.8		64	4.6	
13	5.1		65	5.2	
15	4.9		66	4.9	
16	4.5		67	5.1	
17	4.5		69	4.9	
19	4.6		70	5.4	
21	4.6		71	5.4	
22	4.9		73	5.1	
23	4.8		74	4.7	
24	4.2		75	4.4	
25	4.7		76	4.8	
26	5.2		77	4.4	
27	5.0		78	5.6	
28	5.0		79	5.1	
29	4.9		80	5.1	
30	4.8		81	6.0	
31	4.6		82	4.6	
32	4.6		83	4.9	
33	4.8		84	5.1	
34	4.7		85	4.6	
36	4.9		86	5.0	
37	4.2		87	5.5	
39	4.8		88	4.9	
40	4.7		90	4.7	
41	4.9		91	4.4	
43	5.3		93	5.1	
44	3.6		94	5.3	
45	4.8		95	4.6	
47	4.8		96	4.2	
48	4.6		97	4.7	
49	4.9		98	4.4	
50	5.1		100	5.2	
51	5.5		103	2.0	Outlier
52	4.8				
53	4.5				
54	4.8				
55	4.8				

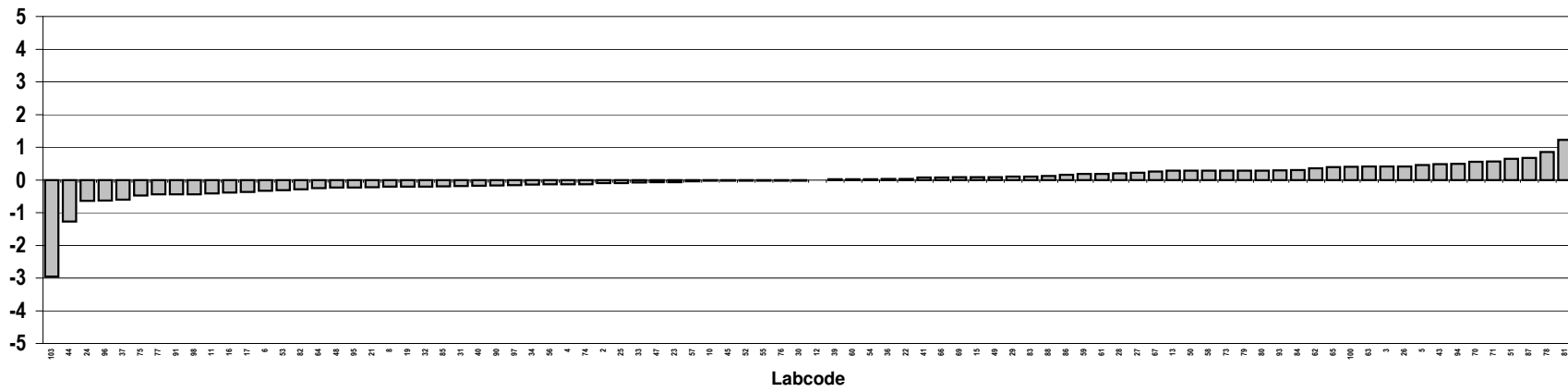
**Consensus statistics**

Consensus median, pg/g	4.8
Median all values pg/g	4.8
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.35
Relative standard deviation, %	7.3
No. of values reported	86
No. of values removed	1
No. of reported non-detects	0

### 1,2,3,7,8 PeCDD



### Z-score: 1,2,3,7,8 PeCDD



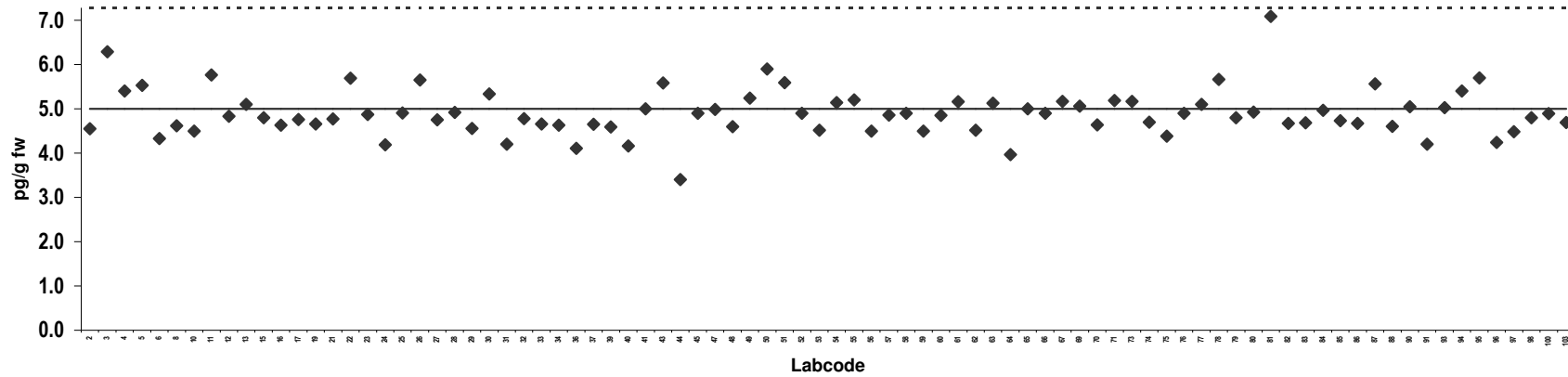
**Analyte solution**  
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4.6		56	4.5	
3	6.3		57	4.9	
4	5.4		58	4.9	
5	5.5		59	4.5	
6	4.3		60	4.9	
8	4.6		61	5.2	
10	4.5		62	4.5	
11	5.8		63	5.1	
12	4.8		64	4.0	
13	5.1		65	5.0	
15	4.8		66	4.9	
16	4.6		67	5.2	
17	4.8		69	5.1	
19	4.7		70	4.6	
21	4.8		71	5.2	
22	5.7		73	5.2	
23	4.9		74	4.7	
24	4.2		75	4.4	
25	4.9		76	4.9	
26	5.6		77	5.1	
27	4.8		78	5.7	
28	4.9		79	4.8	
29	4.6		80	4.9	
30	5.3		81	7.1	
31	4.2		82	4.7	
32	4.8		83	4.7	
33	4.7		84	5.0	
34	4.6		85	4.7	
36	4.1		86	4.7	
37	4.7		87	5.6	
39	4.6		88	4.6	
40	4.2		90	5.0	
41	5.0		91	4.2	
43	5.6		93	5.0	
44	3.4		94	5.4	
45	4.9		95	5.7	
47	5.0		96	4.2	
48	4.6		97	4.5	
49	5.2		98	4.8	
50	5.9		100	4.9	
51	5.6		103	4.7	
52	4.9				
53	4.5				
54	5.1				
55	5.2				

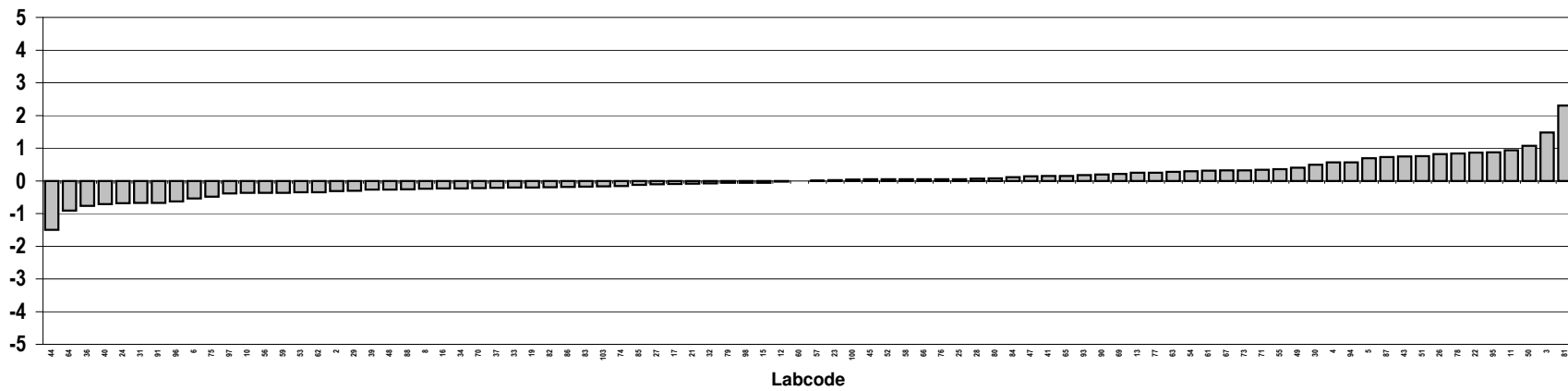
**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.52
Relative standard deviation, %	11
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0

1,2,3,4,7,8 HxCDD



Z-score: 1,2,3,4,7,8 HxCDD



**Analyte solution**  
Congener: 1,2,3,6,7,8 HxCDD

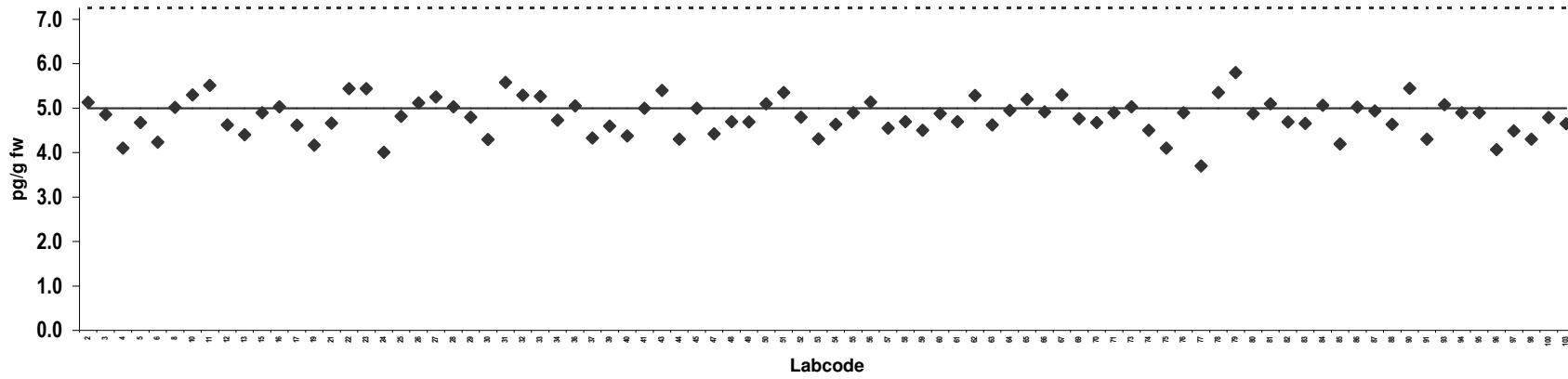
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.1		56	5.1	
3	4.9		57	4.6	
4	4.1		58	4.7	
5	4.7		59	4.5	
6	4.2		60	4.9	
8	5.0		61	4.7	
10	5.3		62	5.3	
11	5.5		63	4.6	
12	4.6		64	5.0	
13	4.4		65	5.2	
15	4.9		66	4.9	
16	5.0		67	5.3	
17	4.6		69	4.8	
19	4.2		70	4.7	
21	4.7		71	4.9	
22	5.4		73	5.0	
23	5.4		74	4.5	
24	4.0		75	4.1	
25	4.8		76	4.9	
26	5.1		77	3.7	
27	5.3		78	5.4	
28	5.0		79	5.8	
29	4.8		80	4.9	
30	4.3		81	5.1	
31	5.6		82	4.7	
32	5.3		83	4.7	
33	5.3		84	5.1	
34	4.7		85	4.2	
36	5.1		86	5.0	
37	4.3		87	4.9	
39	4.6		88	4.6	
40	4.4		90	5.4	
41	5.0		91	4.3	
43	5.4		93	5.1	
44	4.3		94	4.9	
45	5.0		95	4.9	
47	4.4		96	4.1	
48	4.7		97	4.5	
49	4.7		98	4.3	
50	5.1		100	4.8	
51	5.4		103	4.7	
52	4.8				
53	4.3				
54	4.6				
55	4.9				

**Consensus statistics**

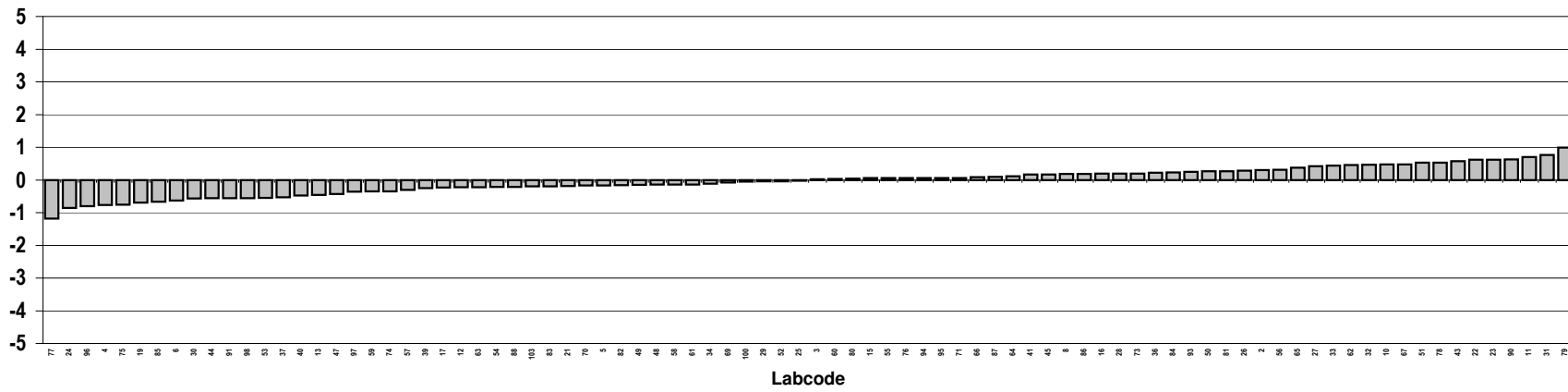
Consensus median, pg/g	4.8
Median all values pg/g	4.8
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.41
Relative standard deviation, %	8.5
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0



1,2,3,6,7,8 HxCDD



Z-score: 1,2,3,6,7,8 HxCDD



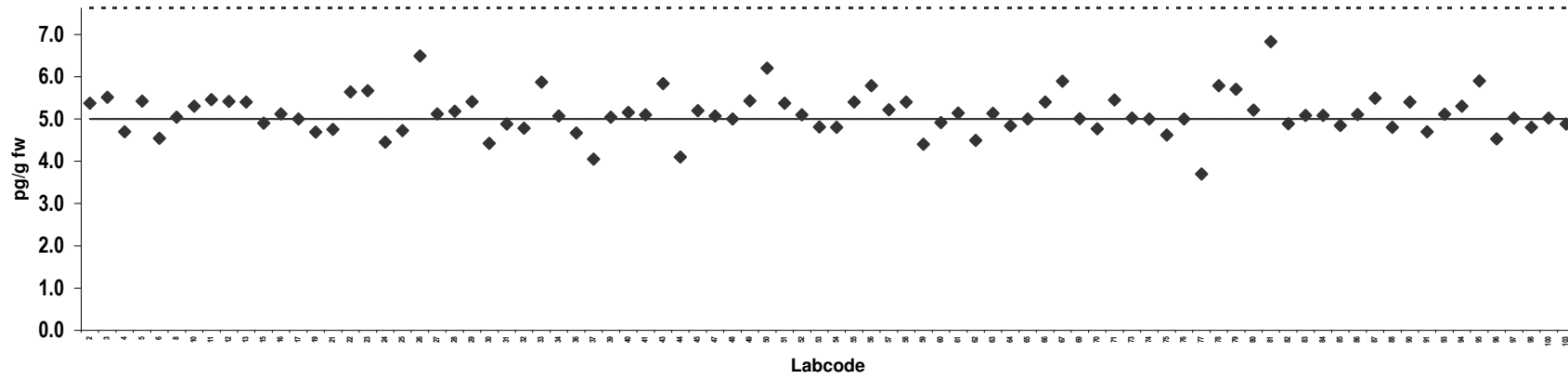
**Analyte solution**  
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.4		56	5.8	
3	5.5		57	5.2	
4	4.7		58	5.4	
5	5.4		59	4.4	
6	4.5		60	4.9	
8	5.0		61	5.1	
10	5.3		62	4.5	
11	5.5		63	5.1	
12	5.4		64	4.8	
13	5.4		65	5.0	
15	4.9		66	5.4	
16	5.1		67	5.9	
17	5.0		69	5.0	
19	4.7		70	4.8	
21	4.8		71	5.4	
22	5.6		73	5.0	
23	5.7		74	5.0	
24	4.5		75	4.6	
25	4.7		76	5.0	
26	6.5		77	3.7	
27	5.1		78	5.8	
28	5.2		79	5.7	
29	5.4		80	5.2	
30	4.4		81	6.8	
31	4.9		82	4.9	
32	4.8		83	5.1	
33	5.9		84	5.1	
34	5.1		85	4.8	
36	4.7		86	5.1	
37	4.1		87	5.5	
39	5.0		88	4.8	
40	5.2		90	5.4	
41	5.1		91	4.7	
43	5.8		93	5.1	
44	4.1		94	5.3	
45	5.2		95	5.9	
47	5.1		96	4.5	
48	5.0		97	5.0	
49	5.4		98	4.8	
50	6.2		100	5.0	
51	5.4		103	4.9	
52	5.1				
53	4.8				
54	4.8				
55	5.4				

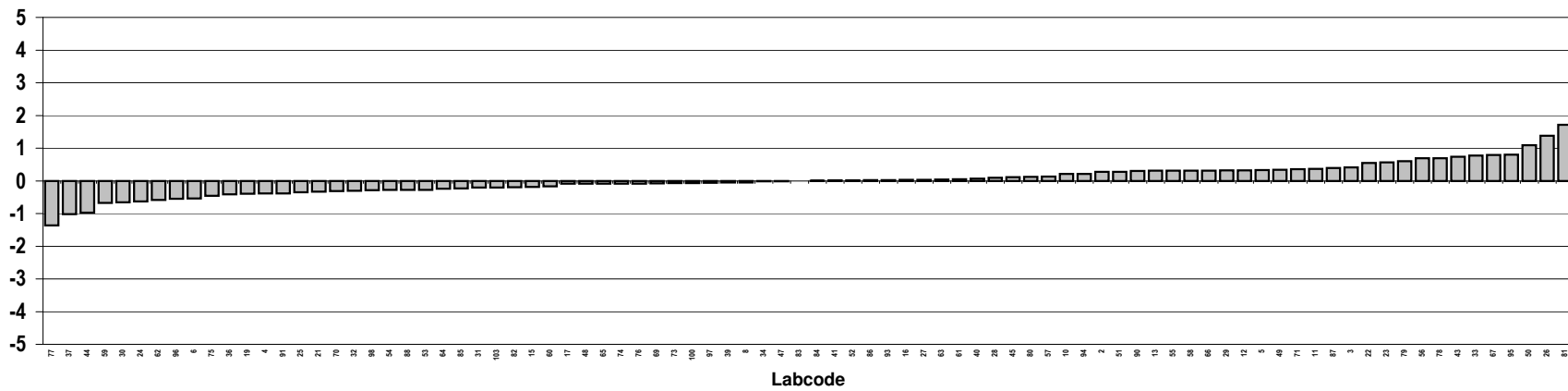
**Consensus statistics**

Consensus median, pg/g	5.1
Median all values pg/g	5.1
Consensus mean, pg/g	5.1
Standard deviation, pg/g	0.49
Relative standard deviation, %	9.6
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0

1,2,3,7,8,9 HxCDD



Z-score: 1,2,3,7,8,9 HxCDD



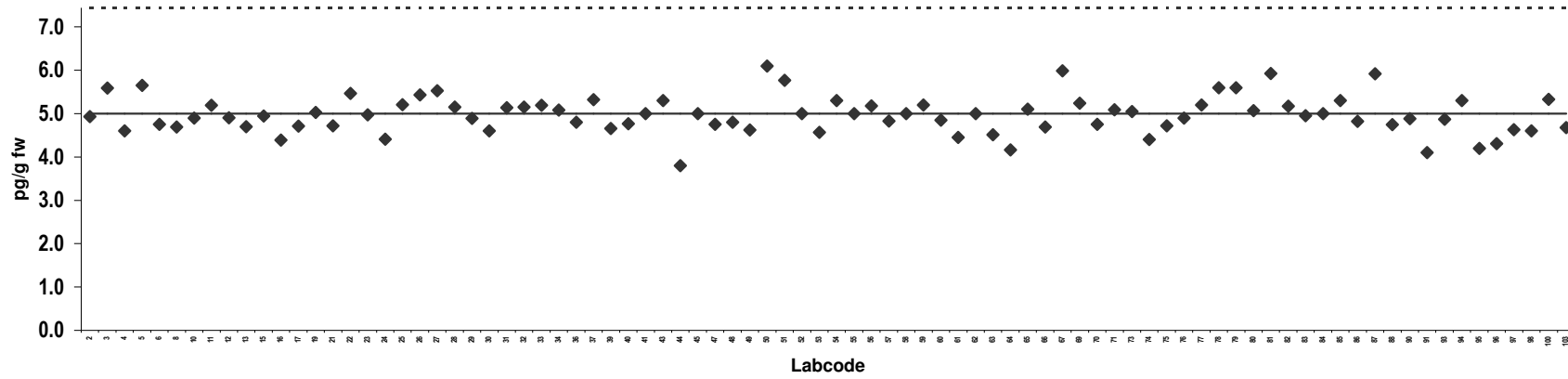
**Analyte solution**  
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4.9		56	5.2	
3	5.6		57	4.8	
4	4.6		58	5.0	
5	5.7		59	5.2	
6	4.8		60	4.9	
8	4.7		61	4.5	
10	4.9		62	5.0	
11	5.2		63	4.5	
12	4.9		64	4.2	
13	4.7		65	5.1	
15	4.9		66	4.7	
16	4.4		67	6.0	
17	4.7		69	5.2	
19	5.0		70	4.8	
21	4.7		71	5.1	
22	5.5		73	5.1	
23	5.0		74	4.4	
24	4.4		75	4.7	
25	5.2		76	4.9	
26	5.4		77	5.2	
27	5.5		78	5.6	
28	5.2		79	5.6	
29	4.9		80	5.1	
30	4.6		81	5.9	
31	5.1		82	5.2	
32	5.2		83	4.9	
33	5.2		84	5.0	
34	5.1		85	5.3	
36	4.8		86	4.8	
37	5.3		87	5.9	
39	4.7		88	4.7	
40	4.8		90	4.9	
41	5.0		91	4.1	
43	5.3		93	4.9	
44	3.8		94	5.3	
45	5.0		95	4.2	
47	4.8		96	4.3	
48	4.8		97	4.6	
49	4.6		98	4.6	
50	6.1		100	5.3	
51	5.8		103	4.7	
52	5.0				
53	4.6				
54	5.3				
55	5.0				

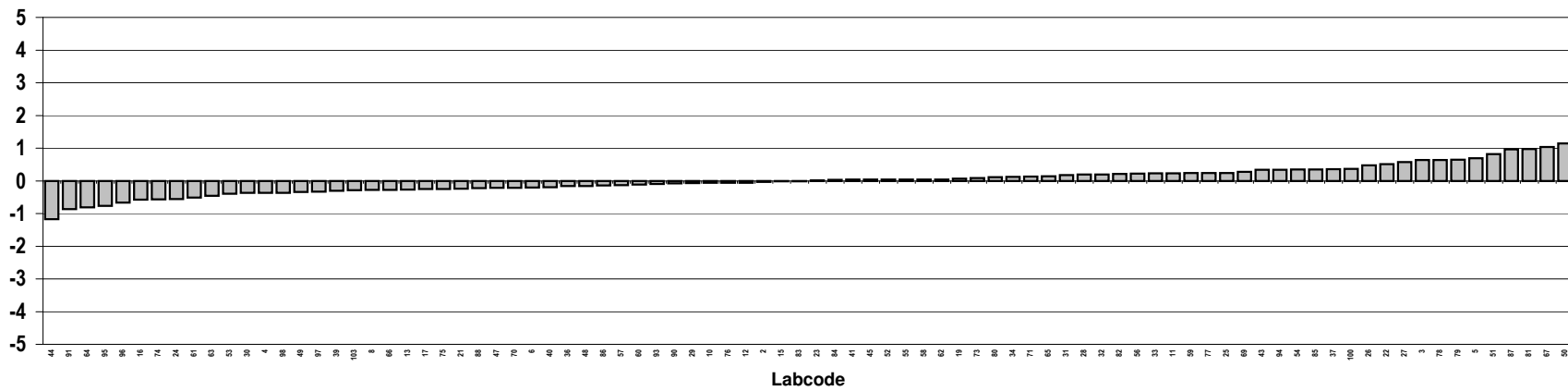
**Consensus statistics**

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.43
Relative standard deviation, %	8.6
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0

1,2,3,4,6,7,8 HpCDD



Z-score: 1,2,3,4,6,7,8 HpCDD



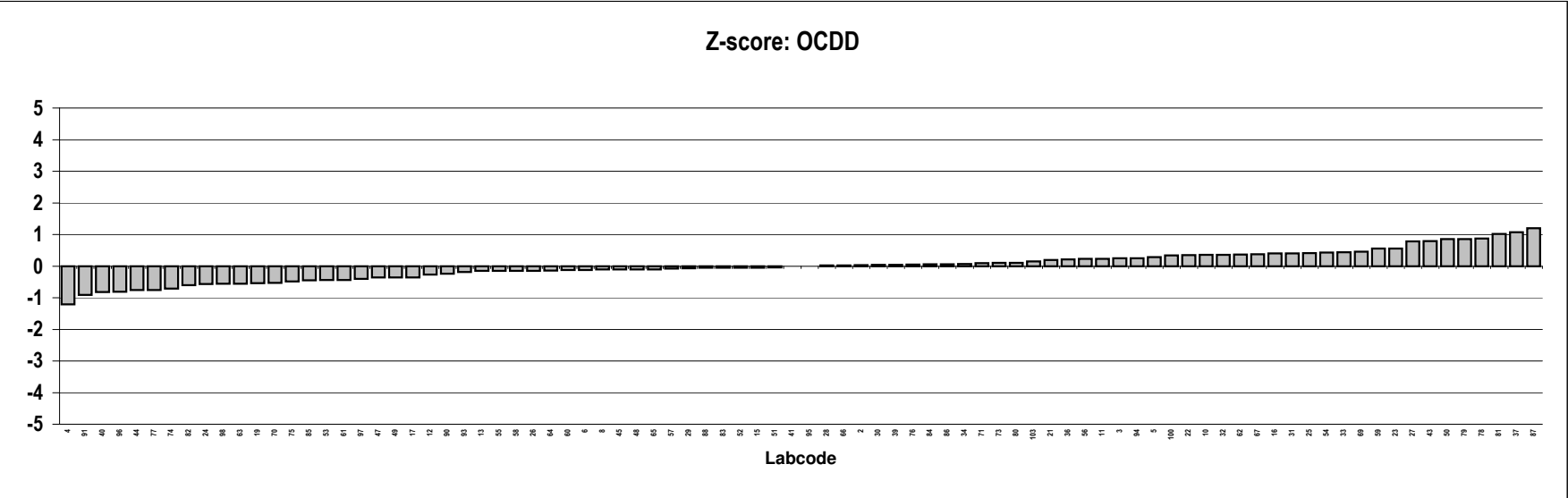
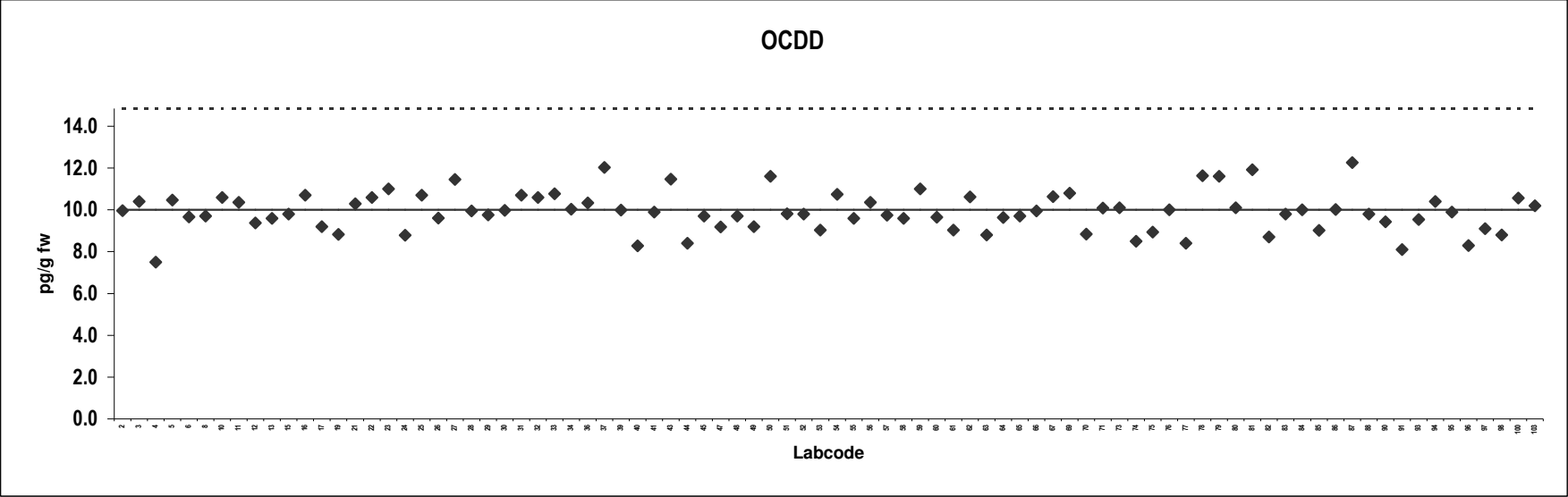
## Analyte solution

Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	10		56	10	
3	10		57	9.7	
4	7.5		58	9.6	
5	10		59	11	
6	9.7		60	9.7	
8	9.7		61	9.0	
10	11		62	11	
11	10		63	8.8	
12	9.4		64	9.6	
13	9.6		65	9.7	
15	9.8		66	10	
16	11		67	11	
17	9.2		69	11	
19	8.8		70	8.8	
21	10		71	10	
22	11		73	10	
23	11		74	8.5	
24	8.8		75	8.9	
25	11		76	10	
26	9.6		77	8.4	
27	11		78	12	
28	10		79	12	
29	9.8		80	10	
30	10		81	12	
31	11		82	8.7	
32	11		83	9.8	
33	11		84	10	
34	10		85	9.0	
36	10		86	10	
37	12		87	12	
39	10		88	9.8	
40	8.3		90	9.4	
41	9.9		91	8.1	
43	11		93	9.5	
44	8.4		94	10	
45	9.7		95	9.9	
47	9.2		96	8.3	
48	9.7		97	9.1	
49	9.2		98	8.8	
50	12		100	11	
51	9.8		103	10	
52	9.8				
53	9.0				
54	11				
55	9.6				

### Consensus statistics

Consensus median, pg/g	9.9
Median all values pg/g	9.9
Consensus mean, pg/g	9.9
Standard deviation, pg/g	0.93
Relative standard deviation, %	9.4
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0



**Analyte solution**  
Congener: 2,3,7,8 TCDF

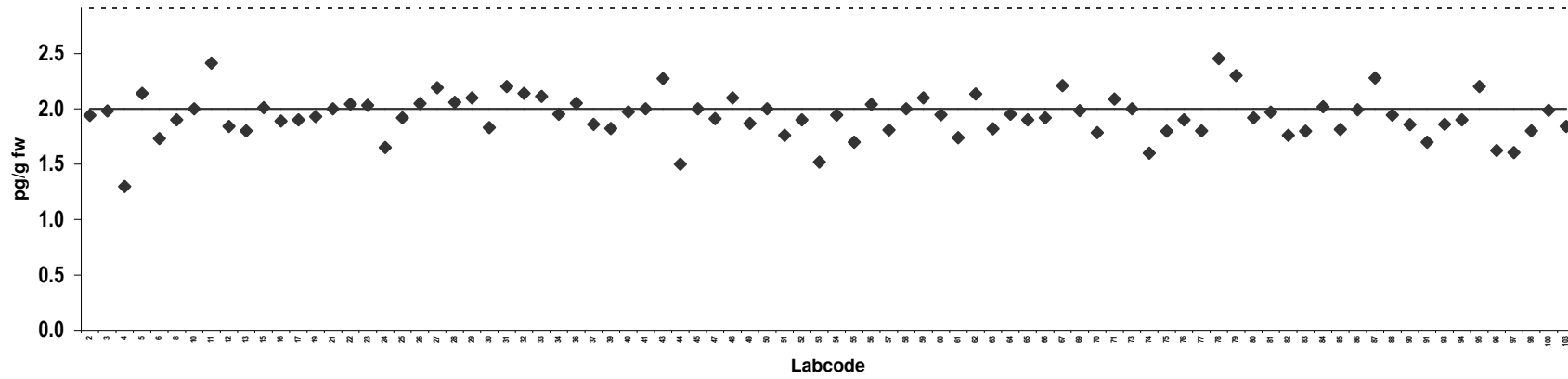
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	1.9		56	2.0	
3	2.0		57	1.8	
4	1.3		58	2.0	
5	2.1		59	2.1	
6	1.7		60	1.9	
8	1.9		61	1.7	
10	2.0		62	2.1	
11	2.4		63	1.8	
12	1.8		64	2.0	
13	1.8		65	1.9	
15	2.0		66	1.9	
16	1.9		67	2.2	
17	1.9		69	2.0	
19	1.9		70	1.8	
21	2.0		71	2.1	
22	2.0		73	2.0	
23	2.0		74	1.6	
24	1.7		75	1.8	
25	1.9		76	1.9	
26	2.0		77	1.8	
27	2.2		78	2.5	
28	2.1		79	2.3	
29	2.1		80	1.9	
30	1.8		81	2.0	
31	2.2		82	1.8	
32	2.1		83	1.8	
33	2.1		84	2.0	
34	2.0		85	1.8	
36	2.1		86	2.0	
37	1.9		87	2.3	
39	1.8		88	1.9	
40	2.0		90	1.9	
41	2.0		91	1.7	
43	2.3		93	1.9	
44	1.5		94	1.9	
45	2.0		95	2.2	
47	1.9		96	1.6	
48	2.1		97	1.6	
49	1.9		98	1.8	
50	2.0		100	2.0	
51	1.8		103	1.8	
52	1.9				
53	1.5				
54	1.9				
55	1.7				

**Consensus statistics**

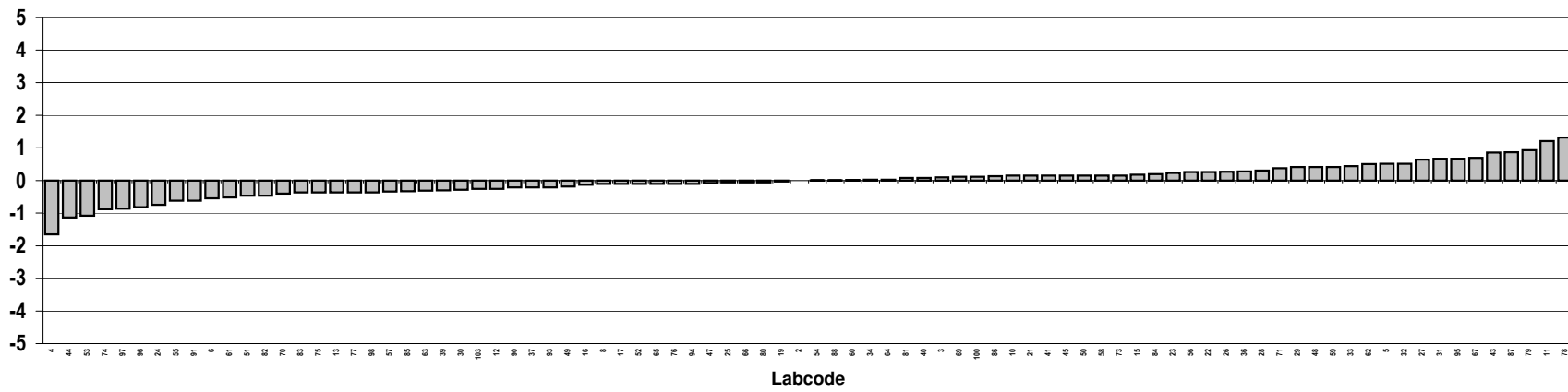
Consensus median, pg/g	1.9
Median all values pg/g	1.9
Consensus mean, pg/g	1.9
Standard deviation, pg/g	0.19
Relative standard deviation, %	10
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0



### 2,3,7,8 TCDF



### Z-score: 2,3,7,8 TCDF



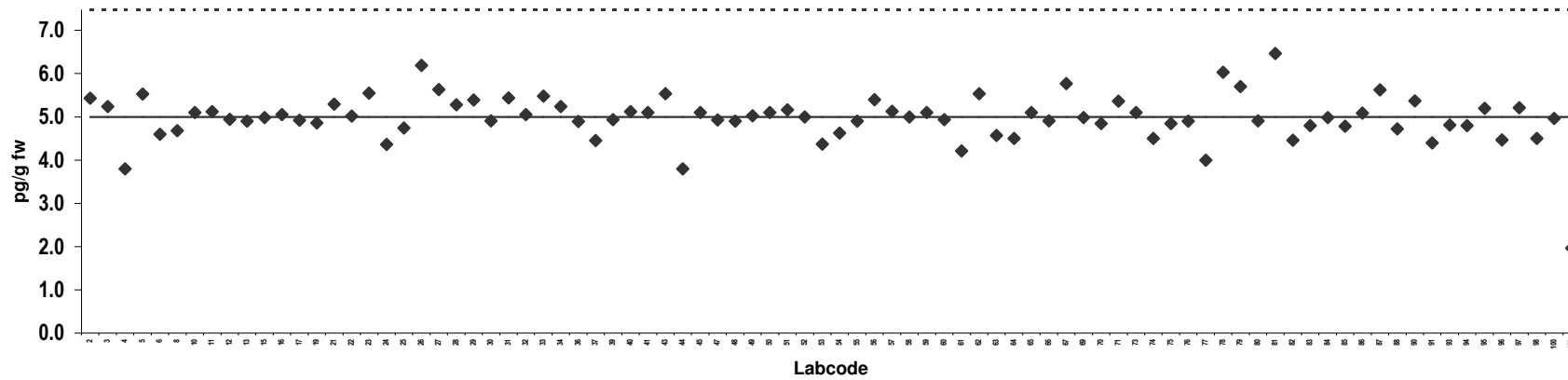
**Analyte solution**  
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.4		56	5.4	
3	5.2		57	5.1	
4	3.8		58	5.0	
5	5.5		59	5.1	
6	4.6		60	4.9	
8	4.7		61	4.2	
10	5.1		62	5.5	
11	5.1		63	4.6	
12	4.9		64	4.5	
13	4.9		65	5.1	
15	5.0		66	4.9	
16	5.1		67	5.8	
17	4.9		69	5.0	
19	4.9		70	4.8	
21	5.3		71	5.4	
22	5.0		73	5.1	
23	5.5		74	4.5	
24	4.4		75	4.8	
25	4.7		76	4.9	
26	6.2		77	4.0	
27	5.6		78	6.0	
28	5.3		79	5.7	
29	5.4		80	4.9	
30	4.9		81	6.5	
31	5.4		82	4.5	
32	5.1		83	4.8	
33	5.5		84	5.0	
34	5.2		85	4.8	
36	4.9		86	5.1	
37	4.5		87	5.6	
39	4.9		88	4.7	
40	5.1		90	5.4	
41	5.1		91	4.4	
43	5.5		93	4.8	
44	3.8		94	4.8	
45	5.1		95	5.2	
47	4.9		96	4.5	
48	4.9		97	5.2	
49	5.0		98	4.5	
50	5.1		100	5.0	
51	5.2		103	2.0	Outlier
52	5.0				
53	4.4				
54	4.6				
55	4.9				

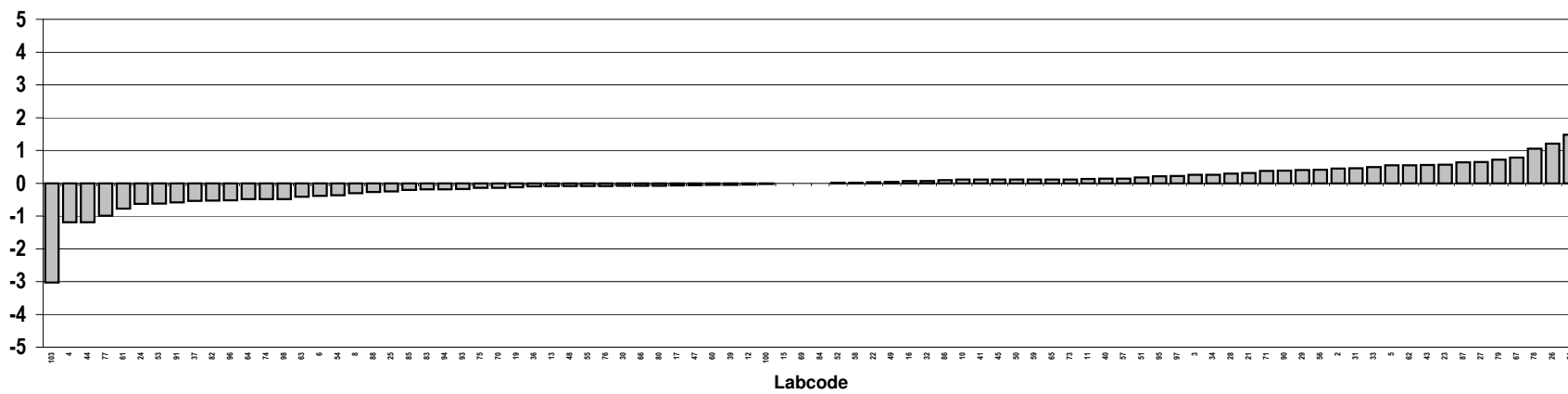
**Consensus statistics**

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.46
Relative standard deviation, %	9.2
No. of values reported	86
No. of values removed	1
No. of reported non-detects	0

1,2,3,7,8 PeCDF



Z-score: 1,2,3,7,8 PeCDF



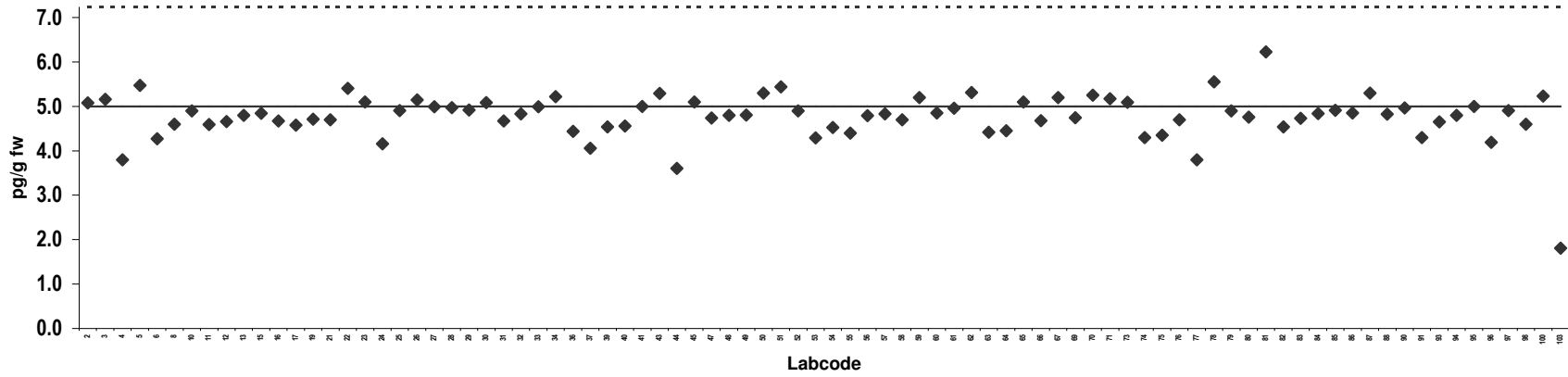
**Analyte solution**  
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.1		56	4.8	
3	5.2		57	4.8	
4	3.8		58	4.7	
5	5.5		59	5.2	
6	4.3		60	4.9	
8	4.6		61	5.0	
10	4.9		62	5.3	
11	4.6		63	4.4	
12	4.7		64	4.5	
13	4.8		65	5.1	
15	4.8		66	4.7	
16	4.7		67	5.2	
17	4.6		69	4.7	
19	4.7		70	5.2	
21	4.7		71	5.2	
22	5.4		73	5.1	
23	5.1		74	4.3	
24	4.2		75	4.4	
25	4.9		76	4.7	
26	5.1		77	3.8	
27	5.0		78	5.6	
28	5.0		79	4.9	
29	4.9		80	4.8	
30	5.1		81	6.2	
31	4.7		82	4.5	
32	4.8		83	4.7	
33	5.0		84	4.8	
34	5.2		85	4.9	
36	4.4		86	4.9	
37	4.1		87	5.3	
39	4.5		88	4.8	
40	4.6		90	5.0	
41	5.0		91	4.3	
43	5.3		93	4.7	
44	3.6		94	4.8	
45	5.1		95	5.0	
47	4.7		96	4.2	
48	4.8		97	4.9	
49	4.8		98	4.6	
50	5.3		100	5.2	
51	5.4		103	1.8	Outlier
52	4.9				
53	4.3				
54	4.5				
55	4.4				

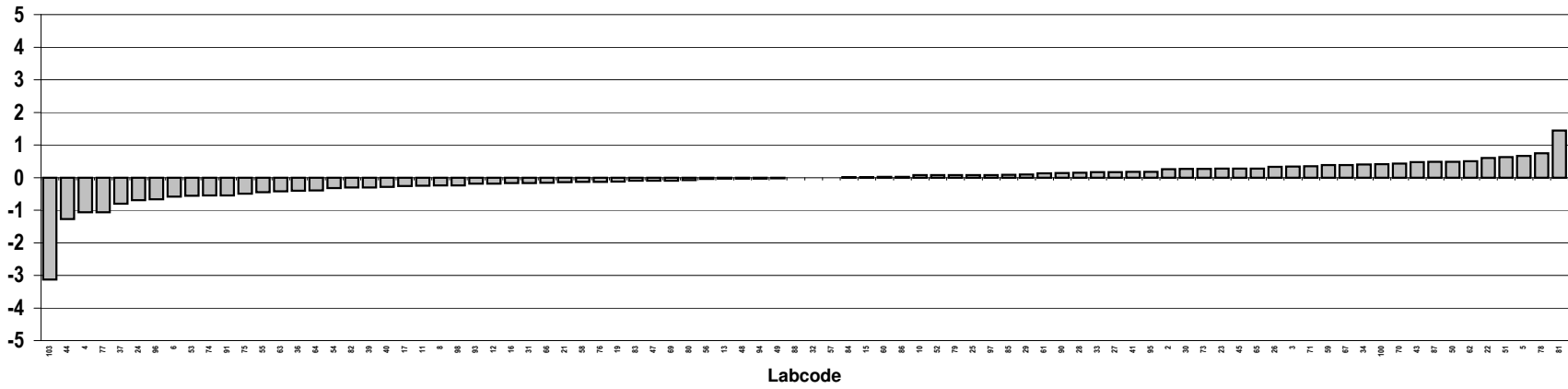
**Consensus statistics**

Consensus median, pg/g	4.8
Median all values pg/g	4.8
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.41
Relative standard deviation, %	8.5
No. of values reported	86
No. of values removed	1
No. of reported non-detects	0

### 2,3,4,7,8 PeCDF



### Z-score: 2,3,4,7,8 PeCDF



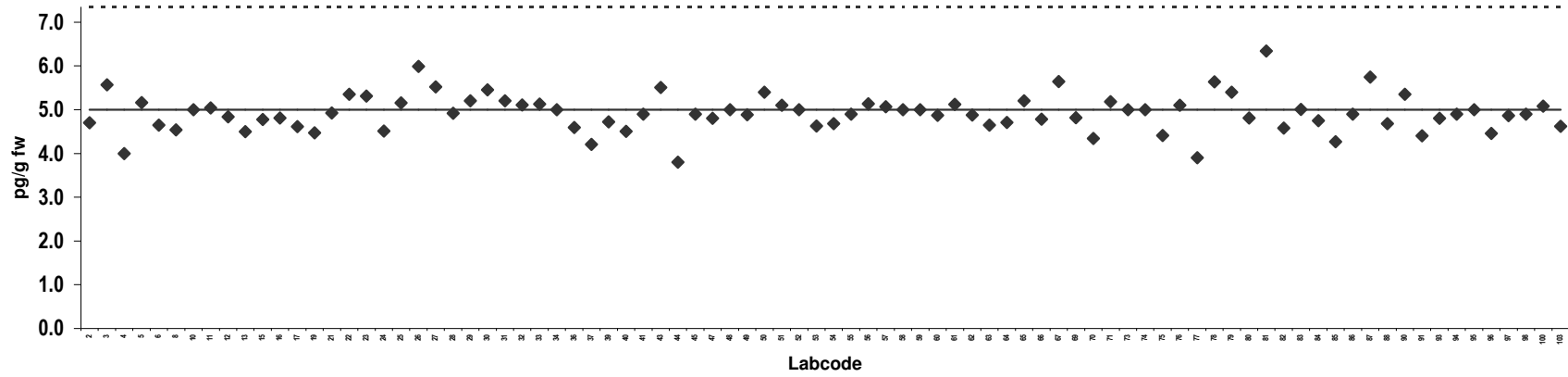
**Analyte solution**  
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4.7		56	5.1	
3	5.6		57	5.1	
4	4.0		58	5.0	
5	5.2		59	5.0	
6	4.6		60	4.9	
8	4.5		61	5.1	
10	5.0		62	4.9	
11	5.0		63	4.6	
12	4.8		64	4.7	
13	4.5		65	5.2	
15	4.8		66	4.8	
16	4.8		67	5.6	
17	4.6		69	4.8	
19	4.5		70	4.3	
21	4.9		71	5.2	
22	5.4		73	5.0	
23	5.3		74	5.0	
24	4.5		75	4.4	
25	5.2		76	5.1	
26	6.0		77	3.9	
27	5.5		78	5.6	
28	4.9		79	5.4	
29	5.2		80	4.8	
30	5.5		81	6.3	
31	5.2		82	4.6	
32	5.1		83	5.0	
33	5.1		84	4.7	
34	5.0		85	4.3	
36	4.6		86	4.9	
37	4.2		87	5.7	
39	4.7		88	4.7	
40	4.5		90	5.4	
41	4.9		91	4.4	
43	5.5		93	4.8	
44	3.8		94	4.9	
45	4.9		95	5.0	
47	4.8		96	4.5	
48	5.0		97	4.9	
49	4.9		98	4.9	
50	5.4		100	5.1	
51	5.1		103	4.6	
52	5.0				
53	4.6				
54	4.7				
55	4.9				

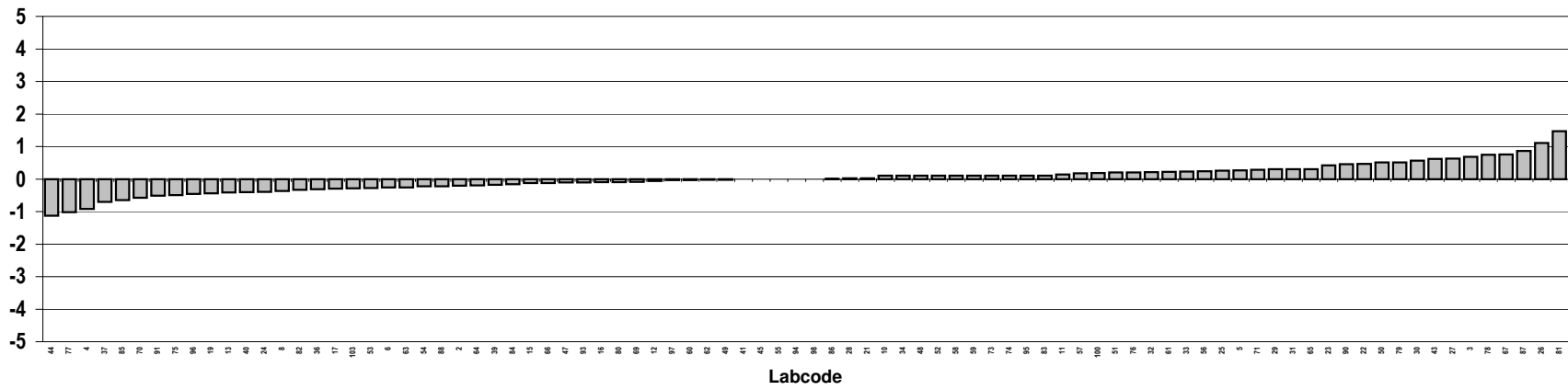
**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.42
Relative standard deviation, %	8.6
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0

1,2,3,4,7,8 HxCDF



Z-score: 1,2,3,4,7,8 HxCDF



**Analyte solution**  
Congener: 1,2,3,6,7,8 HxCDF

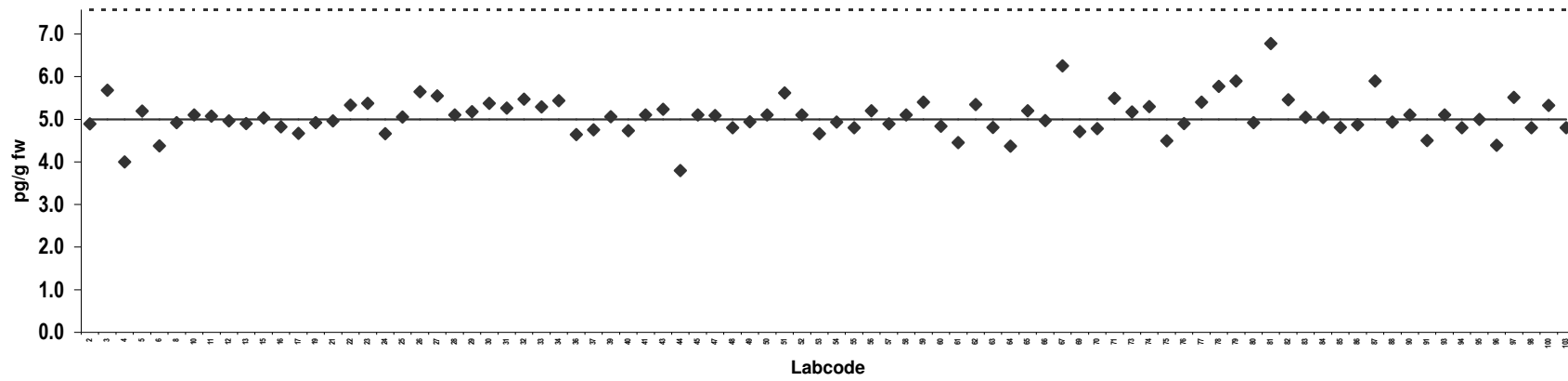
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4.9		56	5.2	
3	5.7		57	4.9	
4	4.0		58	5.1	
5	5.2		59	5.4	
6	4.4		60	4.8	
8	4.9		61	4.5	
10	5.1		62	5.3	
11	5.1		63	4.8	
12	5.0		64	4.4	
13	4.9		65	5.2	
15	5.0		66	5.0	
16	4.8		67	6.3	
17	4.7		69	4.7	
19	4.9		70	4.8	
21	5.0		71	5.5	
22	5.3		73	5.2	
23	5.4		74	5.3	
24	4.7		75	4.5	
25	5.1		76	4.9	
26	5.6		77	5.4	
27	5.6		78	5.8	
28	5.1		79	5.9	
29	5.2		80	4.9	
30	5.4		81	6.8	
31	5.3		82	5.5	
32	5.5		83	5.0	
33	5.3		84	5.0	
34	5.4		85	4.8	
36	4.6		86	4.9	
37	4.8		87	5.9	
39	5.1		88	4.9	
40	4.7		90	5.1	
41	5.1		91	4.5	
43	5.2		93	5.1	
44	3.8		94	4.8	
45	5.1		95	5.0	
47	5.1		96	4.4	
48	4.8		97	5.5	
49	4.9		98	4.8	
50	5.1		100	5.3	
51	5.6		103	4.8	
52	5.1				
53	4.7				
54	4.9				
55	4.8				

**Consensus statistics**

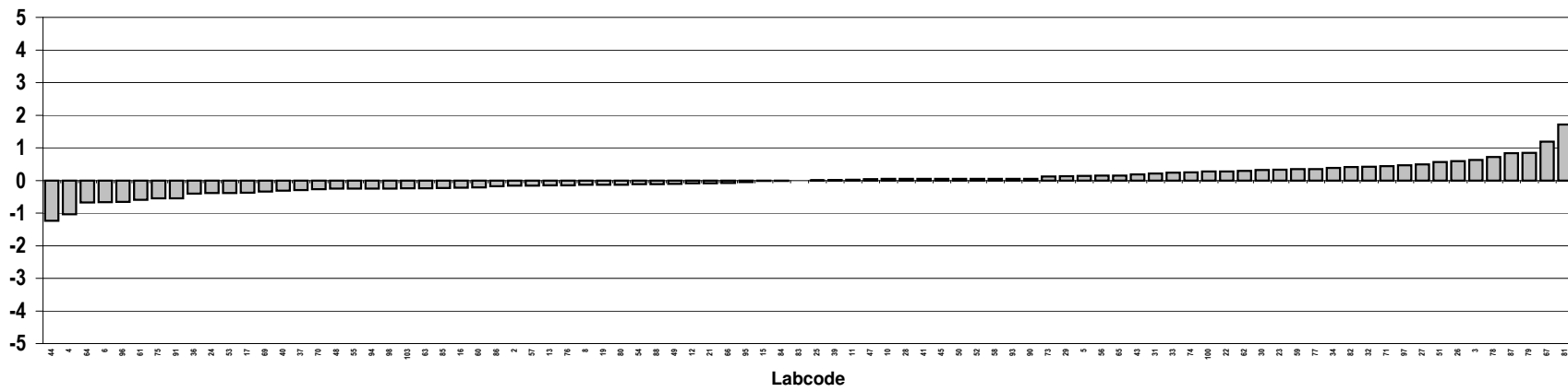
Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.1
Standard deviation, pg/g	0.44
Relative standard deviation, %	8.7
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0



1,2,3,6,7,8 HxCDF



Z-score: 1,2,3,6,7,8 HxCDF



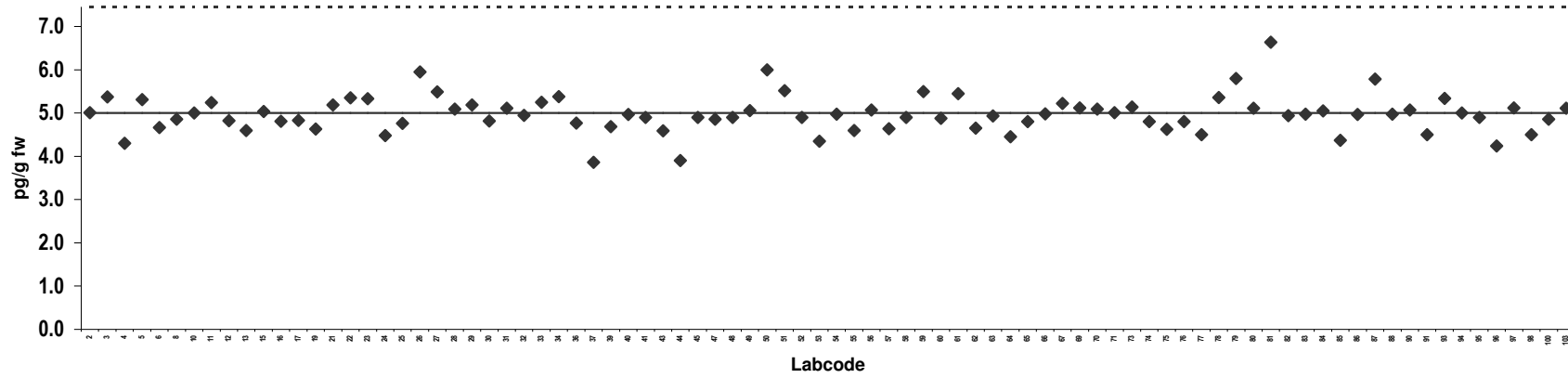
**Analyte solution**  
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.0		56	5.1	
3	5.4		57	4.6	
4	4.3		58	4.9	
5	5.3		59	5.5	
6	4.7		60	4.9	
8	4.9		61	5.4	
10	5.0		62	4.6	
11	5.2		63	4.9	
12	4.8		64	4.5	
13	4.6		65	4.8	
15	5.0		66	5.0	
16	4.8		67	5.2	
17	4.8		69	5.1	
19	4.6		70	5.1	
21	5.2		71	5.0	
22	5.4		73	5.1	
23	5.3		74	4.8	
24	4.5		75	4.6	
25	4.8		76	4.8	
26	5.9		77	4.5	
27	5.5		78	5.4	
28	5.1		79	5.8	
29	5.2		80	5.1	
30	4.8		81	6.6	
31	5.1		82	4.9	
32	5.0		83	5.0	
33	5.2		84	5.0	
34	5.4		85	4.4	
36	4.8		86	5.0	
37	3.9		87	5.8	
39	4.7		88	5.0	
40	5.0		90	5.1	
41	4.9		91	4.5	
43	4.6		93	5.3	
44	3.9		94	5.0	
45	4.9		95	4.9	
47	4.9		96	4.2	
48	4.9		97	5.1	
49	5.1		98	4.5	
50	6.0		100	4.9	
51	5.5		103	5.1	
52	4.9				
53	4.4				
54	5.0				
55	4.6				

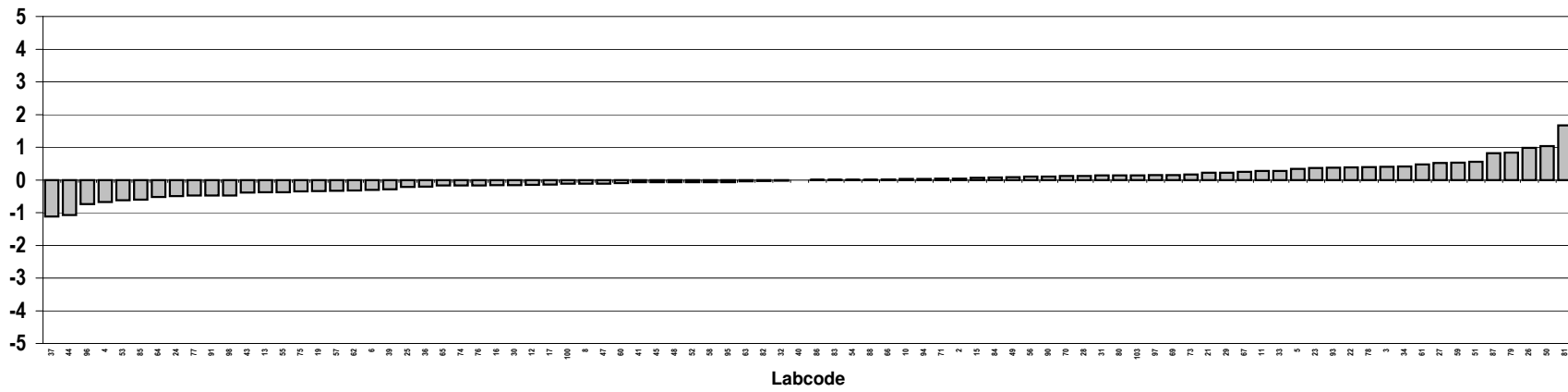
**Consensus statistics**

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.43
Relative standard deviation, %	8.6
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0

2,3,4,6,7,8 HxCDF



Z-score: 2,3,4,6,7,8 HxCDF



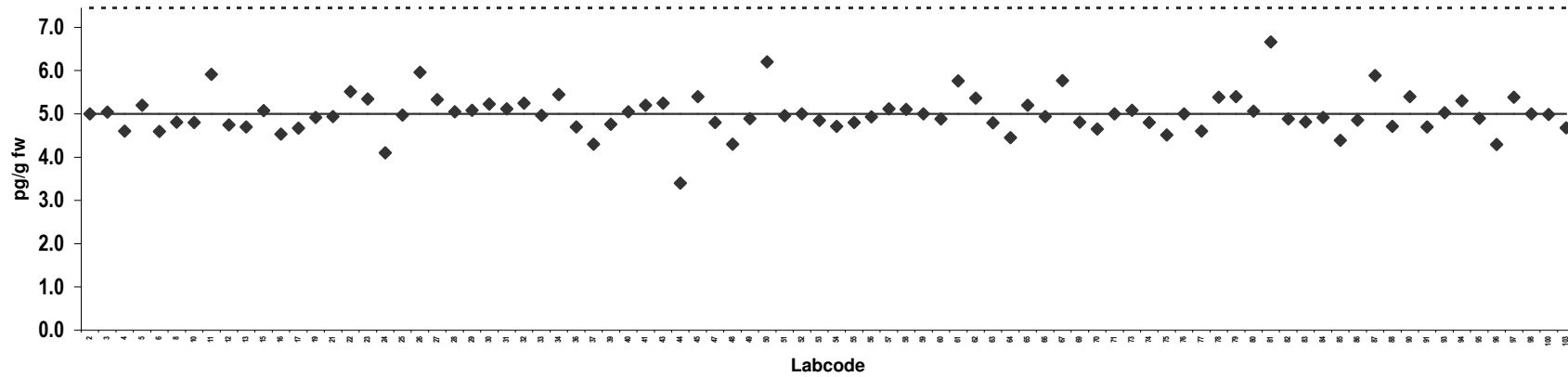
**Analyte solution**  
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.0		56	4.9	
3	5.0		57	5.1	
4	4.6		58	5.1	
5	5.2		59	5.0	
6	4.6		60	4.9	
8	4.8		61	5.8	
10	4.8		62	5.4	
11	5.9		63	4.8	
12	4.7		64	4.5	
13	4.7		65	5.2	
15	5.1		66	4.9	
16	4.5		67	5.8	
17	4.7		69	4.8	
19	4.9		70	4.6	
21	4.9		71	5.0	
22	5.5		73	5.1	
23	5.3		74	4.8	
24	4.1		75	4.5	
25	5.0		76	5.0	
26	6.0		77	4.6	
27	5.3		78	5.4	
28	5.1		79	5.4	
29	5.1		80	5.1	
30	5.2		81	6.7	
31	5.1		82	4.9	
32	5.3		83	4.8	
33	5.0		84	4.9	
34	5.5		85	4.4	
36	4.7		86	4.9	
37	4.3		87	5.9	
39	4.8		88	4.7	
40	5.0		90	5.4	
41	5.2		91	4.7	
43	5.2		93	5.0	
44	3.4		94	5.3	
45	5.4		95	4.9	
47	4.8		96	4.3	
48	4.3		97	5.4	
49	4.9		98	5.0	
50	6.2		100	5.0	
51	5.0		103	4.7	
52	5.0				
53	4.9				
54	4.7				
55	4.8				

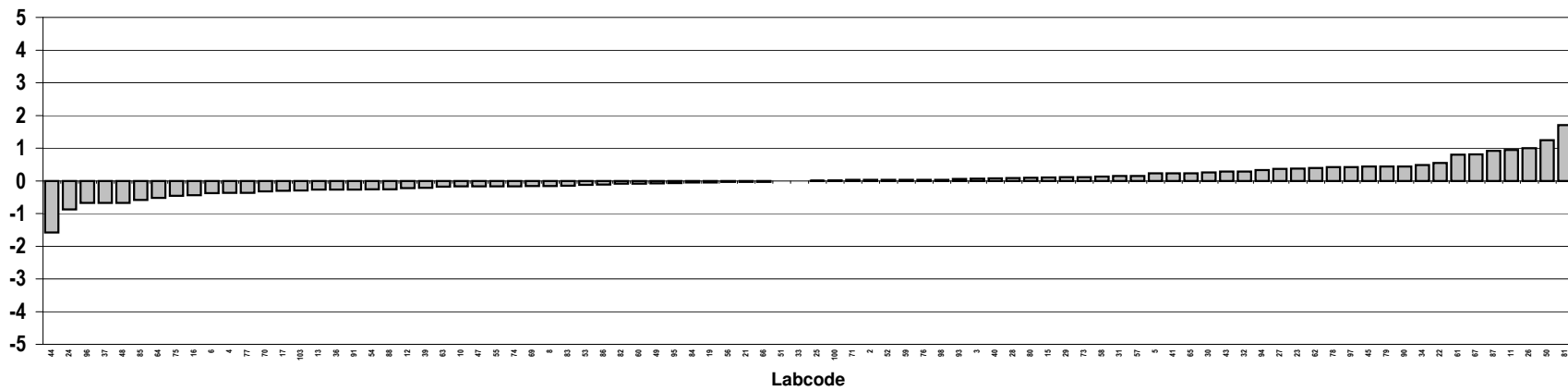
**Consensus statistics**

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.46
Relative standard deviation, %	9.1
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0

1,2,3,7,8,9 HxCDF



Z-score: 1,2,3,7,8,9 HxCDF



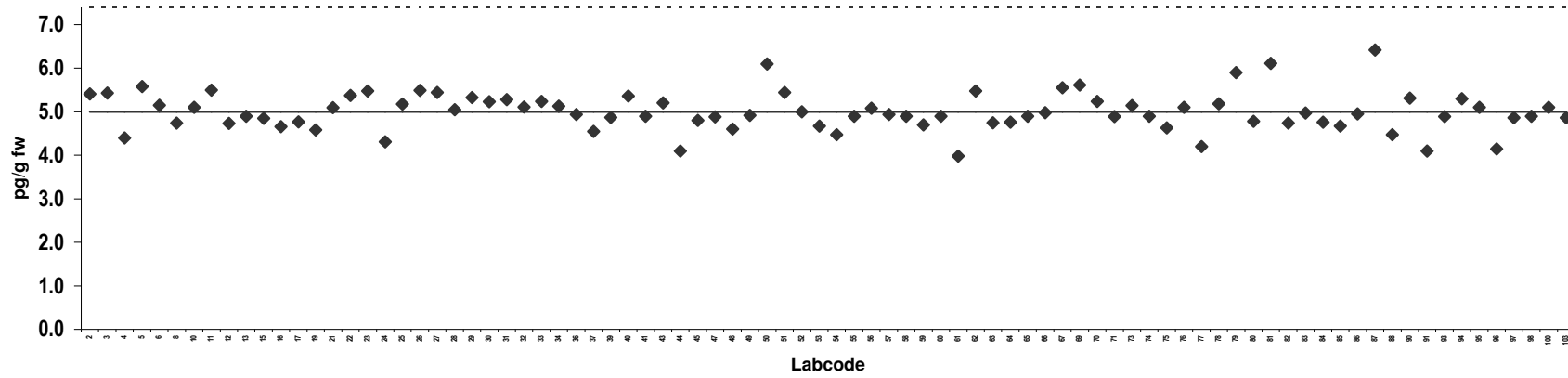
**Analyte solution**  
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.4		56	5.1	
3	5.4		57	4.9	
4	4.4		58	4.9	
5	5.6		59	4.7	
6	5.2		60	4.9	
8	4.7		61	4.0	
10	5.1		62	5.5	
11	5.5		63	4.7	
12	4.7		64	4.8	
13	4.9		65	4.9	
15	4.8		66	5.0	
16	4.7		67	5.6	
17	4.8		69	5.6	
19	4.6		70	5.2	
21	5.1		71	4.9	
22	5.4		73	5.1	
23	5.5		74	4.9	
24	4.3		75	4.6	
25	5.2		76	5.1	
26	5.5		77	4.2	
27	5.4		78	5.2	
28	5.1		79	5.9	
29	5.3		80	4.8	
30	5.2		81	6.1	
31	5.3		82	4.7	
32	5.1		83	5.0	
33	5.2		84	4.8	
34	5.1		85	4.7	
36	4.9		86	5.0	
37	4.6		87	6.4	
39	4.9		88	4.5	
40	5.4		90	5.3	
41	4.9		91	4.1	
43	5.2		93	4.9	
44	4.1		94	5.3	
45	4.8		95	5.1	
47	4.9		96	4.1	
48	4.6		97	4.9	
49	4.9		98	4.9	
50	6.1		100	5.1	
51	5.4		103	4.9	
52	5.0				
53	4.7				
54	4.5				
55	4.9				

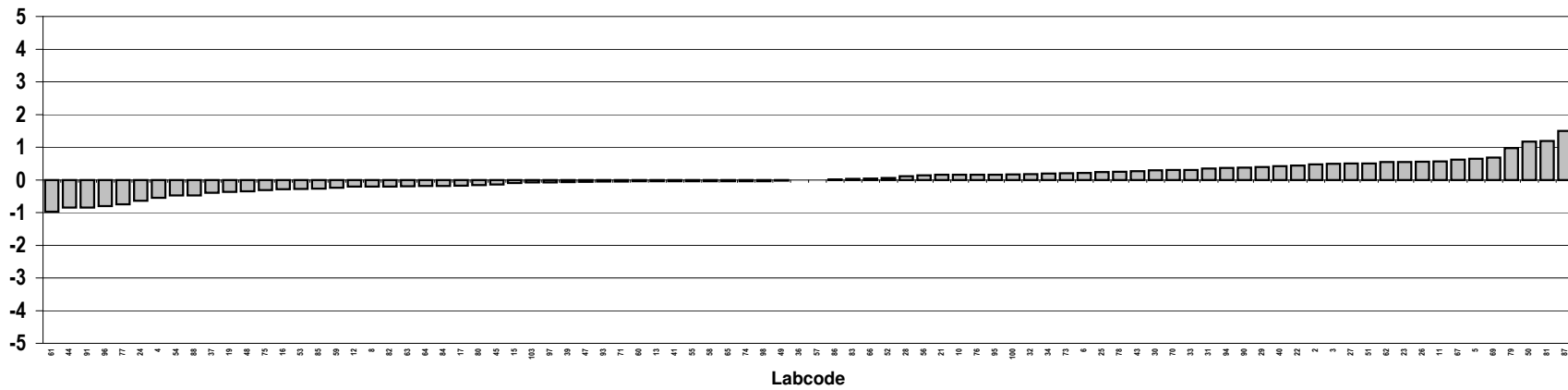
**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.44
Relative standard deviation, %	8.7
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0

### 1,2,3,4,6,7,8 HpCDF



### Z-score: 1,2,3,4,6,7,8 HpCDF



**Analyte solution**  
Congener: 1,2,3,4,7,8,9 HpCDF

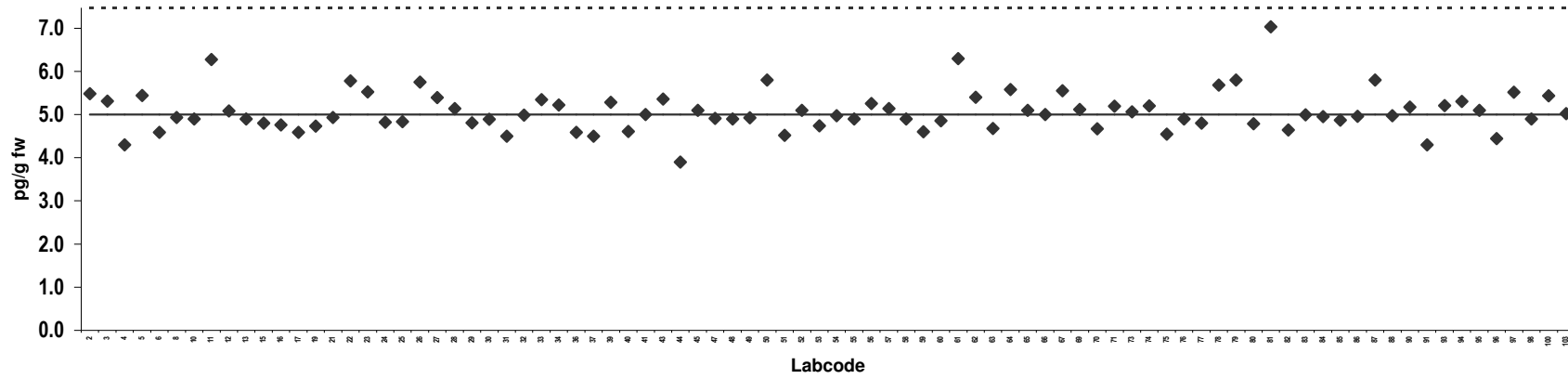
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5.5		56	5.3	
3	5.3		57	5.1	
4	4.3		58	4.9	
5	5.4		59	4.6	
6	4.6		60	4.9	
8	4.9		61	6.3	
10	4.9		62	5.4	
11	6.3		63	4.7	
12	5.1		64	5.6	
13	4.9		65	5.1	
15	4.8		66	5.0	
16	4.8		67	5.6	
17	4.6		69	5.1	
19	4.7		70	4.7	
21	4.9		71	5.2	
22	5.8		73	5.1	
23	5.5		74	5.2	
24	4.8		75	4.5	
25	4.8		76	4.9	
26	5.8		77	4.8	
27	5.4		78	5.7	
28	5.1		79	5.8	
29	4.8		80	4.8	
30	4.9		81	7.0	
31	4.5		82	4.6	
32	5.0		83	5.0	
33	5.3		84	5.0	
34	5.2		85	4.9	
36	4.6		86	5.0	
37	4.5		87	5.8	
39	5.3		88	5.0	
40	4.6		90	5.2	
41	5.0		91	4.3	
43	5.4		93	5.2	
44	3.9		94	5.3	
45	5.1		95	5.1	
47	4.9		96	4.4	
48	4.9		97	5.5	
49	4.9		98	4.9	
50	5.8		100	5.4	
51	4.5		103	5.0	
52	5.1				
53	4.7				
54	5.0				
55	4.9				

**Consensus statistics**

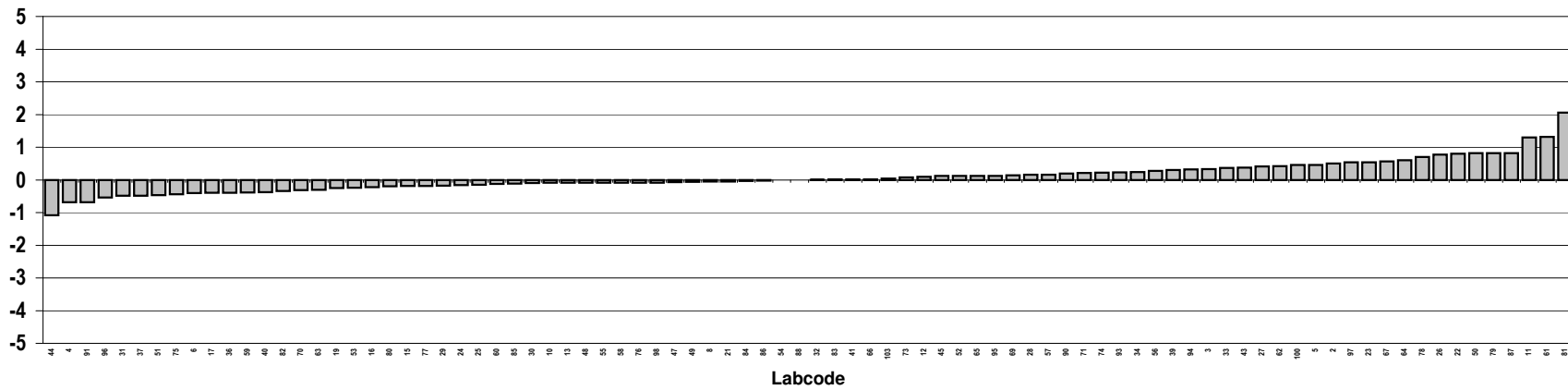
Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.1
Standard deviation, pg/g	0.47
Relative standard deviation, %	9.3
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0



1,2,3,4,7,8,9 HpCDF



Z-score: 1,2,3,4,7,8,9 HpCDF



## Analyte solution

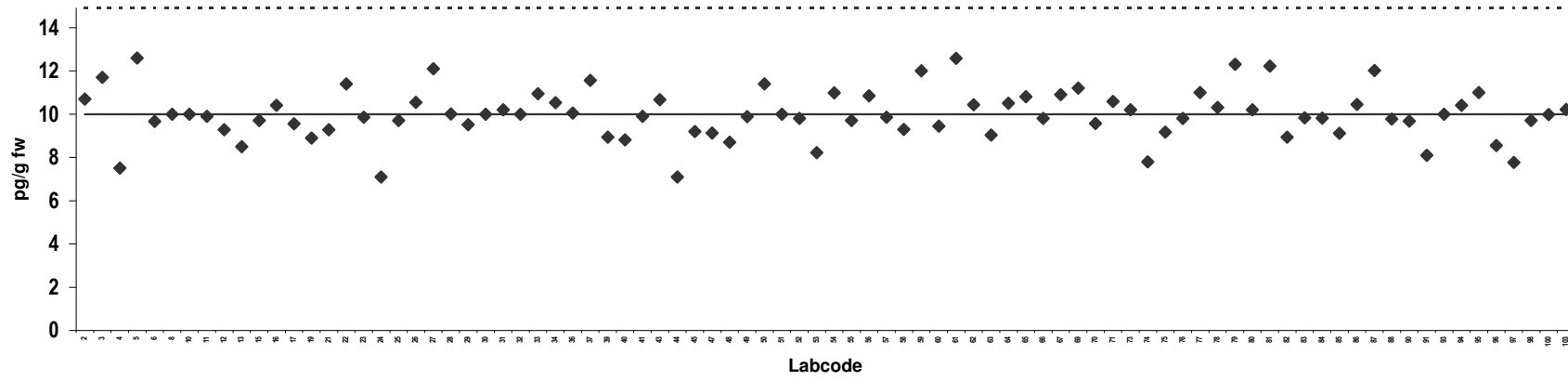
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	11		56	11	
3	12		57	9.9	
4	7.5		58	9.3	
5	13		59	12	
6	9.7		60	9.5	
8	10		61	13	
10	10		62	10	
11	9.9		63	9.0	
12	9.3		64	11	
13	8.5		65	11	
15	9.7		66	9.8	
16	10		67	11	
17	9.6		69	11	
19	8.9		70	9.6	
21	9.3		71	11	
22	11		73	10	
23	9.9		74	7.8	
24	7.1		75	9.2	
25	9.7		76	9.8	
26	11		77	11	
27	12		78	10	
28	10		79	12	
29	9.5		80	10	
30	10		81	12	
31	10		82	8.9	
32	10		83	9.8	
33	11		84	9.8	
34	11		85	9.1	
36	10		86	10	
37	12		87	12	
39	8.9		88	9.8	
40	8.8		90	9.7	
41	9.9		91	8.1	
43	11		93	10	
44	7.1		94	10	
45	9.2		95	11	
47	9.1		96	8.6	
48	8.7		97	7.8	
49	9.9		98	9.7	
50	11		100	10	
51	10		103	10	
52	9.8				
53	8.2				
54	11				
55	9.7				

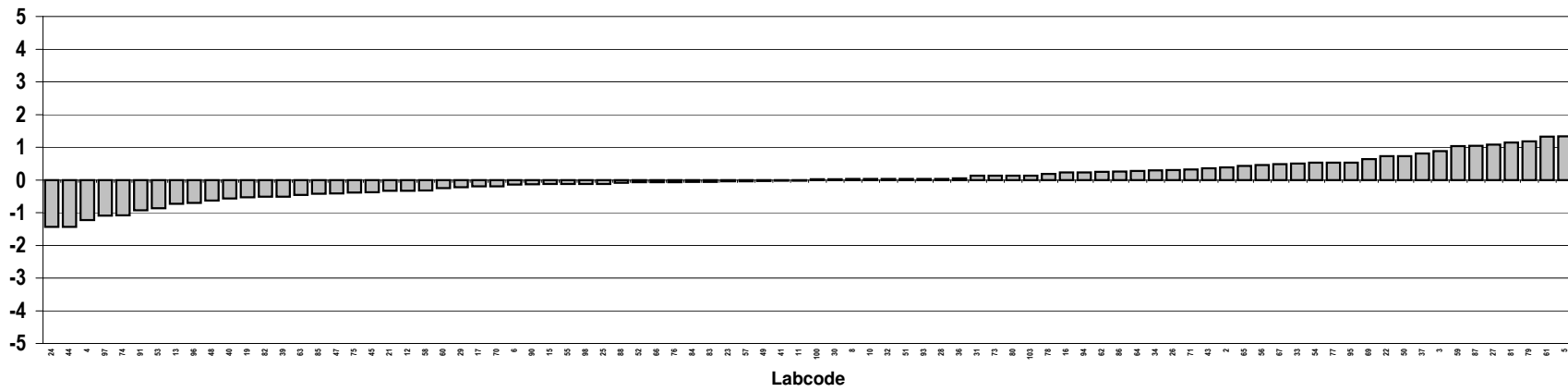
### Consensus statistics

Consensus median, pg/g	9.9
Median all values pg/g	9.9
Consensus mean, pg/g	10
Standard deviation, pg/g	1.2
Relative standard deviation, %	12
No. of values reported	86
No. of values removed	0
No. of reported non-detects	0

### OCDF



### Z-score: OCDF



## Analyte solution

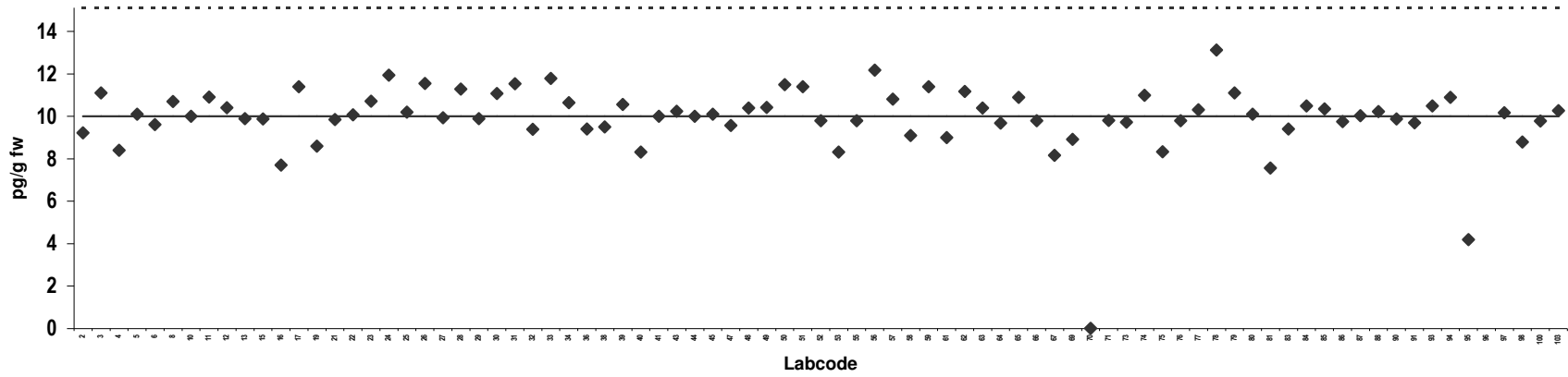
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	9.2		57	11	
3	11		58	9.1	
4	8.4		59	11	
5	10		61	9.0	
6	9.6		62	11	
8	11		63	10	
10	10		64	9.7	
11	11		65	11	
12	10		66	9.8	
13	9.9		67	8.2	
15	9.9		69	8.9	
16	7.7		70	0.011	Outlier
17	11		71	9.8	
19	8.6		73	9.7	
21	9.9		74	11	
22	10		75	8.3	
23	11		76	9.8	
24	12		77	10	
25	10		78	13	
26	12		79	11	
27	9.9		80	10	
28	11		81	7.6	
29	9.9		83	9.4	
30	11		84	11	
31	12		85	10	
32	9.4		86	9.8	
33	12		87	10	
34	11		88	10	
36	9.4		90	9.9	
38	9.5		91	9.7	
39	11		93	11	
40	8.3		94	11	
41	10		95	4.2	Outlier
43	10		96	21	Outlier
44	10		97	10	
45	10		98	8.8	
47	9.6		100	9.8	
48	10		103	10	
49	10				
50	12				
51	11				
52	9.8				
53	8.3				
55	9.8				
56	12				

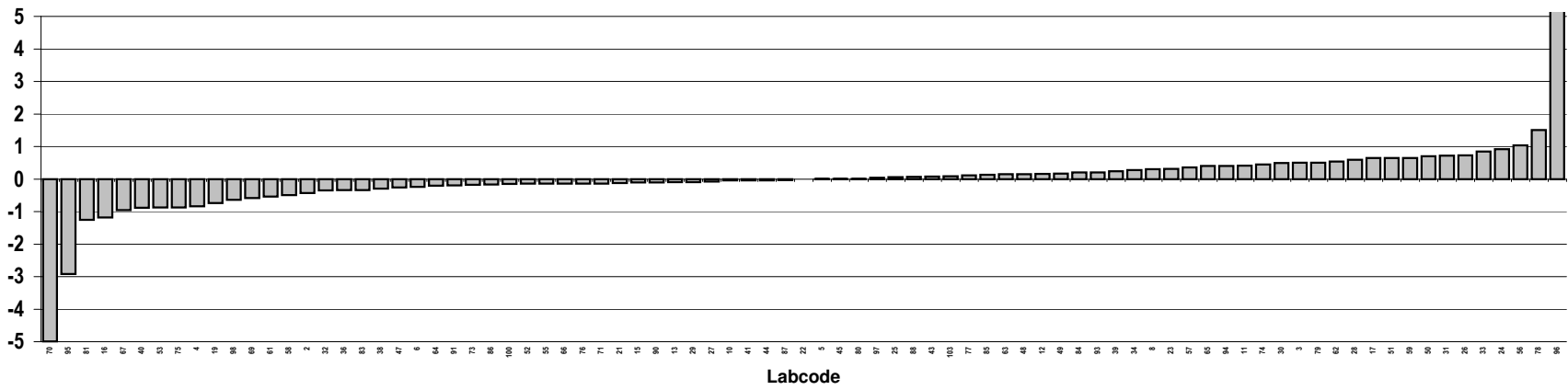
### Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	1.0
Relative standard deviation, %	10
No. of values reported	83
No. of values removed	3
No. of reported non-detects	0

### PCB 77



### Z-score: PCB 77



## Analyte solution

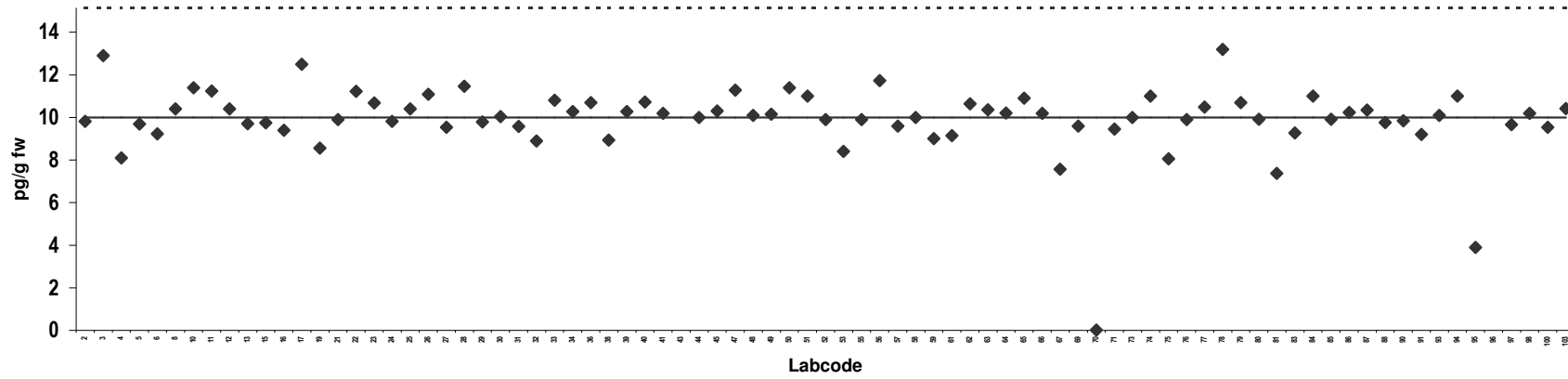
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	9.8		57	9.6	
3	13		58	10	
4	8.1		59	9.0	
5	9.7		61	9.1	
6	9.2		62	11	
8	10		63	10	
10	11		64	10	
11	11		65	11	
12	10		66	10	
13	9.7		67	7.6	
15	9.7		69	9.6	
16	9.4		70	0.0098	Outlier
17	13		71	9.4	
19	8.6		73	10	
21	9.9		74	11	
22	11		75	8.1	
23	11		76	9.9	
24	9.8		77	10	
25	10		78	13	
26	11		79	11	
27	9.5		80	9.9	
28	11		81	7.4	
29	9.8		83	9.3	
30	10		84	11	
31	9.6		85	9.9	
32	8.9		86	10	
33	11		87	10	
34	10		88	9.8	
36	11		90	9.8	
38	8.9		91	9.2	
39	10		93	10	
40	11		94	11	
41	10		95	3.9	Outlier
43	9.4	Outlier	96	21	Outlier
44	10		97	9.7	
45	10		98	10	
47	11		100	9.5	
48	10		103	10	
49	10				
50	11				
51	11				
52	9.9				
53	8.4				
55	9.9				
56	12				

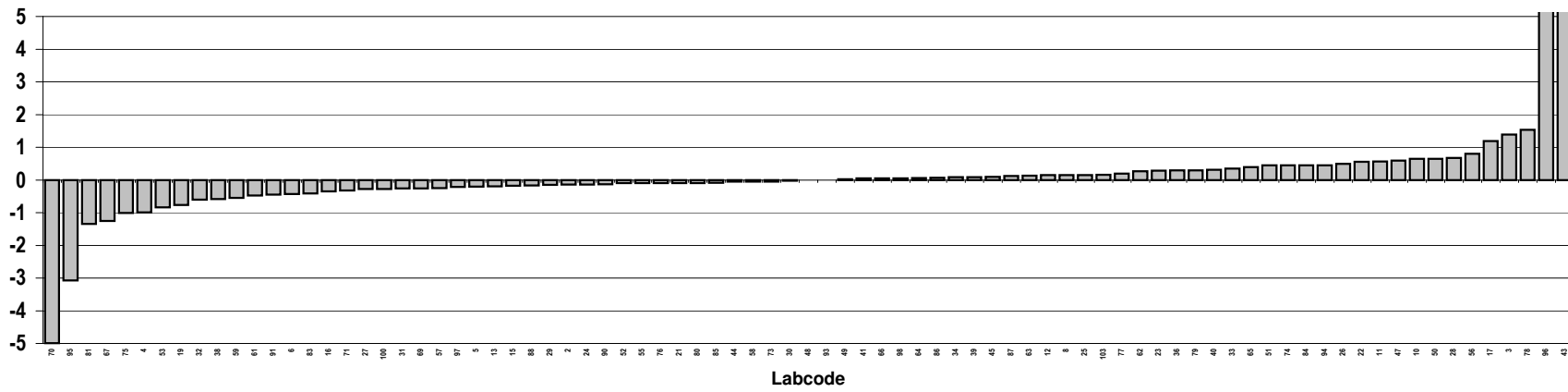
### Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	1.0
Relative standard deviation, %	10
No. of values reported	83
No. of values removed	4
No. of reported non-detects	0

### PCB 126



### Z-score: PCB 126



## Analyte solution

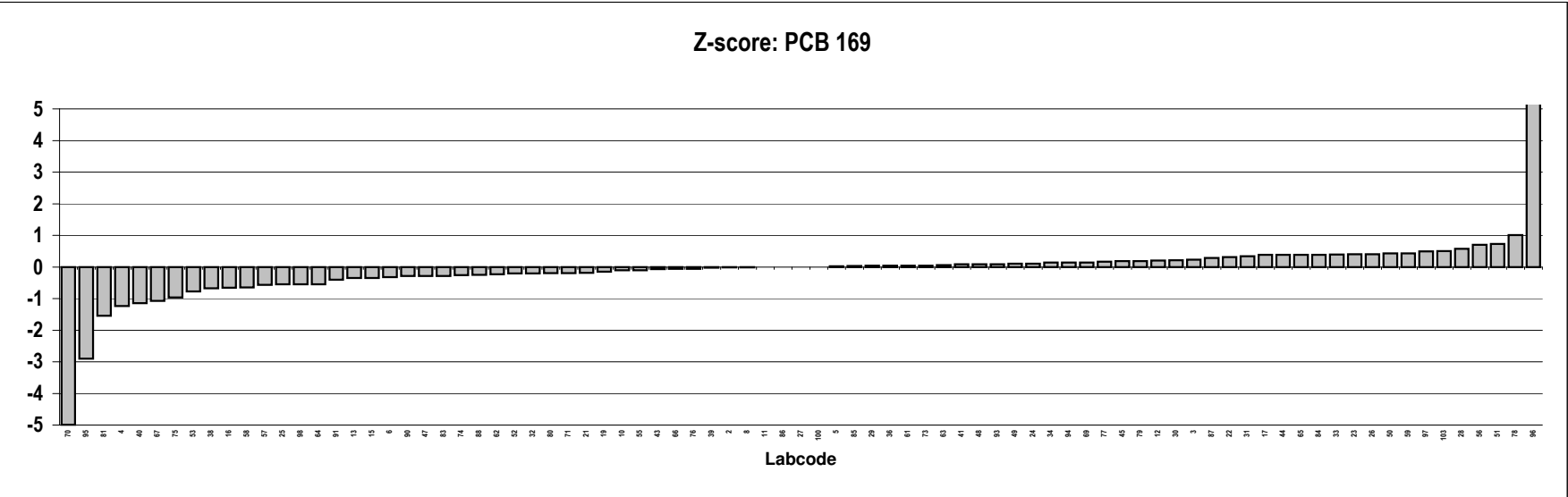
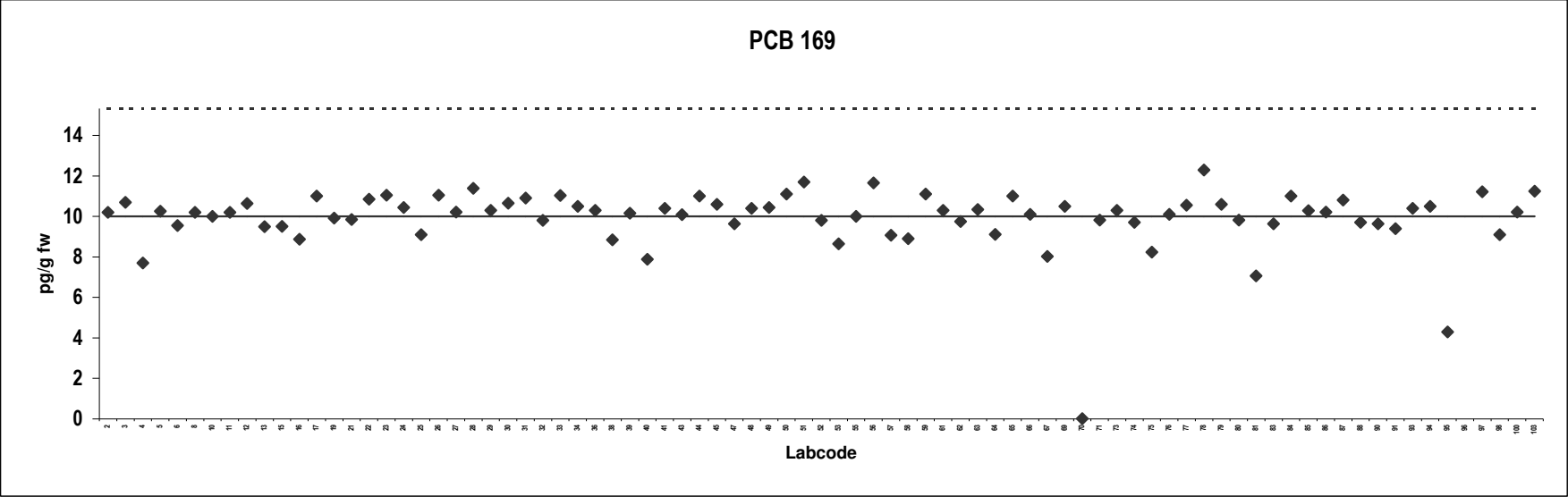
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	10		57	9.1	
3	11		58	8.9	
4	7.7		59	11	
5	10		61	10	
6	9.6		62	9.7	
8	10		63	10	
10	10		64	9.1	
11	10		65	11	
12	11		66	10	
13	9.5		67	8.0	
15	9.5		69	11	
16	8.9		70	0.0094	Outlier
17	11		71	9.8	
19	9.9		73	10	
21	9.8		74	9.7	
22	11		75	8.2	
23	11		76	10	
24	10		77	11	
25	9.1		78	12	
26	11		79	11	
27	10		80	9.8	
28	11		81	7.1	
29	10		83	9.6	
30	11		84	11	
31	11		85	10	
32	9.8		86	10	
33	11		87	11	
34	11		88	9.7	
36	10		90	9.6	
38	8.8		91	9.4	
39	10		93	10	
40	7.9		94	11	
41	10		95	4.3	Outlier
43	10		96	22	Outlier
44	11		97	11	
45	11		98	9.1	
47	9.6		100	10	
48	10		103	11	
49	10				
50	11				
51	12				
52	9.8				
53	8.6				
55	10				
56	12				

### Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.93
Relative standard deviation, %	9.2
No. of values reported	83
No. of values removed	3
No. of reported non-detects	0





## Analyte solution

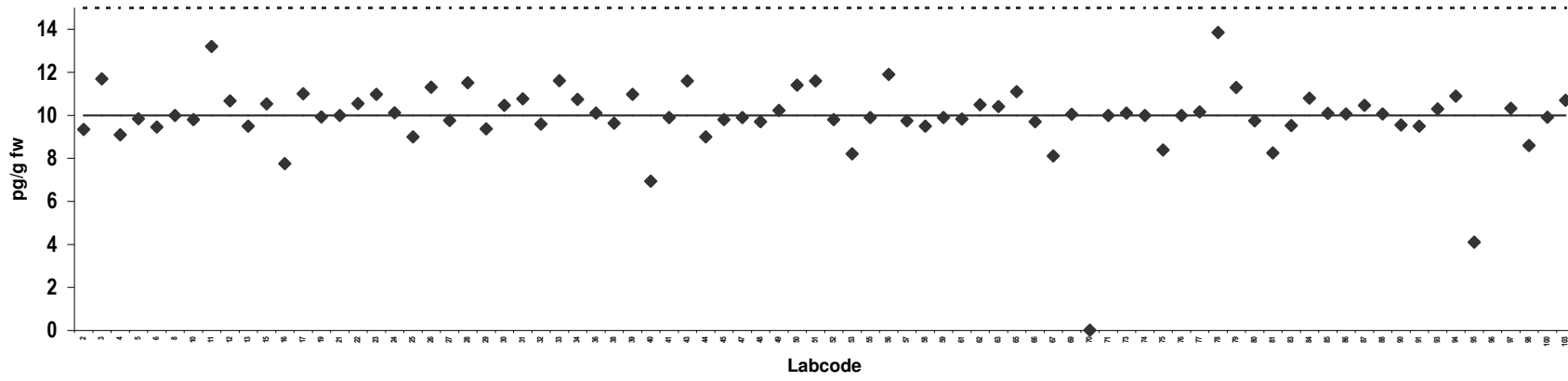
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	9.3		57	9.8	
3	12		58	9.5	
4	9.1		59	9.9	
5	9.8		61	9.8	
6	9.5		62	10	
8	10		63	10	
10	9.8		65	11	
11	13		66	9.7	
12	11		67	8.1	
13	9.5		69	10	
15	11		70	0.010	Outlier
16	7.8		71	10	
17	11		73	10	
19	9.9		74	10	
21	10		75	8.4	
22	11		76	10	
23	11		77	10	
24	10		78	14	
25	9.0		79	11	
26	11		80	9.8	
27	9.8		81	8.3	
28	12		83	9.5	
29	9.4		84	11	
30	10		85	10	
31	11		86	10	
32	9.6		87	10	
33	12		88	10	
34	11		90	9.6	
36	10		91	9.5	
38	9.6		93	10	
39	11		94	11	
40	6.9		95	4.1	Outlier
41	9.9		96	21	Outlier
43	12		97	10	
44	9.0		98	8.6	
45	9.8		100	9.9	
47	9.9		103	11	
48	9.7				
49	10				
50	11				
51	12				
52	9.8				
53	8.2				
55	9.9				
56	12				

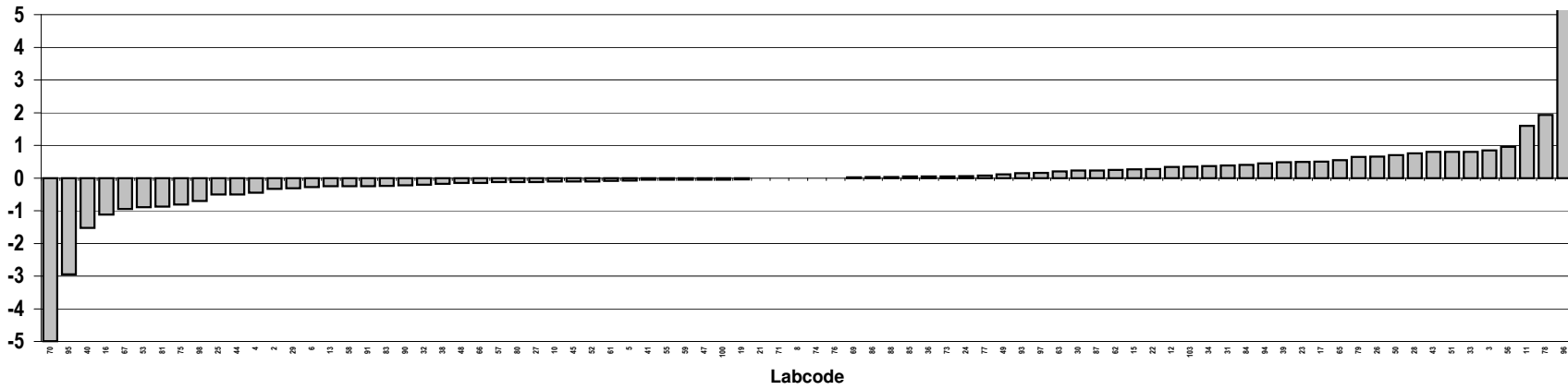
### Consensus statistics

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	1.1
Relative standard deviation, %	11
No. of values reported	82
No. of values removed	3
No. of reported non-detects	0

### PCB 81



### Z-score: PCB 81



## Analyte solution

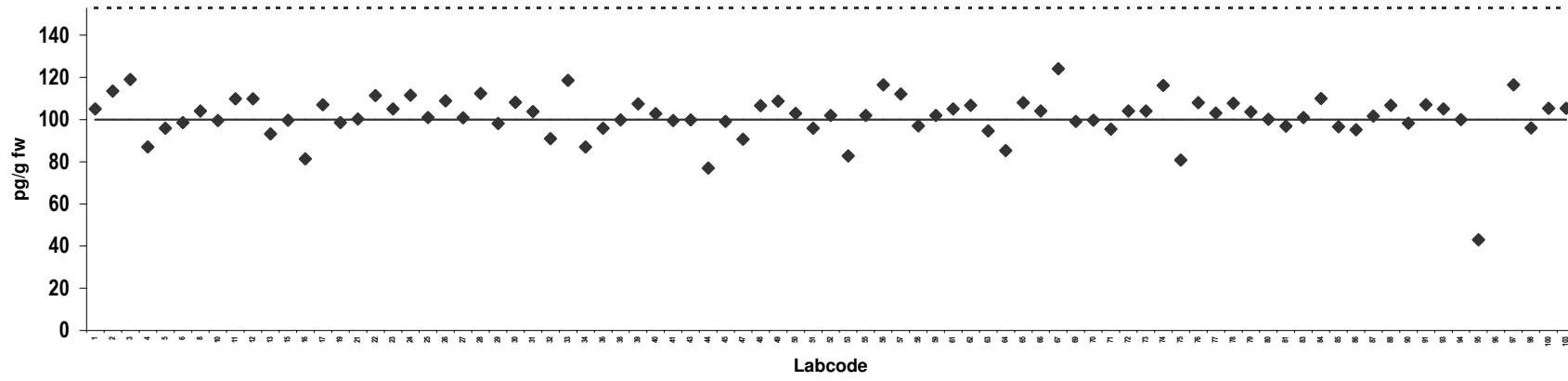
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	105		56	117	
2	114		57	112	
3	119		58	97	
4	87		59	102	
5	96		61	105	
6	99		62	107	
8	104		63	95	
10	100		64	85	
11	110		65	108	
12	110		66	104	
13	93		67	124	
15	100		69	99	
16	81		70	100	
17	107		71	95	
19	99		72	104	
21	100		73	104	
22	111		74	116	
23	105		75	81	
24	112		76	108	
25	101		77	103	
26	109		78	108	
27	101		79	104	
28	112		80	100	
29	98		81	97	
30	108		83	101	
31	104		84	110	
32	91		85	97	
33	119		86	95	
34	87		87	102	
36	96		88	107	
38	100		90	98	
39	107		91	107	
40	103		93	105	
41	100		94	100	
43	100		95	43	Outlier
44	77		96	219	Outlier
45	99		97	116	
47	91		98	96	
48	107		100	105	
49	109		103	105	
50	103				
51	96				
52	102				
53	83				
55	102				

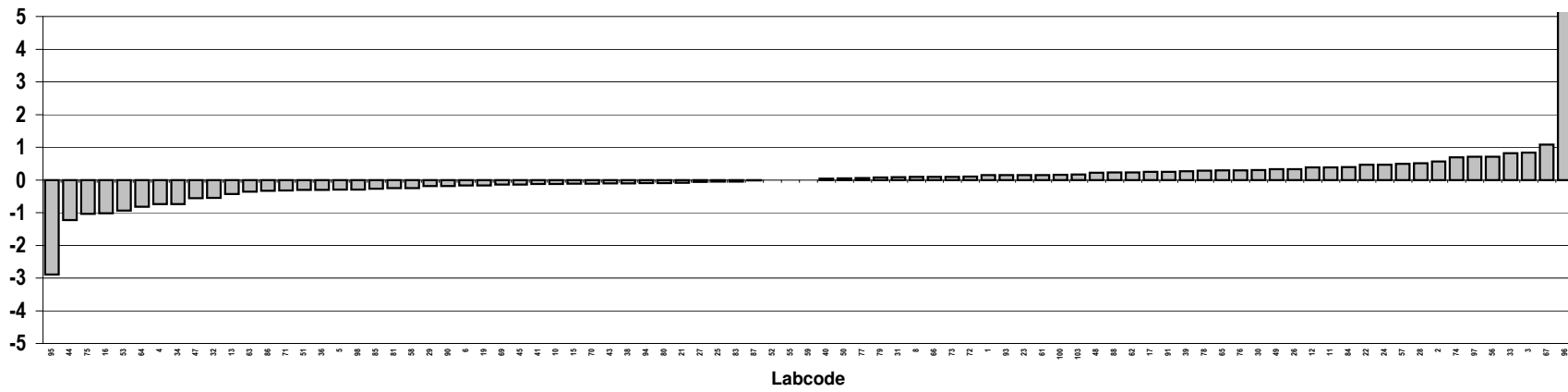
### Consensus statistics

Consensus median, pg/g	102
Median all values pg/g	102
Consensus mean, pg/g	102
Standard deviation, pg/g	8.7
Relative standard deviation, %	8.6
No. of values reported	85
No. of values removed	2
No. of reported non-detects	0

### PCB 105



### Z-score: PCB 105



## Analyte solution

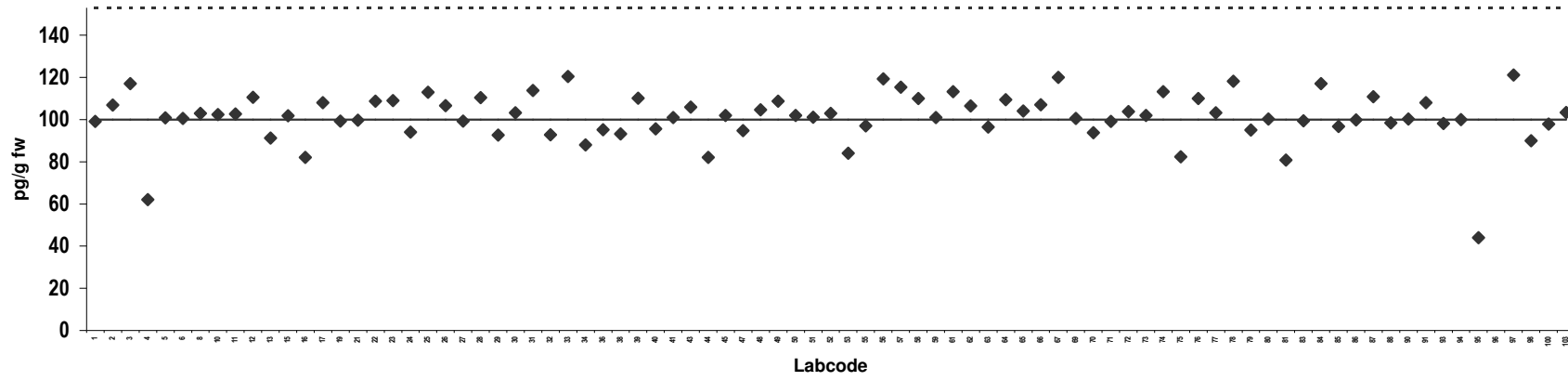
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	99		56	119	
2	107		57	115	
3	117		58	110	
4	62		59	101	
5	101		61	113	
6	101		62	106	
8	103		63	96	
10	102		64	109	
11	103		65	104	
12	110		66	107	
13	91		67	120	
15	102		69	101	
16	82		70	94	
17	108		71	99	
19	99		72	104	
21	100		73	102	
22	109		74	113	
23	109		75	82	
24	94		76	110	
25	113		77	103	
26	107		78	118	
27	99		79	95	
28	110		80	100	
29	93		81	81	
30	103		83	99	
31	114		84	117	
32	93		85	97	
33	120		86	100	
34	88		87	111	
36	95		88	98	
38	93		90	100	
39	110		91	108	
40	96		93	98	
41	101		94	100	
43	106		95	44	Outlier
44	82		96	220	Outlier
45	102		97	121	
47	95		98	90	
48	105		100	98	
49	109		103	103	
50	102				
51	101				
52	103				
53	84				
55	97				

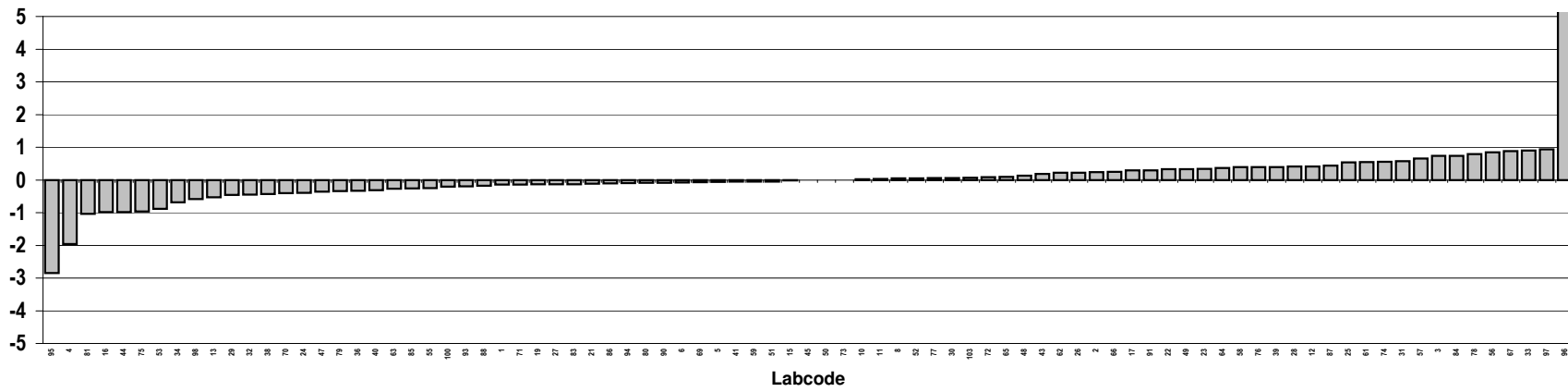
### Consensus statistics

Consensus median, pg/g	102
Median all values pg/g	102
Consensus mean, pg/g	102
Standard deviation, pg/g	10
Relative standard deviation, %	9.9
No. of values reported	85
No. of values removed	2
No. of reported non-detects	0

### PCB 114



### Z-score: PCB 114



## Analyte solution

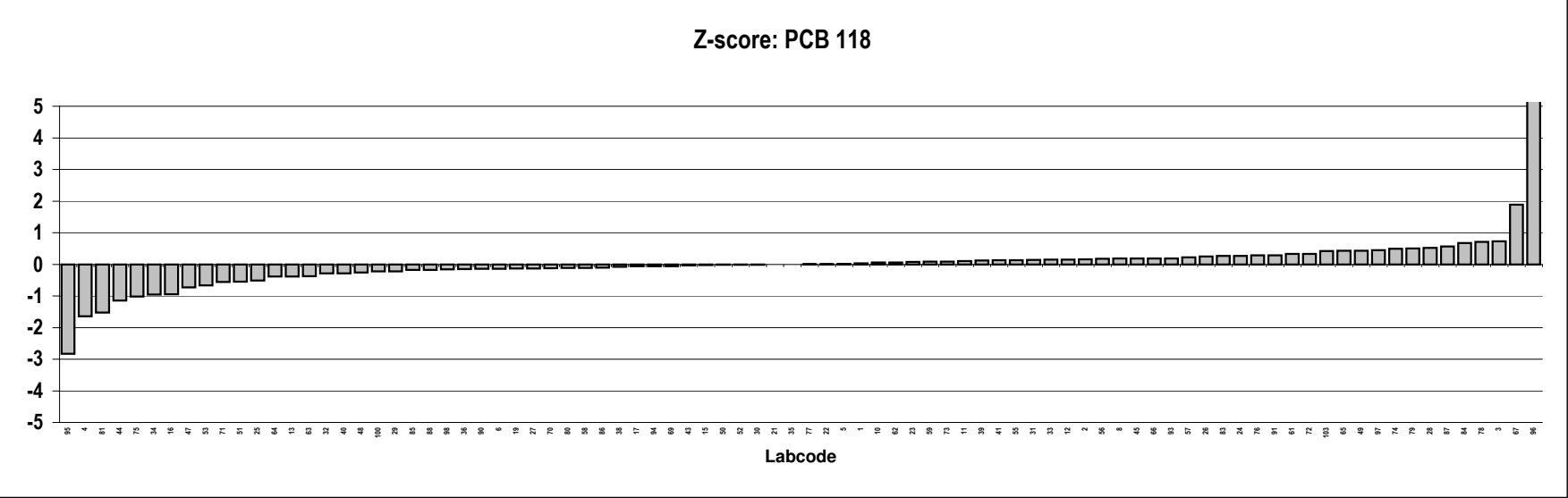
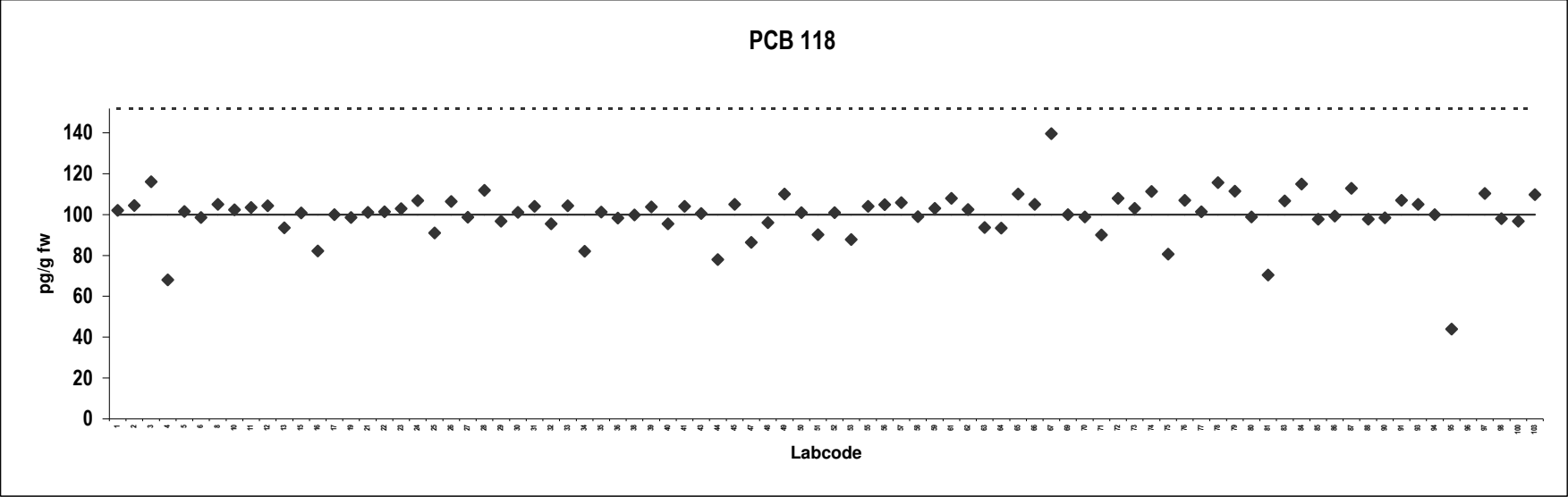
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	102		55	104	
2	105		56	105	
3	116		57	106	
4	68		58	99	
5	102		59	103	
6	99		61	108	
8	105		62	103	
10	102		63	94	
11	103		64	93	
12	104		65	110	
13	94		66	105	
15	101		67	140	
16	82		69	100	
17	100		70	99	
19	99		71	90	
21	101		72	108	
22	101		73	103	
23	103		74	111	
24	107		75	81	
25	91		76	107	
26	106		77	101	
27	99		78	116	
28	112		79	111	
29	97		80	99	
30	101		81	70	
31	104		83	107	
32	95		84	115	
33	104		85	98	
34	82		86	99	
35	101		87	113	
36	98		88	98	
38	100		90	98	
39	104		91	107	
40	96		93	105	
41	104		94	100	
43	101		95	44	Outlier
44	78		96	208	Outlier
45	105		97	110	
47	86		98	98	
48	96		100	97	
49	110		103	110	
50	101				
51	90				
52	101				
53	88				

### Consensus statistics

Consensus median, pg/g	101
Median all values pg/g	101
Consensus mean, pg/g	101
Standard deviation, pg/g	9.9
Relative standard deviation, %	9.8
No. of values reported	86
No. of values removed	2
No. of reported non-detects	0





## Analyte solution

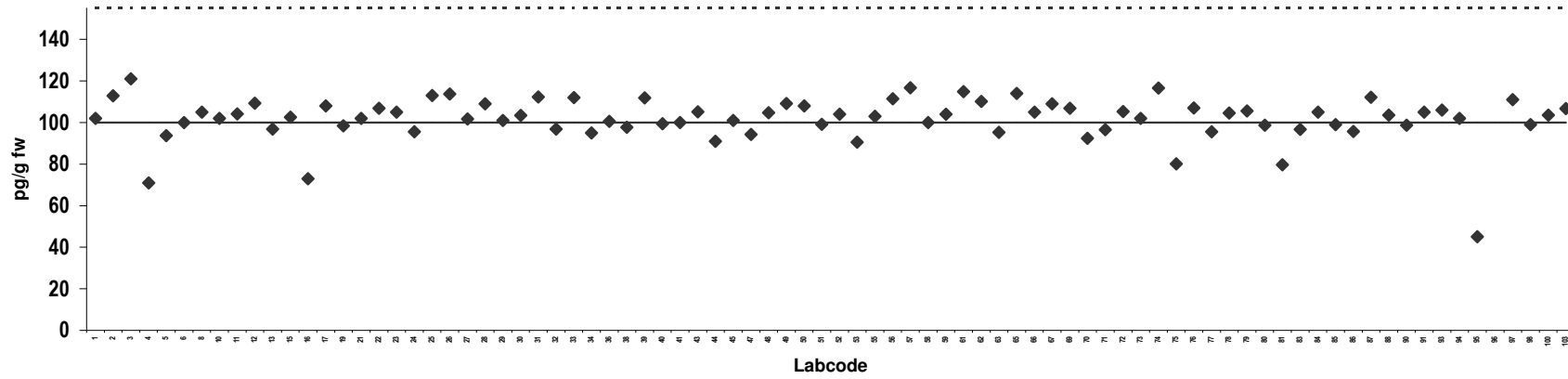
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	102		56	111	
2	113		57	117	
3	121		58	100	
4	71		59	104	
5	94		61	115	
6	100		62	110	
8	105		63	95	
10	102		65	114	
11	104		66	105	
12	109		67	109	
13	97		69	107	
15	103		70	92	
16	73		71	97	
17	108		72	105	
19	98		73	102	
21	102		74	117	
22	107		75	80	
23	105		76	107	
24	96		77	96	
25	113		78	104	
26	114		79	106	
27	102		80	99	
28	109		81	80	
29	101		83	97	
30	103		84	105	
31	112		85	99	
32	97		86	96	
33	112		87	112	
34	95		88	104	
36	101		90	99	
38	98		91	105	
39	112		93	106	
40	99		94	102	
41	100		95	45	Outlier
43	105		96	235	Outlier
44	91		97	111	
45	101		98	99	
47	94		100	104	
48	105		103	107	
49	109				
50	108				
51	99				
52	104				
53	91				
55	103				

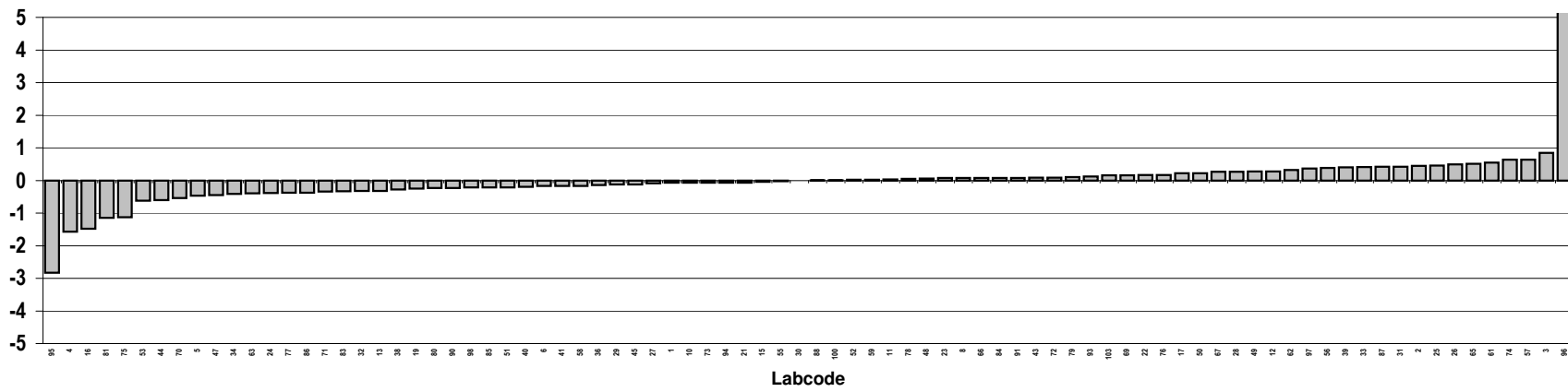
### Consensus statistics

Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	102
Standard deviation, pg/g	8.8
Relative standard deviation, %	8.6
No. of values reported	84
No. of values removed	2
No. of reported non-detects	0

### PCB 123



### Z-score: PCB 123



## Analyte solution

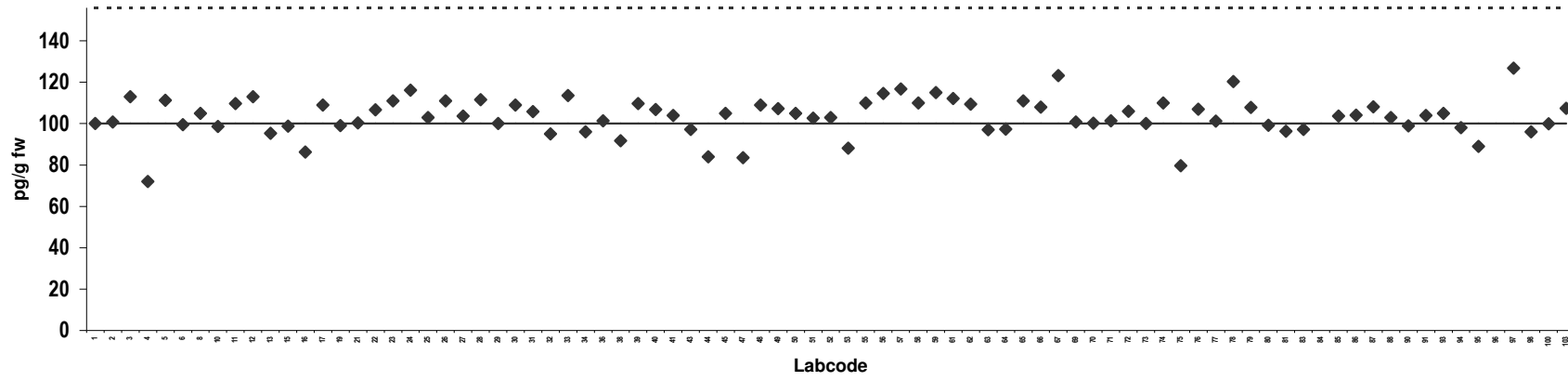
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	100		56	115	
2	101		57	117	
3	113		58	110	
4	72		59	115	
5	111		61	112	
6	100		62	109	
8	105		63	97	
10	99		64	97	
11	110		65	111	
12	113		66	108	
13	95		67	123	
15	99		69	101	
16	86		70	100	
17	109		71	101	
19	99		72	106	
21	100		73	100	
22	107		74	110	
23	111		75	80	
24	116		76	107	
25	103		77	101	
26	111		78	120	
27	104		79	108	
28	112		80	99	
29	100		81	96	
30	109		83	97	
31	106		84	226	Outlier
32	95		85	104	
33	114		86	104	
34	96		87	108	
36	101		88	103	
38	92		90	99	
39	110		91	104	
40	107		93	105	
41	104		94	98	
43	97		95	89	
44	84		96	228	Outlier
45	105		97	127	
47	84		98	96	
48	109		100	100	
49	107		103	107	
50	105				
51	103				
52	103				
53	88				
55	110				

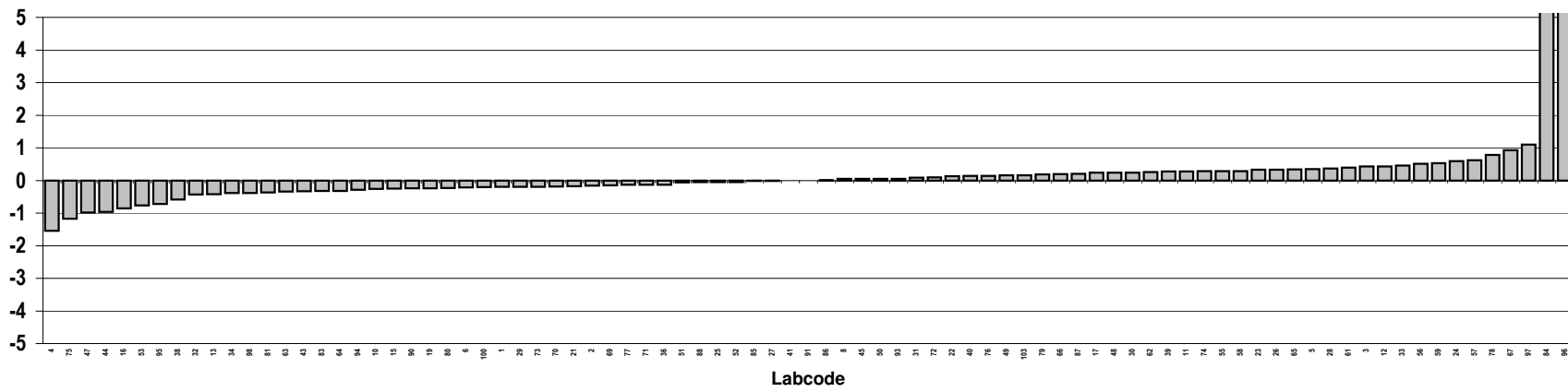
### Consensus statistics

Consensus median, pg/g	104
Median all values pg/g	104
Consensus mean, pg/g	103
Standard deviation, pg/g	9.1
Relative standard deviation, %	8.8
No. of values reported	85
No. of values removed	2
No. of reported non-detects	0

### PCB 156



### Z-score: PCB 156



## Analyte solution

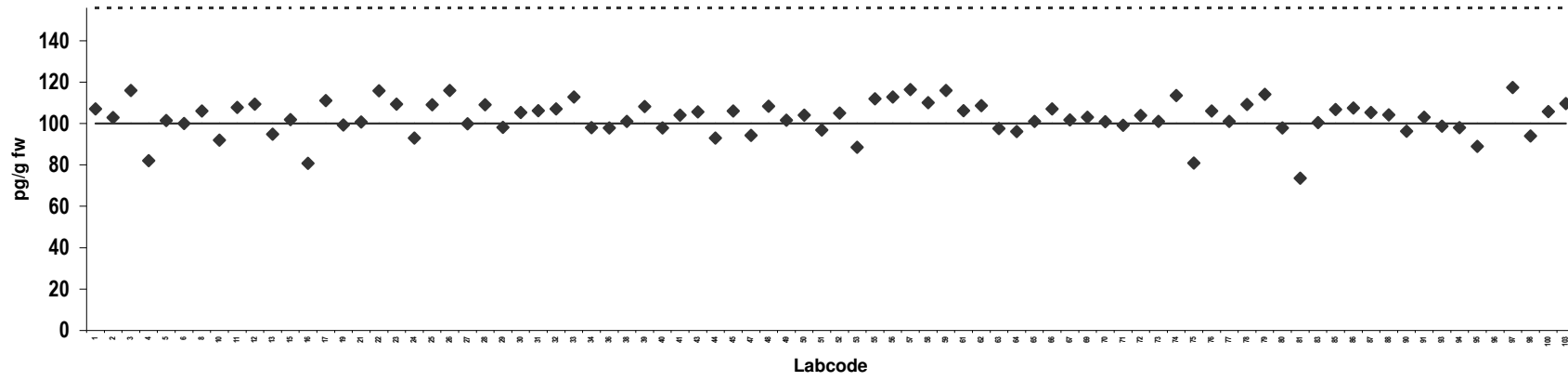
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	107		56	113	
2	103		57	116	
3	116		58	110	
4	82		59	116	
5	102		61	106	
6	100		62	109	
8	106		63	98	
10	92		64	96	
11	108		65	101	
12	109		66	107	
13	95		67	102	
15	102		69	103	
16	81		70	101	
17	111		71	99	
19	99		72	104	
21	101		73	101	
22	116		74	113	
23	109		75	81	
24	93		76	106	
25	109		77	101	
26	116		78	109	
27	100		79	114	
28	109		80	98	
29	98		81	74	
30	105		83	100	
31	106		85	107	
32	107		86	108	
33	113		87	105	
34	98		88	104	
36	98		90	96	
38	101		91	103	
39	108		93	99	
40	98		94	98	
41	104		95	89	
43	106		96	224	Outlier
44	93		97	117	
45	106		98	94	
47	94		100	106	
48	108		103	110	
49	102				
50	104				
51	97				
52	105				
53	88				
55	112				

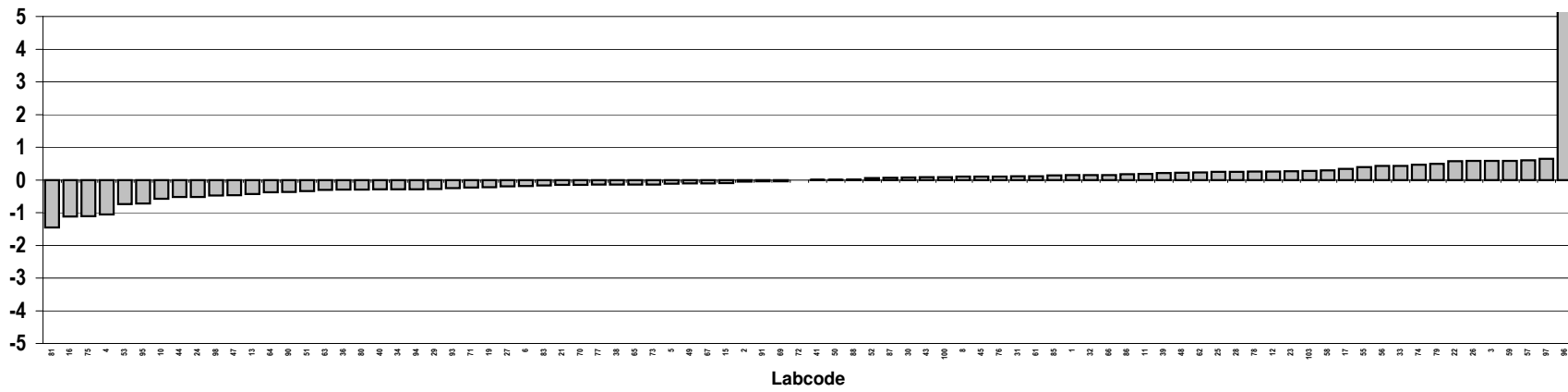
### Consensus statistics

Consensus median, pg/g	104
Median all values pg/g	104
Consensus mean, pg/g	103
Standard deviation, pg/g	8.4
Relative standard deviation, %	8.2
No. of values reported	84
No. of values removed	1
No. of reported non-detects	0

### PCB 157



### Z-score: PCB 157



## Analyte solution

Congener: PCB 167

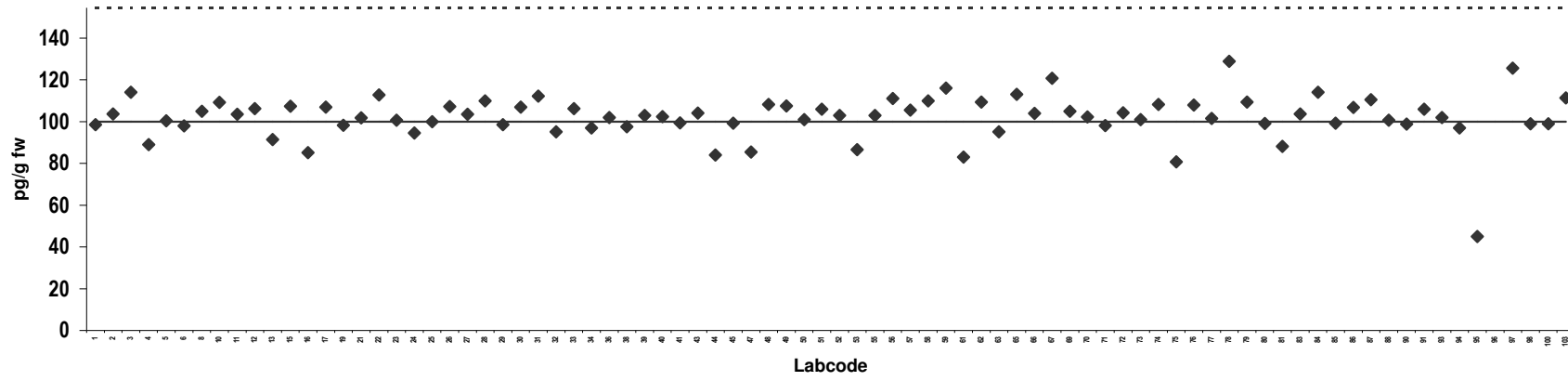
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	99		56	111	
2	104		57	106	
3	114		58	110	
4	89		59	116	
5	100		61	83	
6	98		62	109	
8	105		63	95	
10	109		65	113	
11	104		66	104	
12	106		67	121	
13	91		69	105	
15	107		70	102	
16	85		71	98	
17	107		72	104	
19	98		73	101	
21	102		74	108	
22	113		75	81	
23	101		76	108	
24	95		77	102	
25	100		78	129	
26	107		79	109	
27	104		80	99	
28	110		81	88	
29	99		83	104	
30	107		84	114	
31	112		85	99	
32	95		86	107	
33	106		87	111	
34	97		88	101	
36	102		90	99	
38	98		91	106	
39	103		93	102	
40	102		94	97	
41	99		95	45	Outlier
43	104		96	230	Outlier
44	84		97	126	
45	99		98	99	
47	85		100	99	
48	108		103	111	
49	108				
50	101				
51	106				
52	103				
53	87				
55	103				

### Consensus statistics

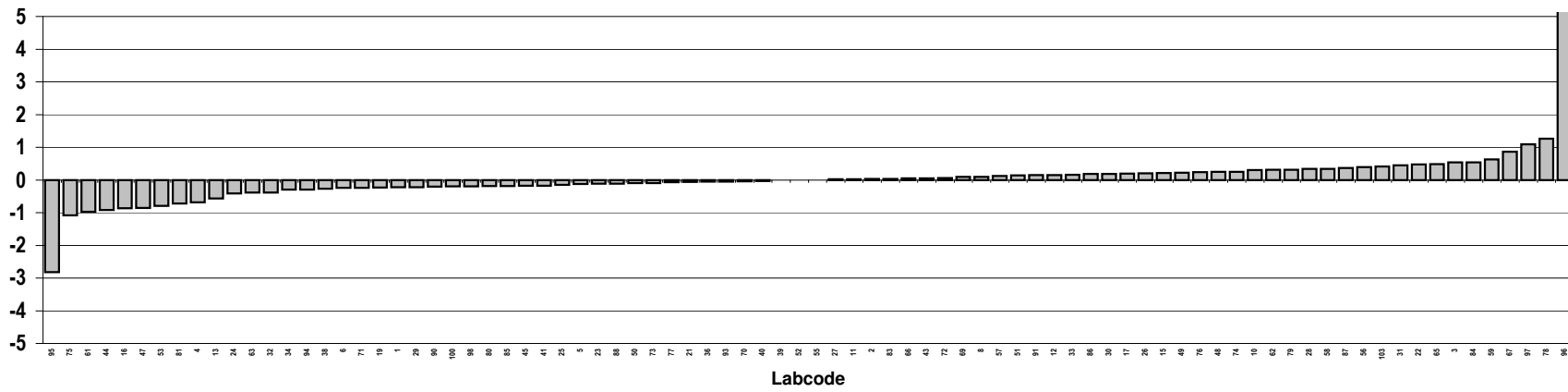
Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	103
Standard deviation, pg/g	8.7
Relative standard deviation, %	8.4
No. of values reported	84
No. of values removed	2
No. of reported non-detects	0



### PCB 167



### Z-score: PCB 167



## Analyte solution

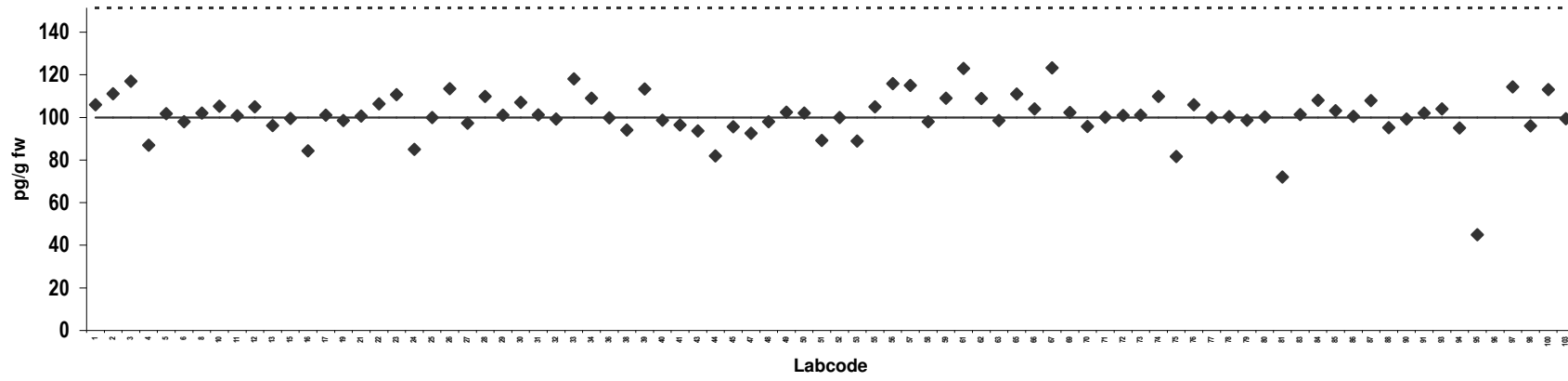
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	106		56	116	
2	111		57	115	
3	117		58	98	
4	87		59	109	
5	102		61	123	
6	98		62	109	
8	102		63	99	
10	105		65	111	
11	101		66	104	
12	105		67	123	
13	96		69	102	
15	99		70	96	
16	84		71	100	
17	101		72	101	
19	99		73	101	
21	101		74	110	
22	106		75	82	
23	111		76	106	
24	85		77	100	
25	100		78	100	
26	113		79	99	
27	97		80	100	
28	110		81	72	
29	101		83	101	
30	107		84	108	
31	101		85	103	
32	99		86	100	
33	118		87	108	
34	109		88	95	
36	100		90	99	
38	94		91	102	
39	113		93	104	
40	99		94	95	
41	96		95	45	Outlier
43	94		96	221	Outlier
44	82		97	114	
45	96		98	96	
47	93		100	113	
48	98		103	99	
49	103				
50	102				
51	89				
52	100				
53	89				
55	105				

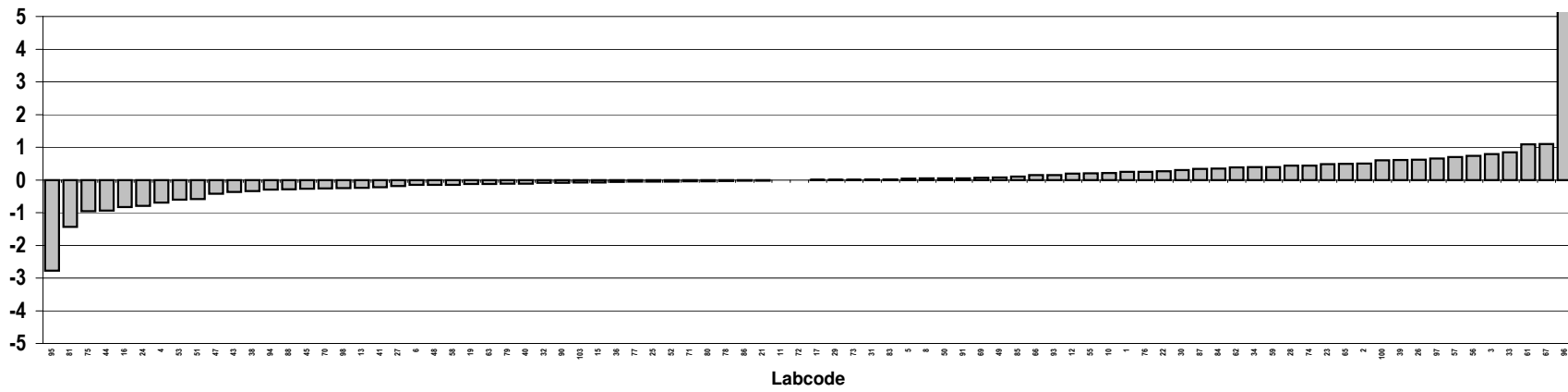
### Consensus statistics

Consensus median, pg/g	101
Median all values pg/g	101
Consensus mean, pg/g	102
Standard deviation, pg/g	9.0
Relative standard deviation, %	8.8
No. of values reported	84
No. of values removed	2
No. of reported non-detects	0

### PCB 189



### Z-score: PCB 189



## Analyte solution

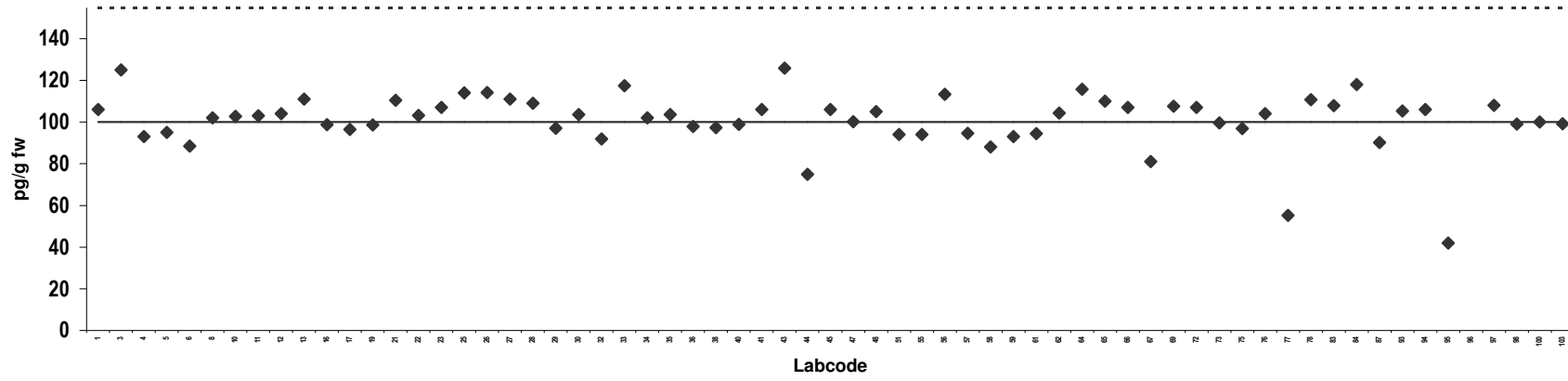
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	106		66	107	
3	125		67	81	
4	93		69	108	
5	95		72	107	
6	89		73	100	
8	102		75	97	
10	103		76	104	
11	103		77	55	
12	104		78	111	
13	111		83	108	
16	99		84	118	
17	97		87	90	
19	99		93	105	
21	110		94	106	
22	103		95	42	Outlier
23	107		96	188	Outlier
25	114		97	108	
26	114		98	99	
27	111		100	100	
28	109		103	99	
29	97				
30	104				
32	92				
33	118				
34	102				
35	104				
36	98				
38	97				
40	99				
41	106				
43	126				
44	75				
45	106				
47	100				
48	105				
51	94				
55	94				
56	113				
57	95				
58	88				
59	93				
61	95				
62	104				
64	116				
65	110				

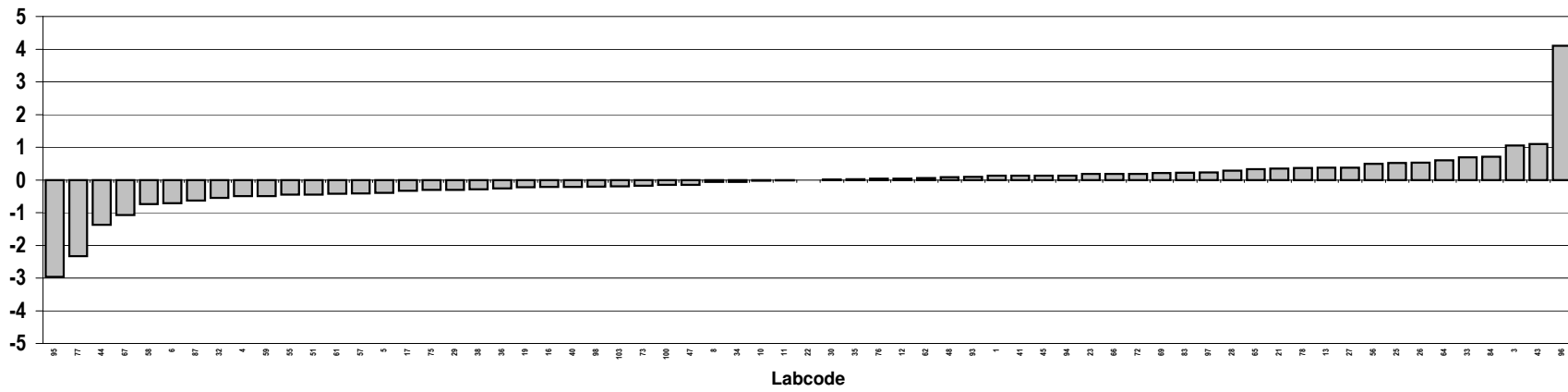
### Consensus statistics

Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	102
Standard deviation, pg/g	11
Relative standard deviation, %	11
No. of values reported	65
No. of values removed	2
No. of reported non-detects	0

### CB 28



### Z-score: CB 28



## Analyte solution

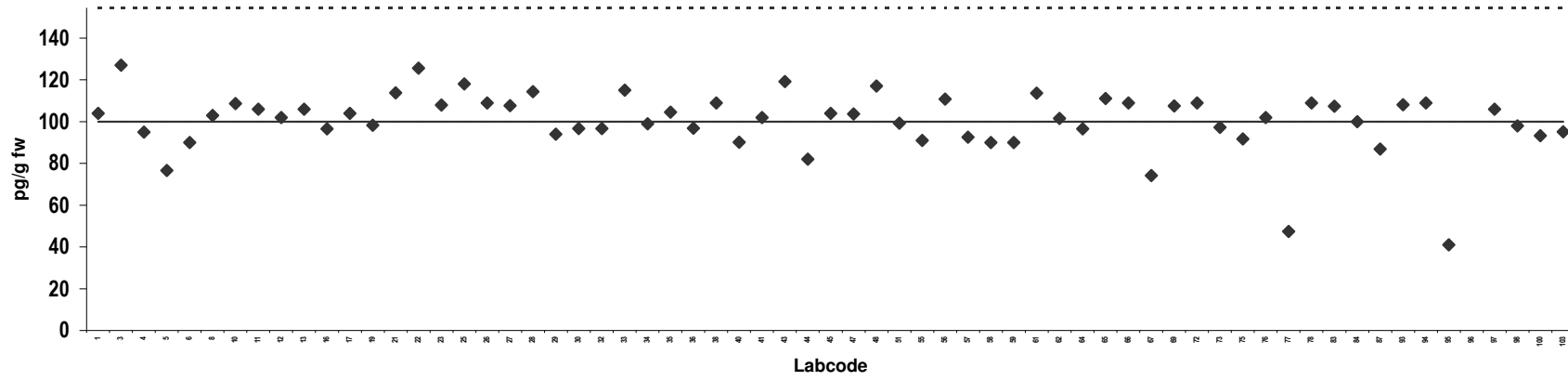
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	104		66	109	
3	127		67	74	
4	95		69	108	
5	77		72	109	
6	90		73	97	
8	103		75	92	
10	109		76	102	
11	106		77	47	Outlier
12	102		78	109	
13	106		83	107	
16	97		84	100	
17	104		87	87	
19	98		93	108	
21	114		94	109	
22	126		95	41	Outlier
23	108		96	175	Outlier
25	118		97	106	
26	109		98	98	
27	108		100	93	
28	114		103	95	
29	94				
30	97				
32	97				
33	115				
34	99				
35	105				
36	97				
38	109				
40	90				
41	102				
43	119				
44	82				
45	104				
47	104				
48	117				
51	99				
55	91				
56	111				
57	93				
58	90				
59	90				
61	114				
62	101				
64	97				
65	111				

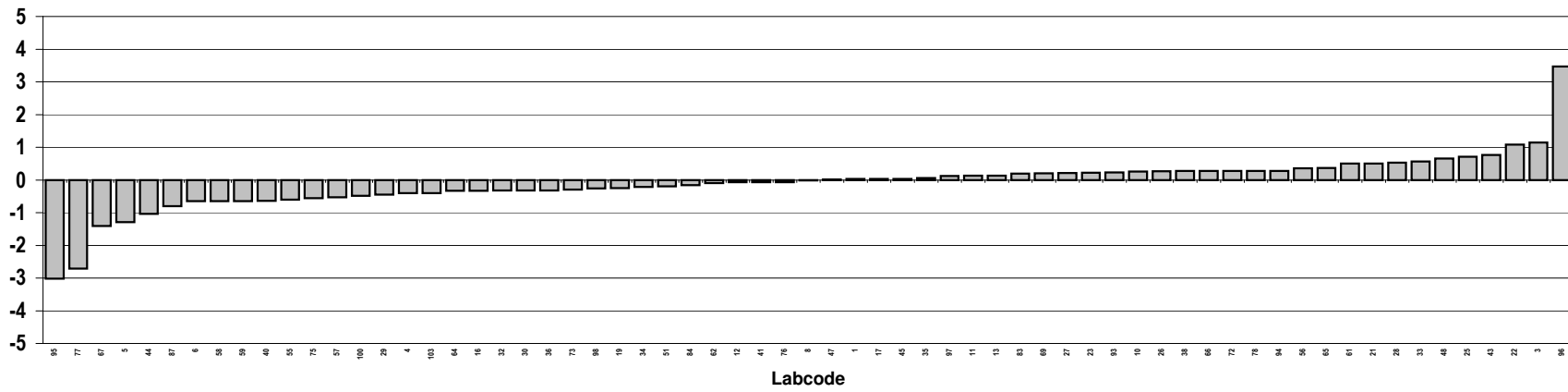
### Consensus statistics

Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	102
Standard deviation, pg/g	10
Relative standard deviation, %	10
No. of values reported	65
No. of values removed	3
No. of reported non-detects	0

### CB 52



### Z-score: CB 52



## Analyte solution

Congener: CB 101

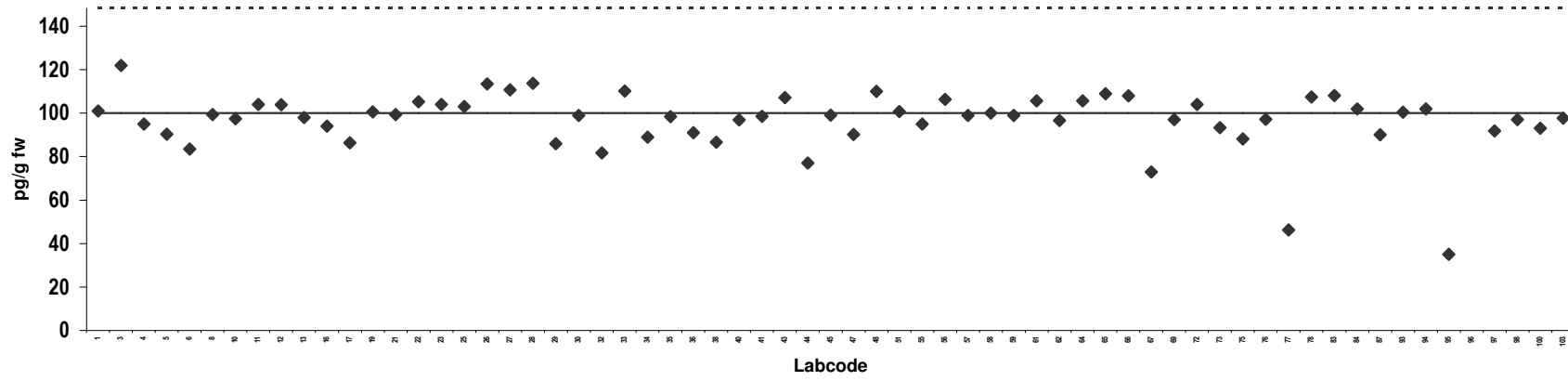
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	101		66	108	
3	122		67	73	
4	95		69	97	
5	90		72	104	
6	84		73	93	
8	99		75	88	
10	97		76	97	
11	104		77	46	Outlier
12	104		78	107	
13	98		83	108	
16	94		84	102	
17	86		87	90	
19	101		93	100	
21	99		94	102	
22	105		95	35	Outlier
23	104		96	167	Outlier
25	103		97	92	
26	113		98	97	
27	111		100	93	
28	114		103	98	
29	86				
30	99				
32	82				
33	110				
34	89				
35	98				
36	91				
38	87				
40	97				
41	99				
43	107				
44	77				
45	99				
47	90				
48	110				
51	101				
55	95				
56	106				
57	99				
58	100				
59	99				
61	106				
62	97				
64	106				
65	109				

### Consensus statistics

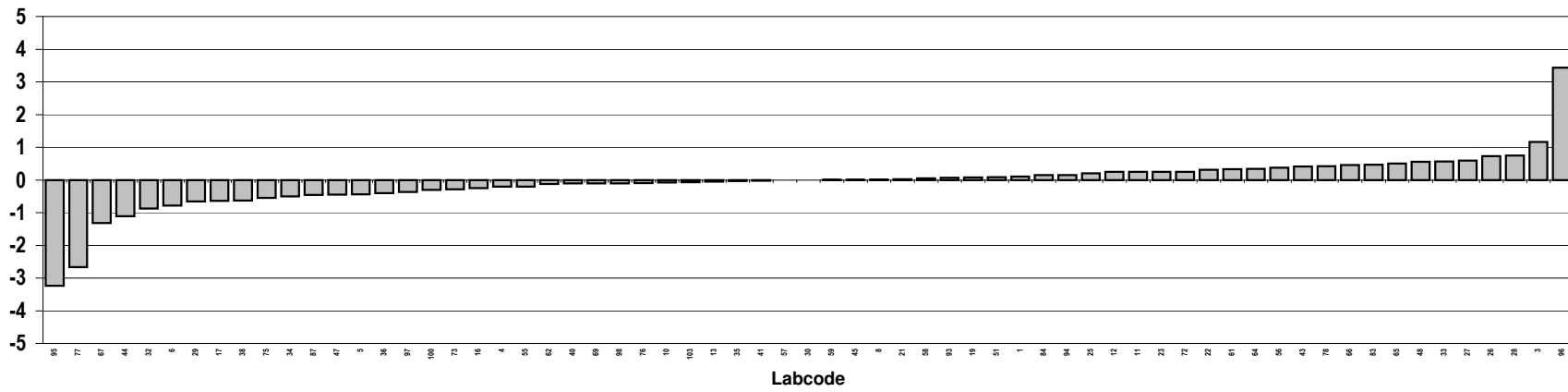
Consensus median, pg/g	99
Median all values pg/g	99
Consensus mean, pg/g	99
Standard deviation, pg/g	9.0
Relative standard deviation, %	9.1
No. of values reported	65
No. of values removed	3
No. of reported non-detects	0



### CB 101



### Z-score: CB 101



## Analyte solution

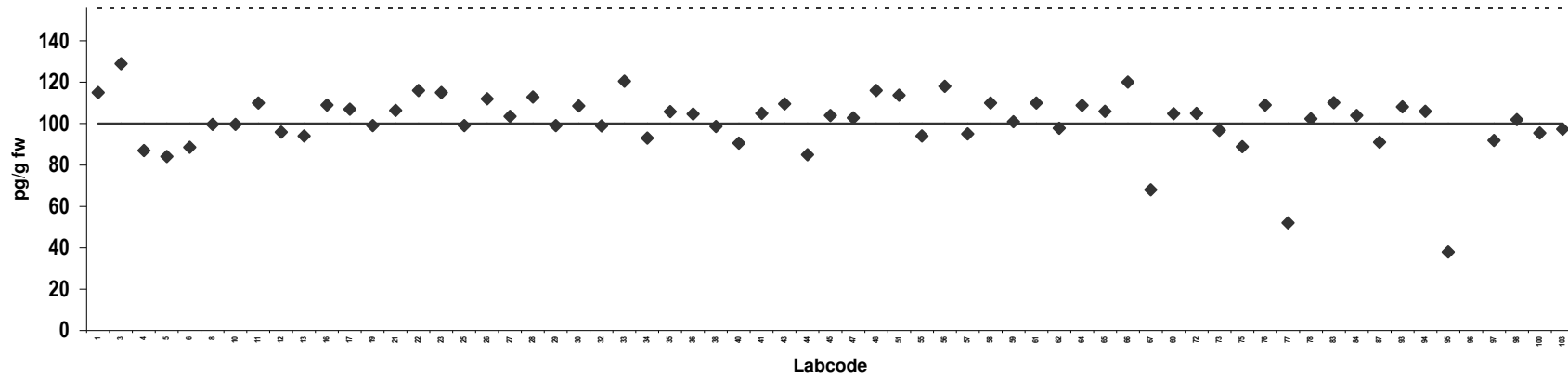
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	115		66	120	
3	129		67	68	
4	87		69	105	
5	84		72	105	
6	89		73	97	
8	100		75	89	
10	100		76	109	
11	110		77	52	
12	96		78	102	
13	94		83	110	
16	109		84	104	
17	107		87	91	
19	99		93	108	
21	106		94	106	
22	116		95	38	Outlier
23	115		96	230	Outlier
25	99		97	92	
26	112		98	102	
27	103		100	95	
28	113		103	97	
29	99				
30	109				
32	99				
33	121				
34	93				
35	106				
36	105				
38	99				
40	91				
41	105				
43	110				
44	85				
45	104				
47	103				
48	116				
51	114				
55	94				
56	118				
57	95				
58	110				
59	101				
61	110				
62	98				
64	109				
65	106				

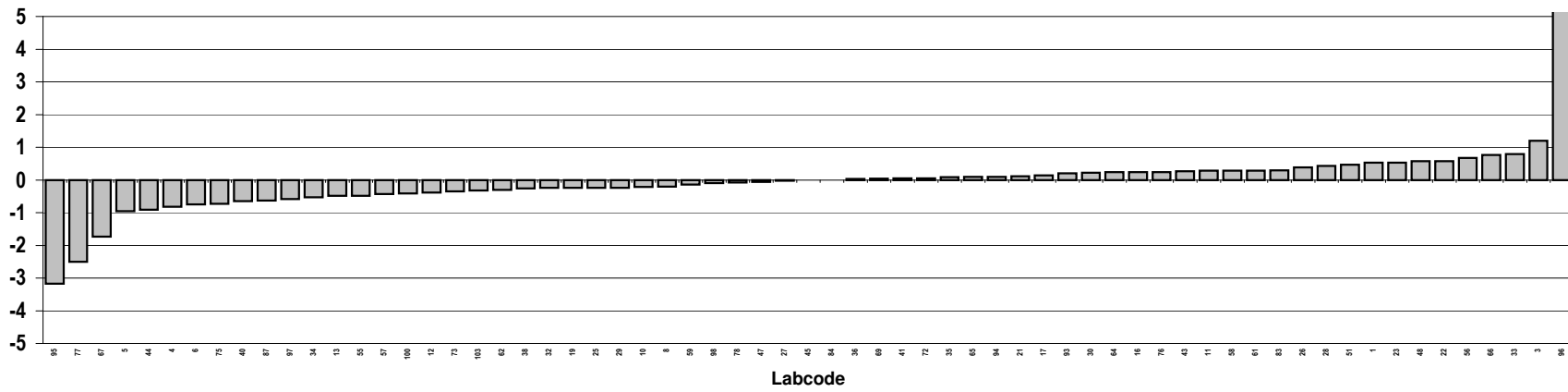
### Consensus statistics

Consensus median, pg/g	104
Median all values pg/g	104
Consensus mean, pg/g	102
Standard deviation, pg/g	12
Relative standard deviation, %	12
No. of values reported	65
No. of values removed	2
No. of reported non-detects	0

### CB 138



### Z-score: CB 138



## Analyte solution

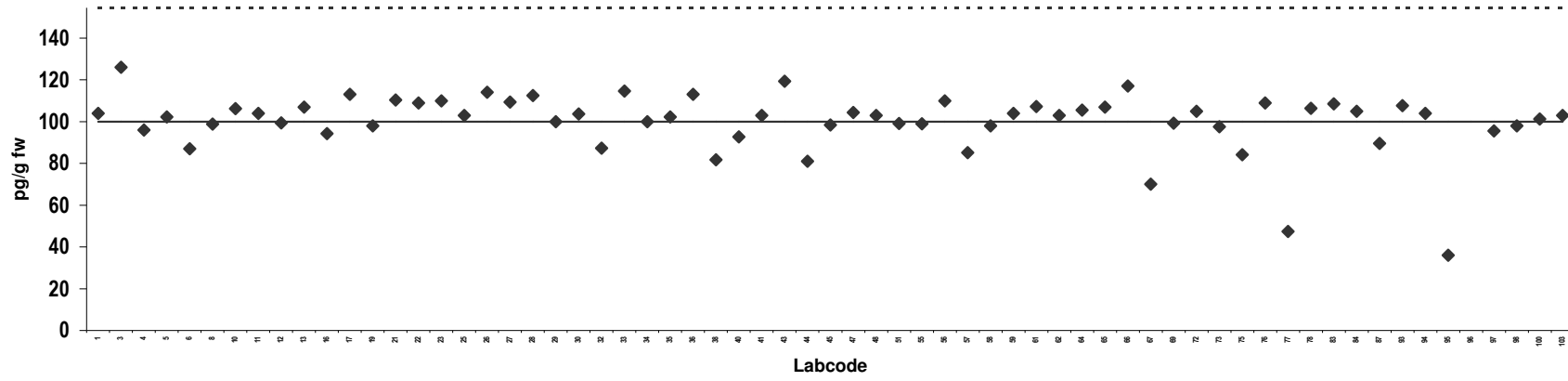
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	104		66	117	
3	126		67	70	
4	96		69	99	
5	102		72	105	
6	87		73	98	
8	99		75	84	
10	106		76	109	
11	104		77	47	Outlier
12	99		78	106	
13	107		83	109	
16	94		84	105	
17	113		87	90	
19	98		93	108	
21	110		94	104	
22	109		95	36	Outlier
23	110		96	177	Outlier
25	103		97	96	
26	114		98	98	
27	109		100	101	
28	113		103	103	
29	100				
30	104				
32	87				
33	115				
34	100				
35	102				
36	113				
38	82				
40	93				
41	103				
43	119				
44	81				
45	98				
47	104				
48	103				
51	99				
55	99				
56	110				
57	85				
58	98				
59	104				
61	107				
62	103				
64	106				
65	107				

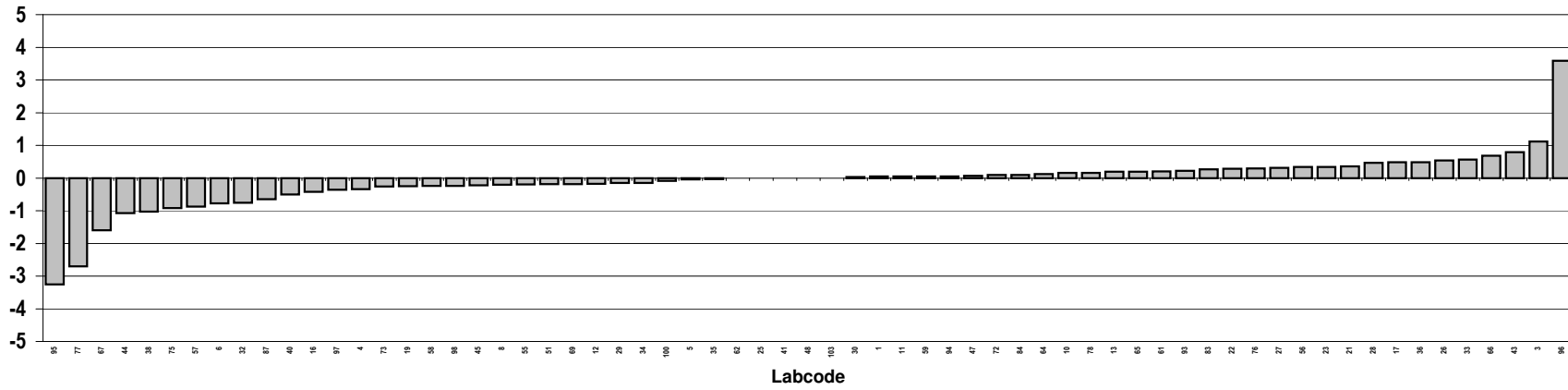
### Consensus statistics

Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	102
Standard deviation, pg/g	9.7
Relative standard deviation, %	9.5
No. of values reported	65
No. of values removed	3
No. of reported non-detects	0

CB 153



Z-score: CB 153



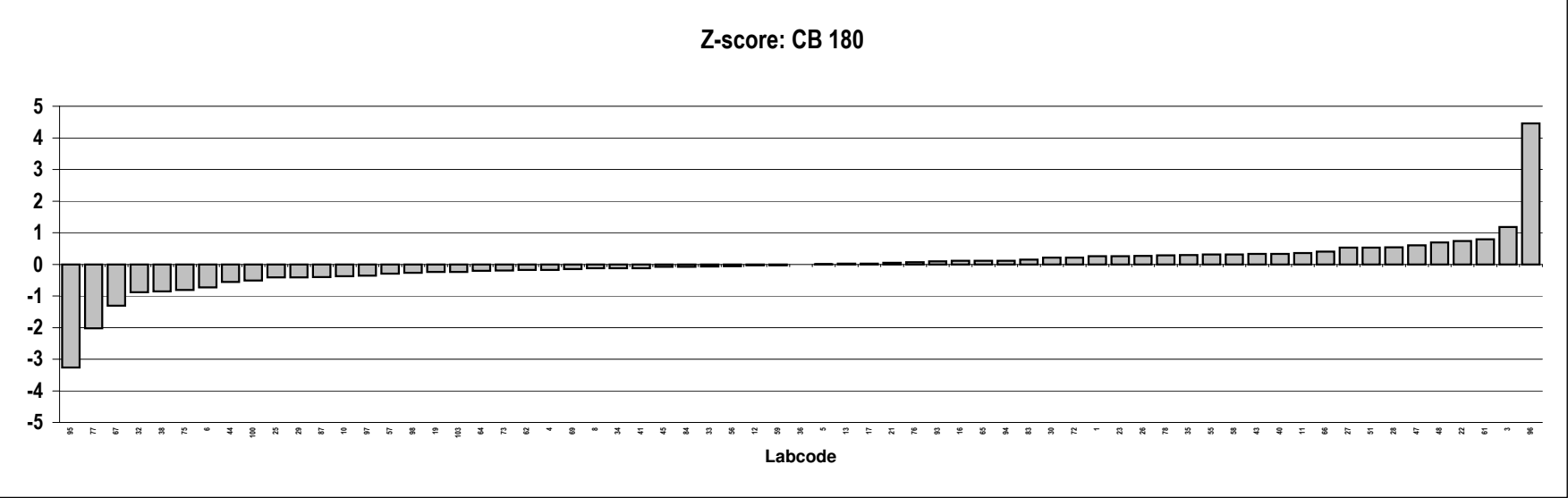
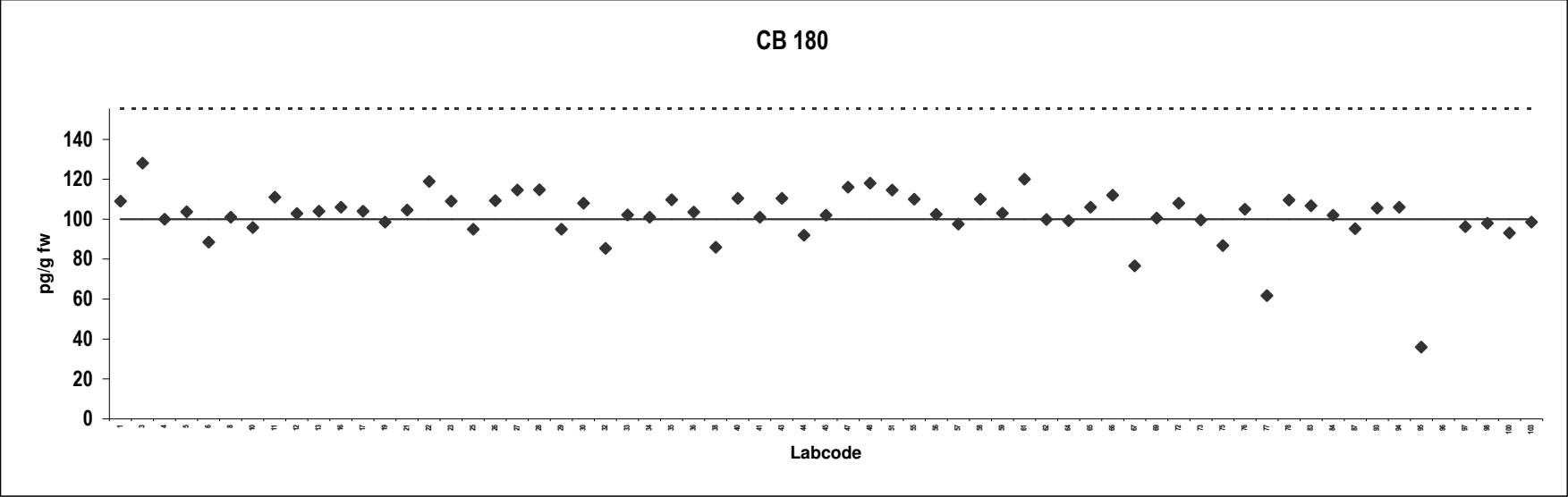
## Analyte solution

Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	109		66	112	
3	128		67	77	
4	100		69	101	
5	104		72	108	
6	89		73	100	
8	101		75	87	
10	96		76	105	
11	111		77	62	
12	103		78	110	
13	104		83	107	
16	106		84	102	
17	104		87	95	
19	99		93	106	
21	105		94	106	
22	119		95	36	Outlier
23	109		96	196	Outlier
25	95		97	96	
26	109		98	98	
27	115		100	93	
28	115		103	99	
29	95				
30	108				
32	85				
33	102				
34	101				
35	110				
36	104				
38	86				
40	110				
41	101				
43	110				
44	92				
45	102				
47	116				
48	118				
51	115				
55	110				
56	102				
57	98				
58	110				
59	103				
61	120				
62	100				
64	99				
65	106				

### Consensus statistics

Consensus median, pg/g	104
Median all values pg/g	104
Consensus mean, pg/g	103
Standard deviation, pg/g	10
Relative standard deviation, %	10
No. of values reported	65
No. of values removed	2
No. of reported non-detects	0



## Analyte solution

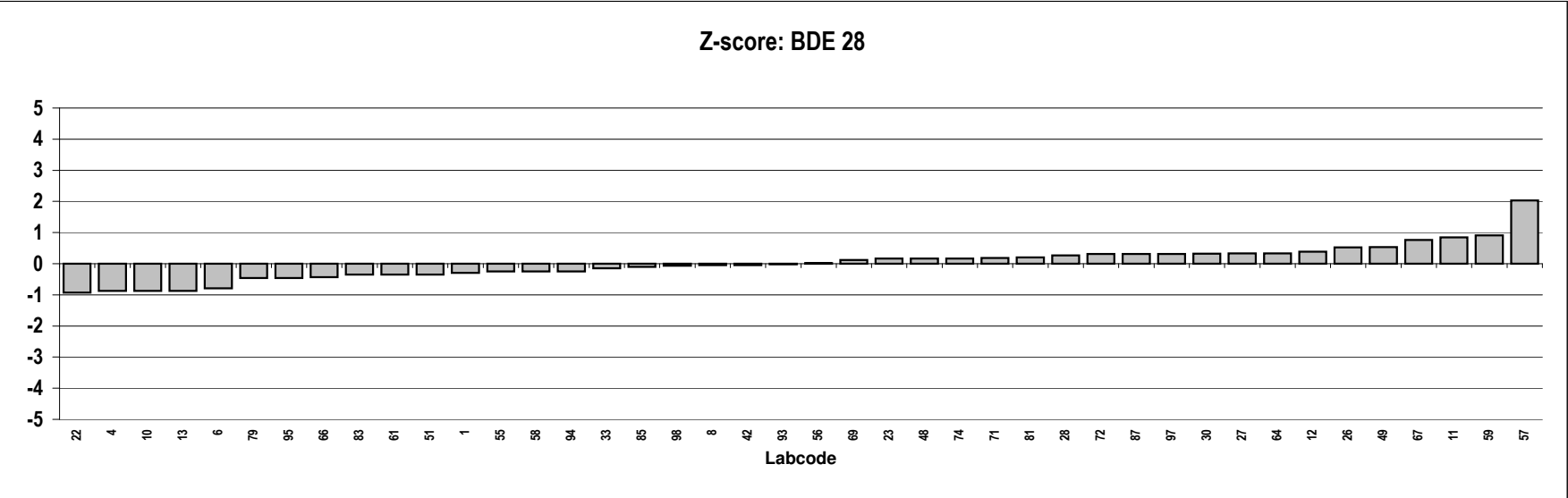
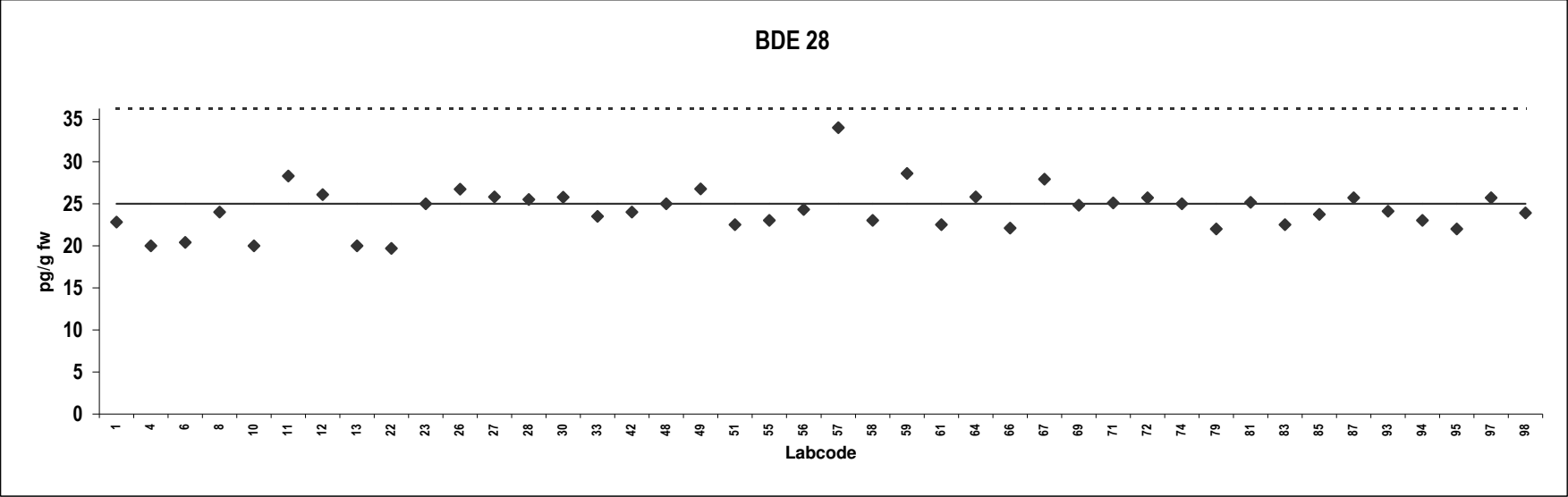
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	23				
4	20				
6	20				
8	24				
10	20				
11	28				
12	26				
13	20				
22	20				
23	25				
26	27				
27	26				
28	25				
30	26				
33	24				
42	24				
48	25				
49	27				
51	23				
55	23				
56	24				
57	34				
58	23				
59	29				
61	23				
64	26				
66	22				
67	28				
69	25				
71	25				
72	26				
74	25				
79	22				
81	25				
83	22				
85	24				
87	26				
93	24				
94	23				
95	22				
97	26				
98	24				

### Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.7
Relative standard deviation, %	11
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0





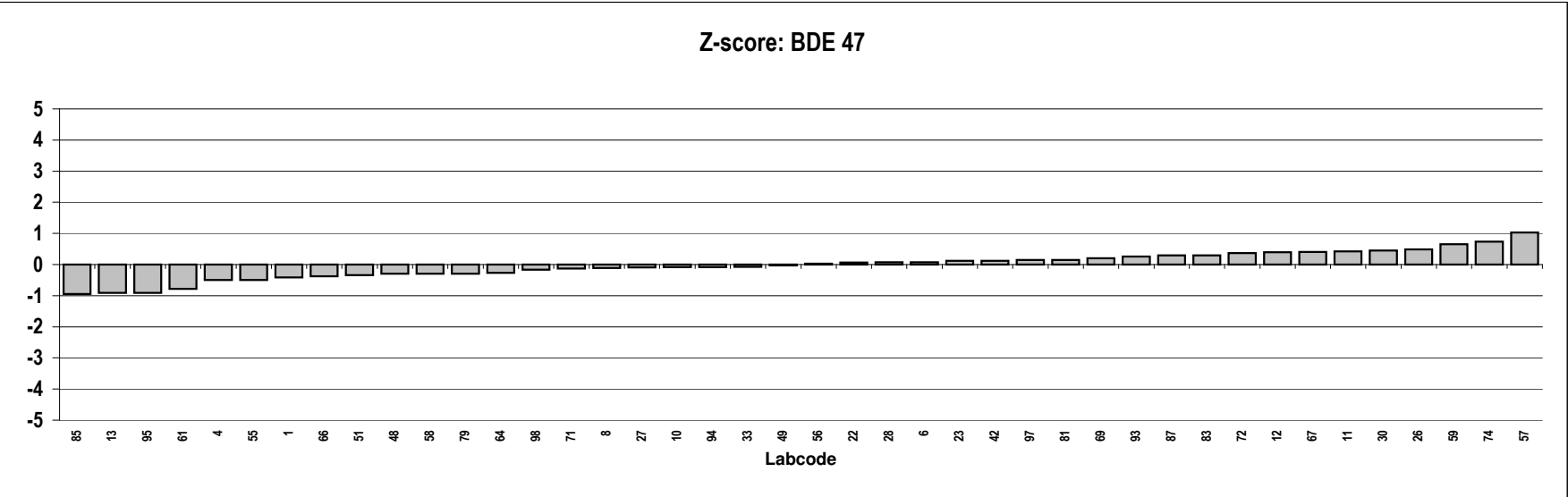
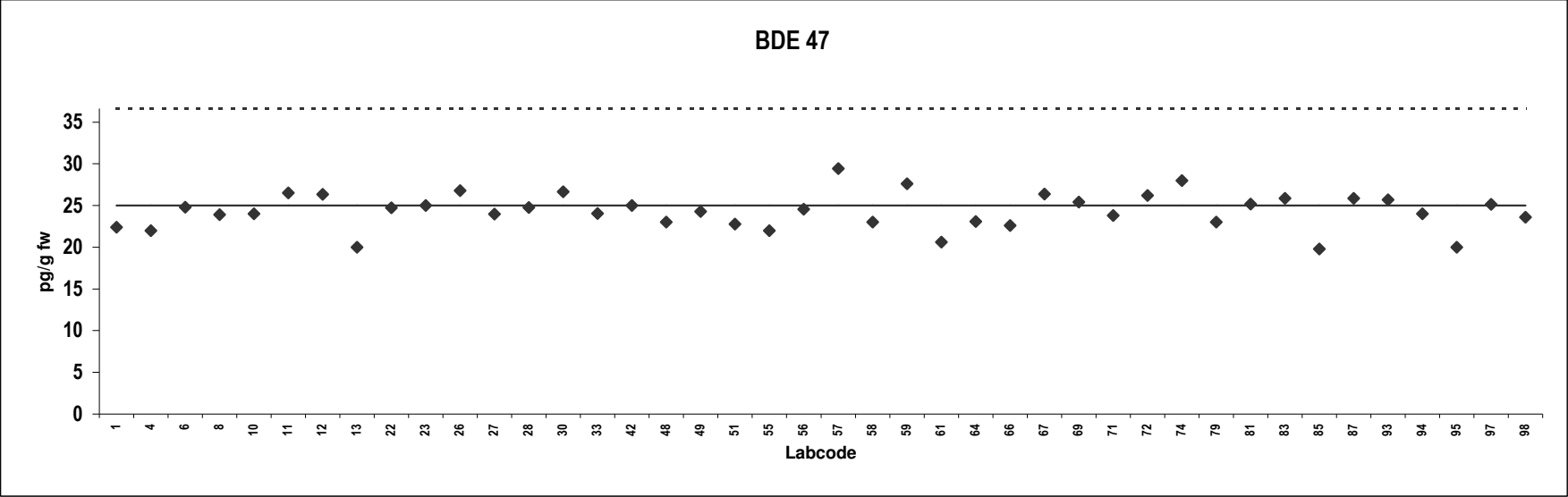
## Analyte solution

Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	22				
4	22				
6	25				
8	24				
10	24				
11	27				
12	26				
13	20				
22	25				
23	25				
26	27				
27	24				
28	25				
30	27				
33	24				
42	25				
48	23				
49	24				
51	23				
55	22				
56	25				
57	29				
58	23				
59	28				
61	21				
64	23				
66	23				
67	26				
69	25				
71	24				
72	26				
74	28				
79	23				
81	25				
83	26				
85	20				
87	26				
93	26				
94	24				
95	20				
97	25				
98	24				

### Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.1
Relative standard deviation, %	8.8
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



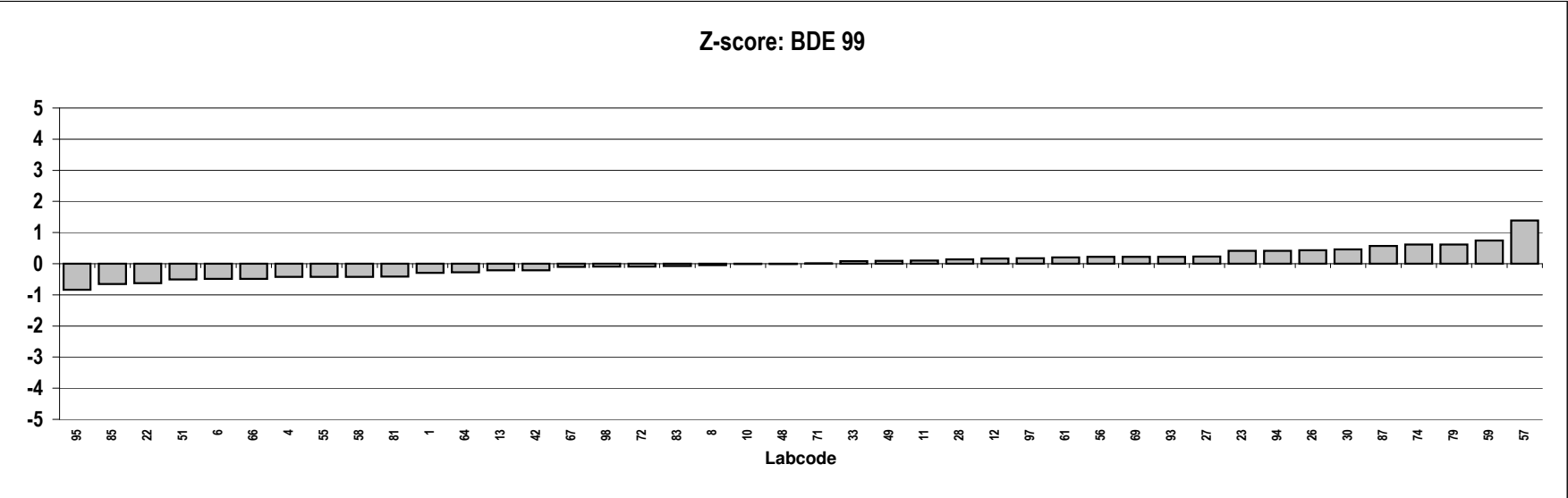
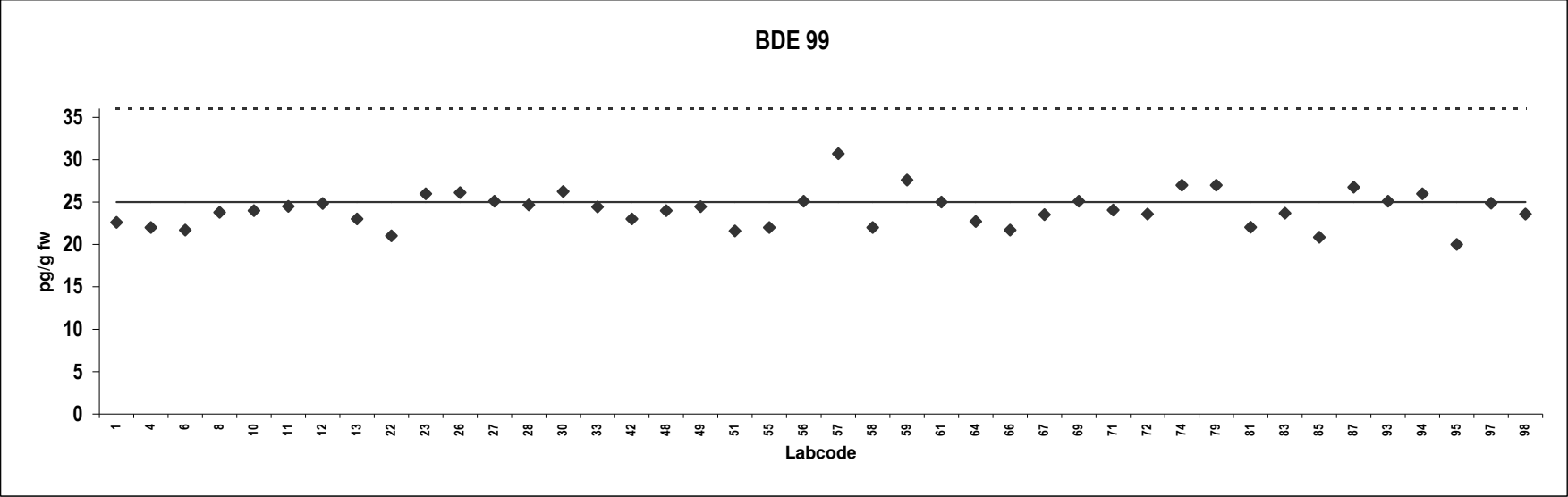
## Analyte solution

Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	23				
4	22				
6	22				
8	24				
10	24				
11	25				
12	25				
13	23				
22	21				
23	26				
26	26				
27	25				
28	25				
30	26				
33	24				
42	23				
48	24				
49	24				
51	22				
55	22				
56	25				
57	31				
58	22				
59	28				
61	25				
64	23				
66	22				
67	24				
69	25				
71	24				
72	24				
74	27				
79	27				
81	22				
83	24				
85	21				
87	27				
93	25				
94	26				
95	20				
97	25				
98	24				

### Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.1
Relative standard deviation, %	8.7
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



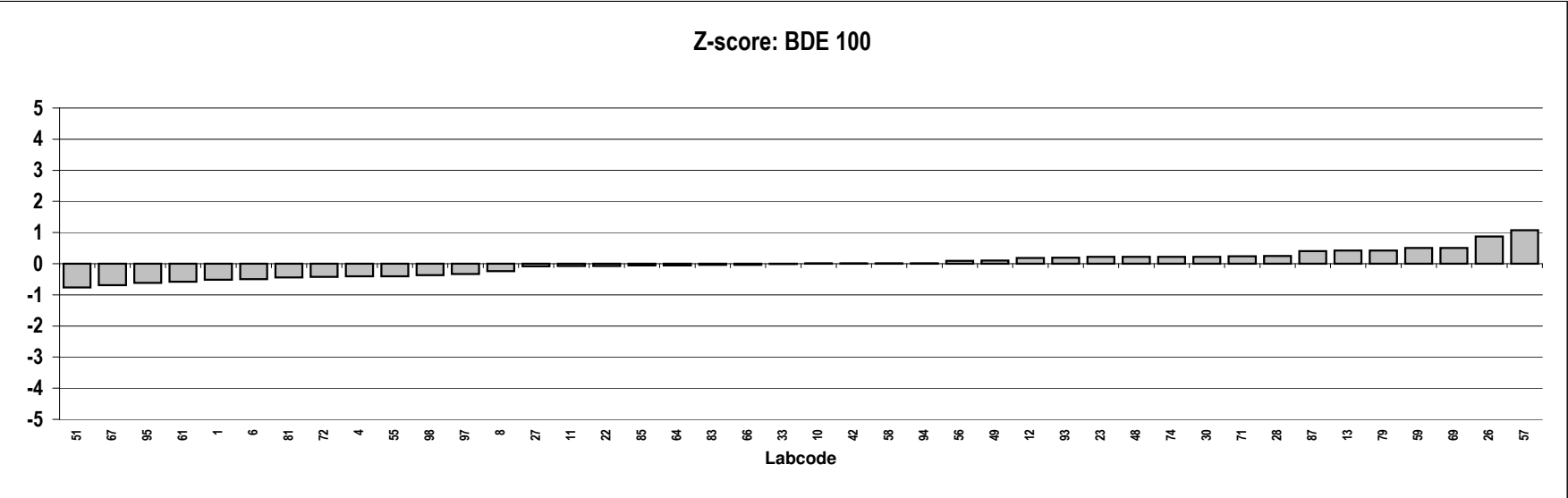
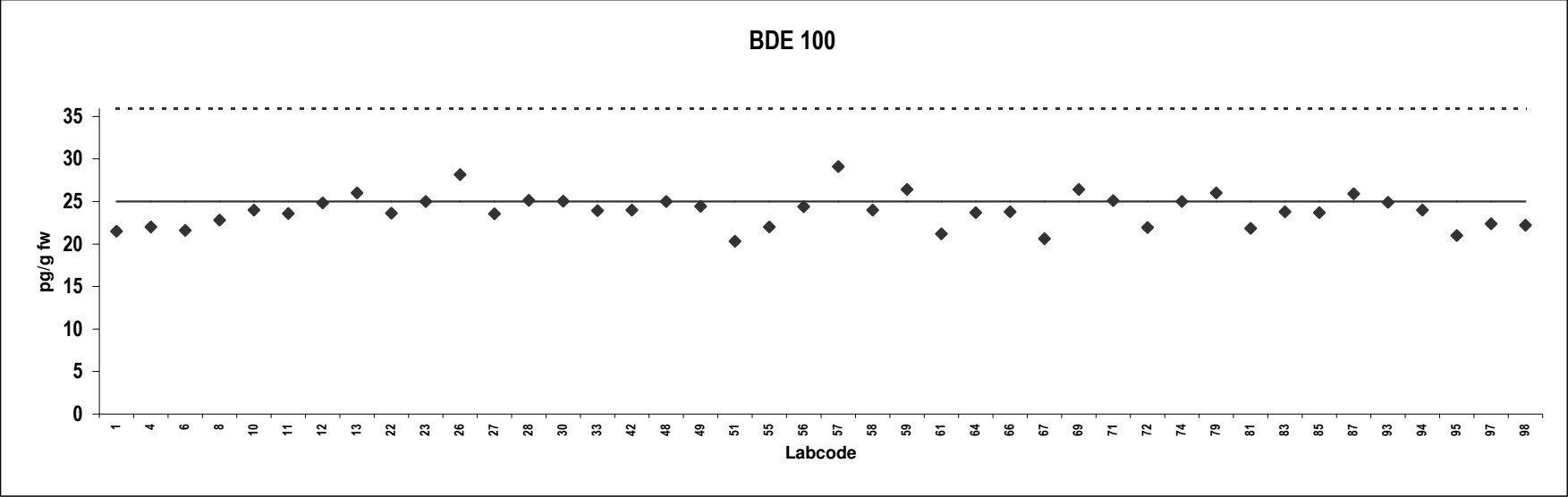
## Analyte solution

Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	22				
4	22				
6	22				
8	23				
10	24				
11	24				
12	25				
13	26				
22	24				
23	25				
26	28				
27	24				
28	25				
30	25				
33	24				
42	24				
48	25				
49	24				
51	20				
55	22				
56	24				
57	29				
58	24				
59	26				
61	21				
64	24				
66	24				
67	21				
69	26				
71	25				
72	22				
74	25				
79	26				
81	22				
83	24				
85	24				
87	26				
93	25				
94	24				
95	21				
97	22				
98	22				

### Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	1.9
Relative standard deviation, %	8.1
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



## Analyte solution

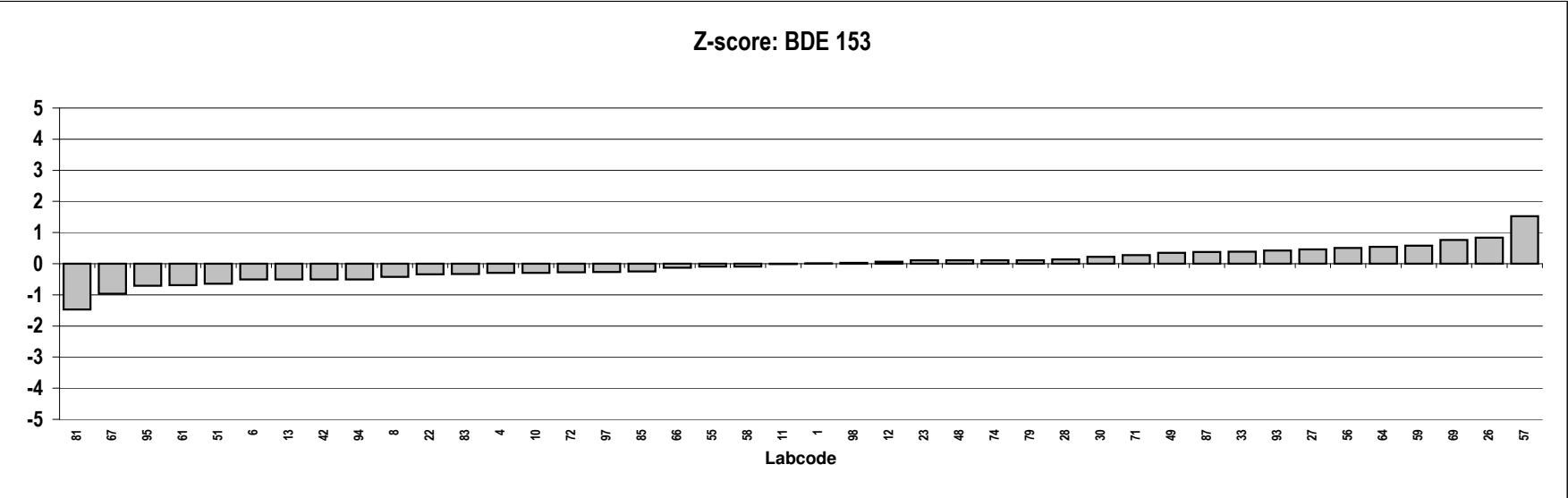
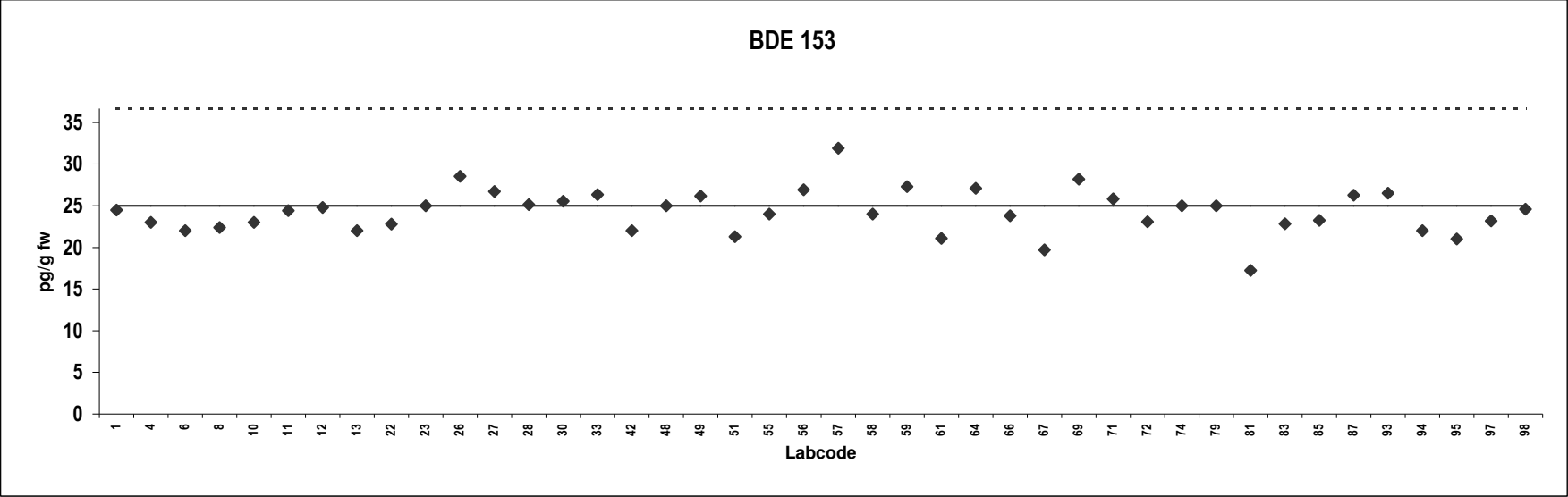
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	25				
4	23				
6	22				
8	22				
10	23				
11	24				
12	25				
13	22				
22	23				
23	25				
26	29				
27	27				
28	25				
30	26				
33	26				
42	22				
48	25				
49	26				
51	21				
55	24				
56	27				
57	32				
58	24				
59	27				
61	21				
64	27				
66	24				
67	20				
69	28				
71	26				
72	23				
74	25				
79	25				
81	17				
83	23				
85	23				
87	26				
93	27				
94	22				
95	21				
97	23				
98	25				

### Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.6
Relative standard deviation, %	11
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0





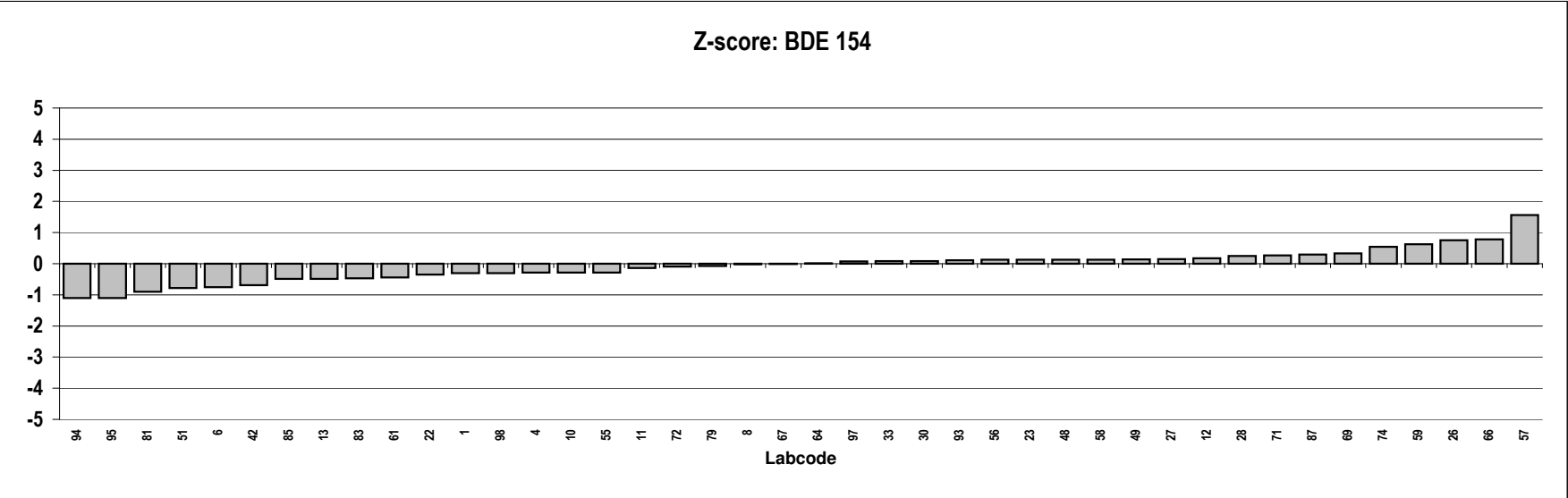
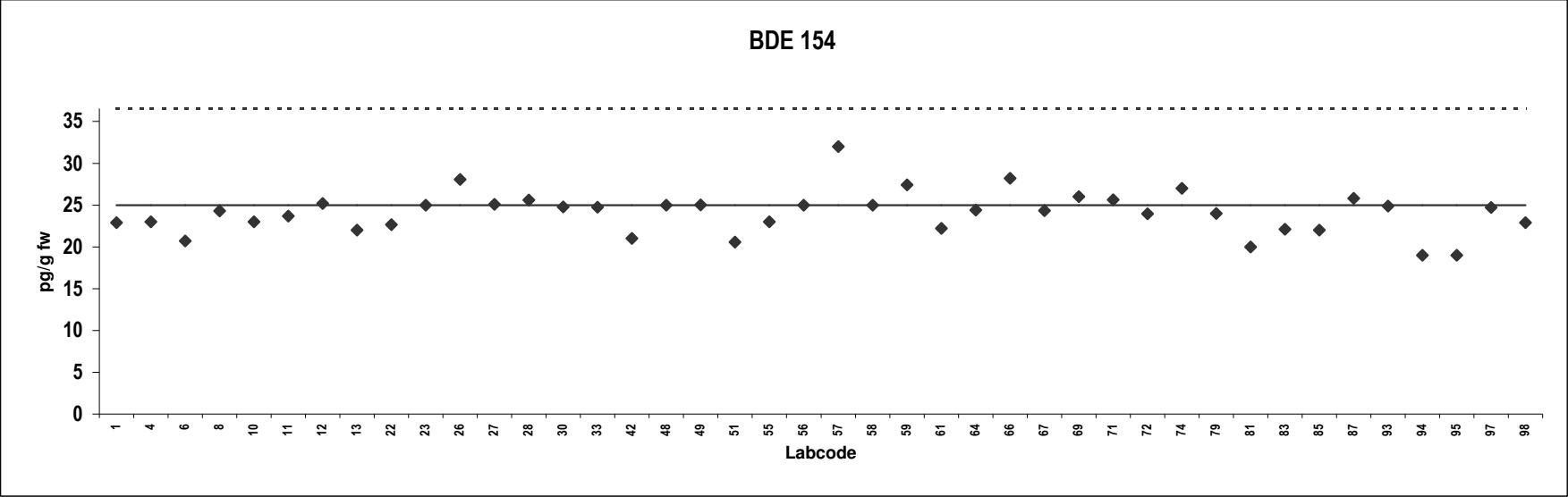
## Analyte solution

Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	23				
4	23				
6	21				
8	24				
10	23				
11	24				
12	25				
13	22				
22	23				
23	25				
26	28				
27	25				
28	26				
30	25				
33	25				
42	21				
48	25				
49	25				
51	21				
55	23				
56	25				
57	32				
58	25				
59	27				
61	22				
64	24				
66	28				
67	24				
69	26				
71	26				
72	24				
74	27				
79	24				
81	20				
83	22				
85	22				
87	26				
93	25				
94	19				
95	19				
97	25				
98	23				

### Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.5
Relative standard deviation, %	10
No. of values reported	42
No. of values removed	0
No. of reported non-detects	0



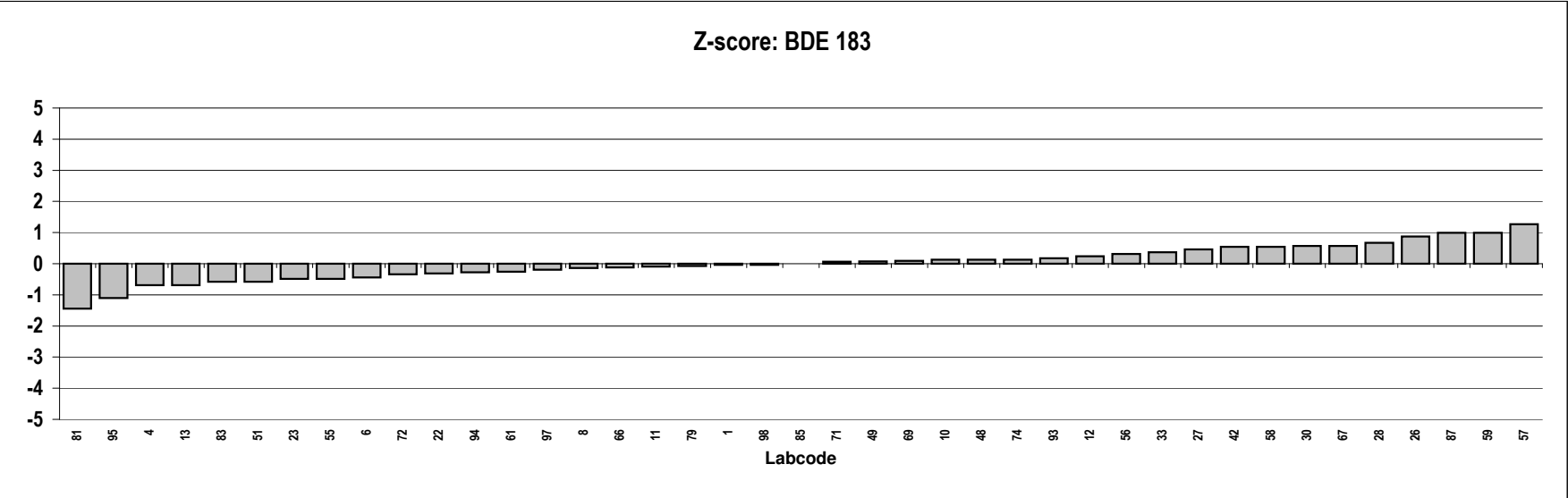
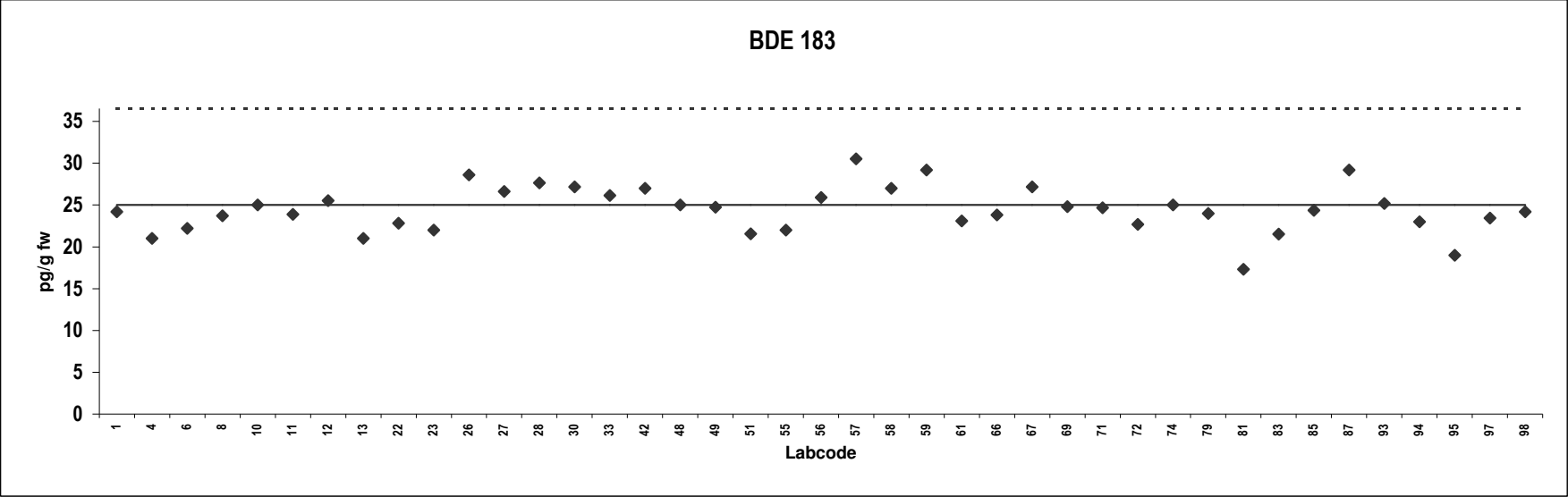
## Analyte solution

Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	24				
4	21				
6	22				
8	24				
10	25				
11	24				
12	26				
13	21				
22	23				
23	22				
26	29				
27	27				
28	28				
30	27				
33	26				
42	27				
48	25				
49	25				
51	22				
55	22				
56	26				
57	31				
58	27				
59	29				
61	23				
66	24				
67	27				
69	25				
71	25				
72	23				
74	25				
79	24				
81	17				
83	22				
85	24				
87	29				
93	25				
94	23				
95	19				
97	23				
98	24				

### Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.7
Relative standard deviation, %	11
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



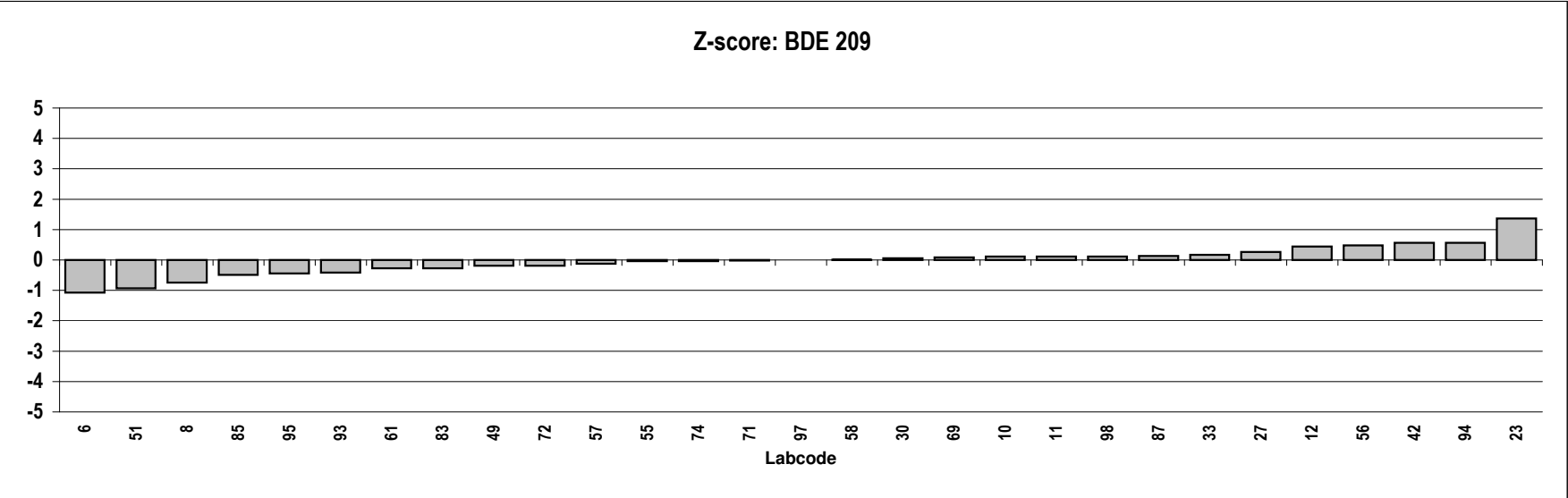
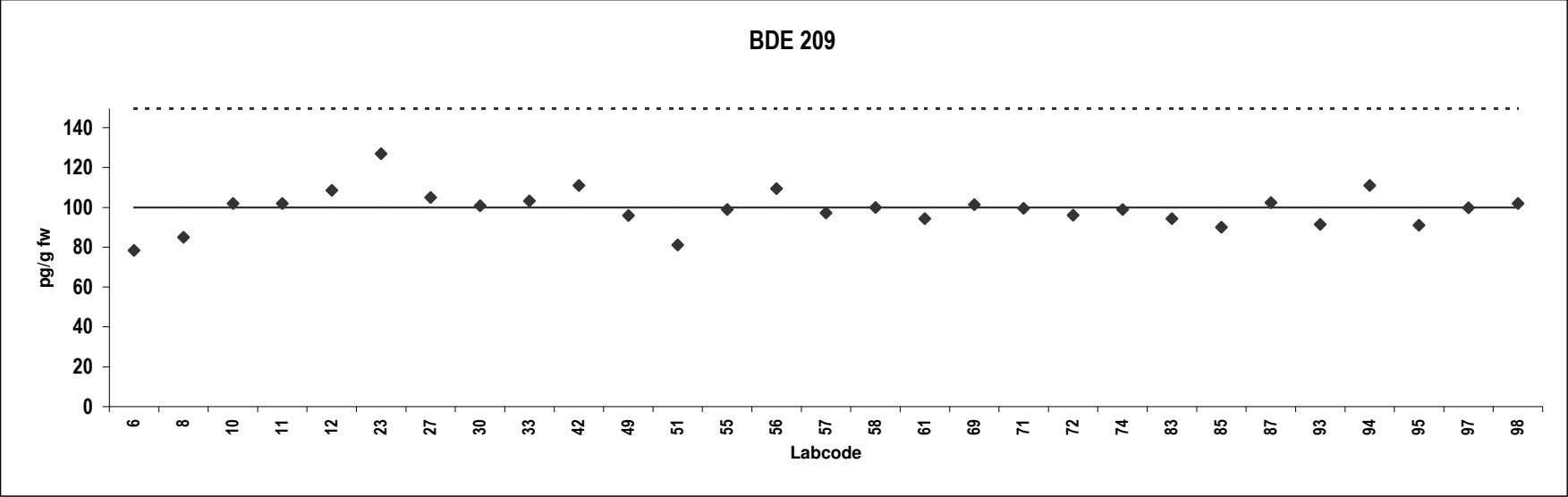
## Analyte solution

Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	78				
8	85				
10	102				
11	102				
12	109				
23	127				
27	105				
30	101				
33	103				
42	111				
49	96				
51	81				
55	99				
56	109				
57	97				
58	100				
61	94				
69	101				
71	99				
72	96				
74	99				
83	94				
85	90				
87	102				
93	92				
94	111				
95	91				
97	100				
98	102				

### Consensus statistics

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	99
Standard deviation, pg/g	9.6
Relative standard deviation, %	9.7
No. of values reported	29
No. of values removed	0
No. of reported non-detects	0



## Analyte solution

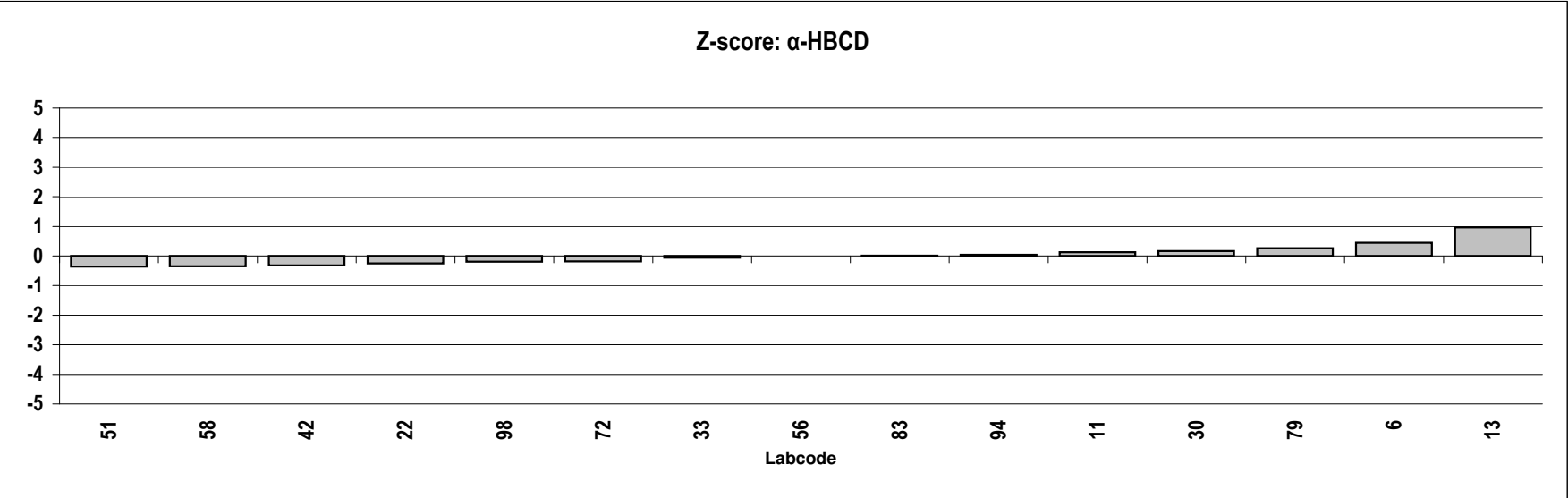
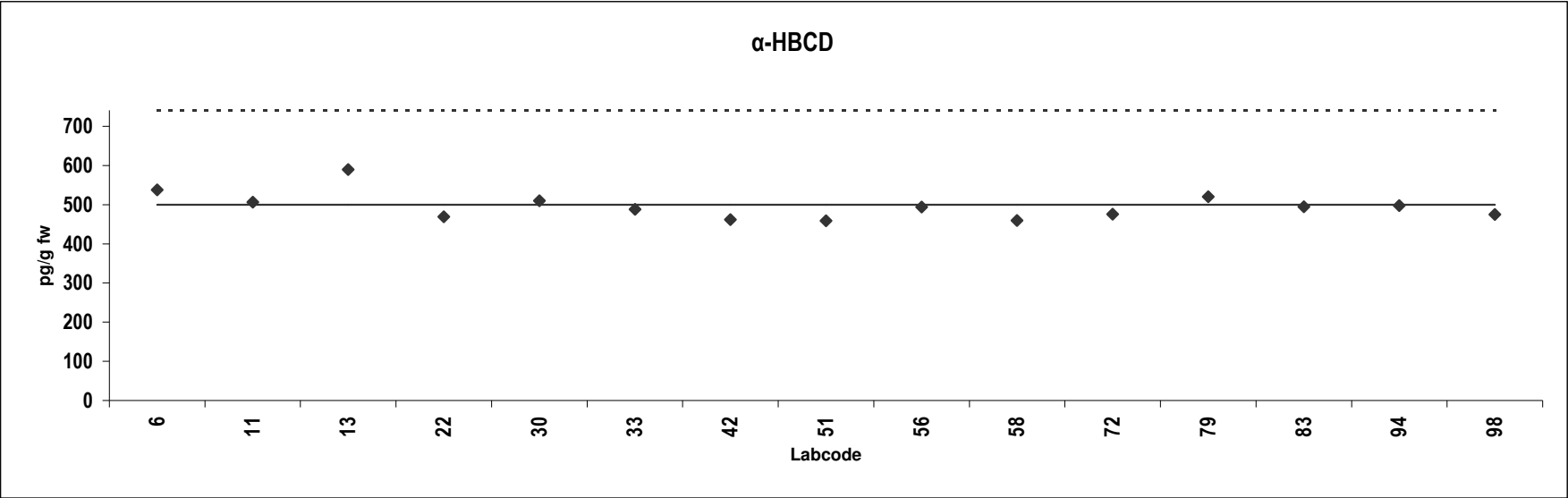
Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	538				
11	506				
13	590				
22	469				
30	510				
33	488				
42	462				
51	459				
56	494				
58	460				
72	476				
79	520				
83	495				
94	498				
98	475				

### Consensus statistics

Consensus median, pg/g	494
Median all values pg/g	494
Consensus mean, pg/g	496
Standard deviation, pg/g	35
Relative standard deviation, %	7.0
No. of values reported	15
No. of values removed	0
No. of reported non-detects	0







## **Appendix 2:**

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Presentation of results  
for salmon



## Appendix 2: Presentation of results: Salmon

### Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

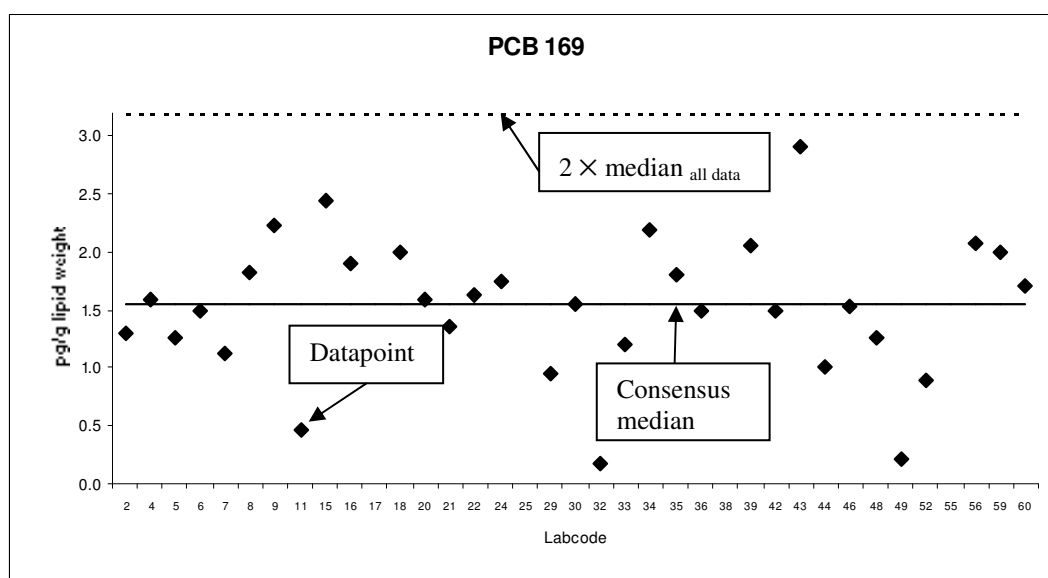
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

### Statistic calculations for indicator PCBs, PBDEs and HBCD

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).
2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set. The NDs were also removed.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

The diagram shows the reported data up to approximately the limit for outliers ( $2 \times$  the first median).



### Z-Scores of individual congeners

Z-scores of each congener were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

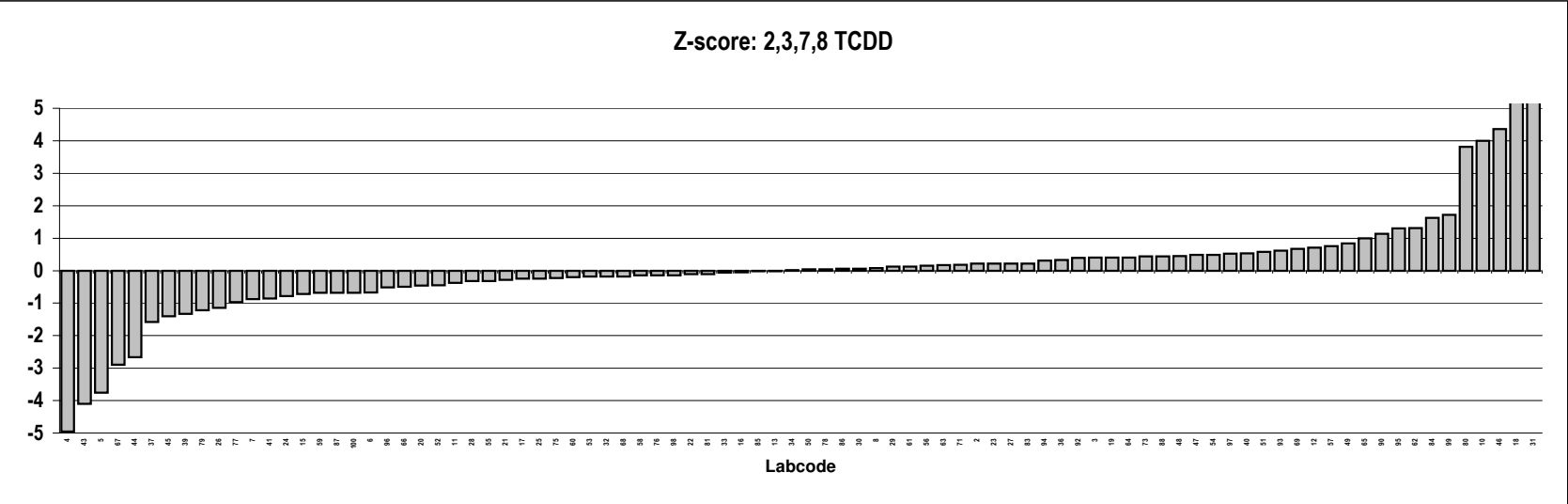
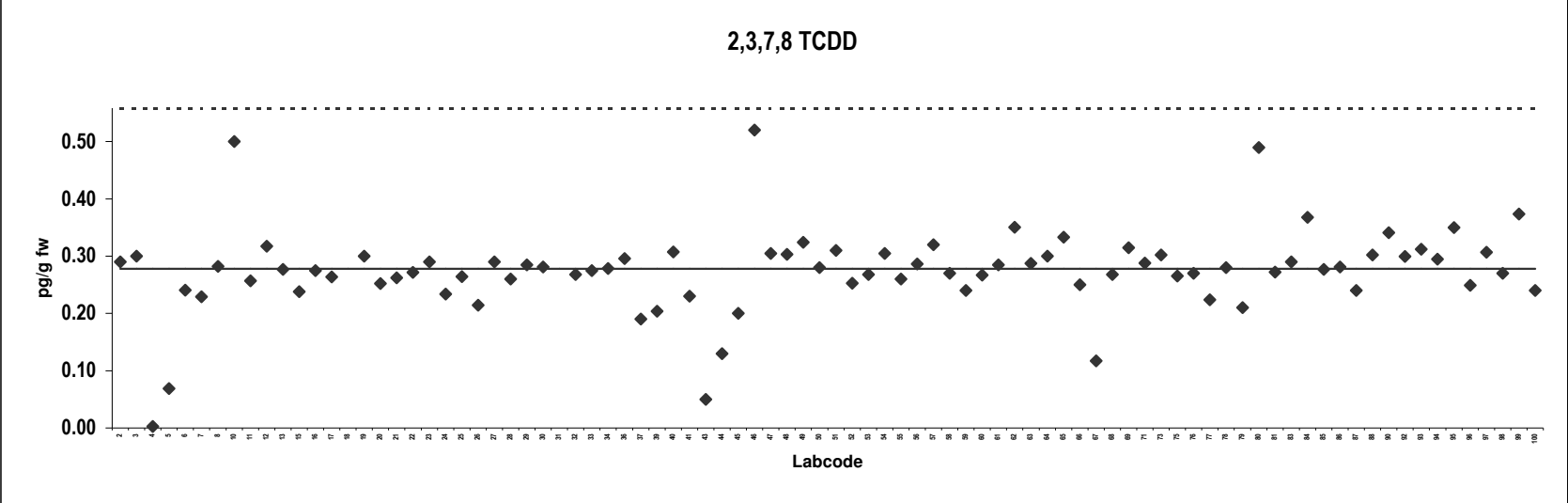
where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

**Salmon**  
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.29		52	0.25	
3	0.30		53	0.27	
4	0.0024	ND	54	0.31	
5	0.069		55	0.26	
6	0.24		56	0.29	
7	0.23		57	0.32	
8	0.28		58	0.27	
10	0.50	ND	59	0.24	
11	0.26		60	0.27	
12	0.32		61	0.29	
13	0.28		62	0.35	
15	0.24		63	0.29	
16	0.28		64	0.30	
17	0.26		65	0.33	
18	3.0	Outlier	66	0.25	
19	0.30		67	0.12	
20	0.25		68	0.27	
21	0.26		69	0.32	
22	0.27		71	0.29	
23	0.29		73	0.30	
24	0.23		75	0.27	
25	0.26		76	0.27	
26	0.21		77	0.22	
27	0.29		78	0.28	
28	0.26		79	0.21	
29	0.29		80	0.49	
30	0.28		81	0.27	
31	3.3	Outlier	83	0.29	
32	0.27		84	0.37	
33	0.27		85	0.28	
34	0.28		86	0.28	
36	0.30		87	0.24	
37	0.19		88	0.30	
39	0.20		90	0.34	
40	0.31		92	0.30	
41	0.23		93	0.31	
43	0.050	ND	94	0.30	
44	0.13	ND	95	0.35	
45	0.20		96	0.25	
46	0.52	ND	97	0.31	
47	0.31		98	0.27	
48	0.30		99	0.37	
49	0.32		100	0.24	
50	0.28				
51	0.31				

**Consensus statistics**

Consensus median, pg/g	0.28
Median all values pg/g	0.28
Consensus mean, pg/g	0.27
Standard deviation, pg/g	0.075
Relative standard deviation, %	27
No. of values reported	88
No. of values removed	2
No. of reported non-detects	5



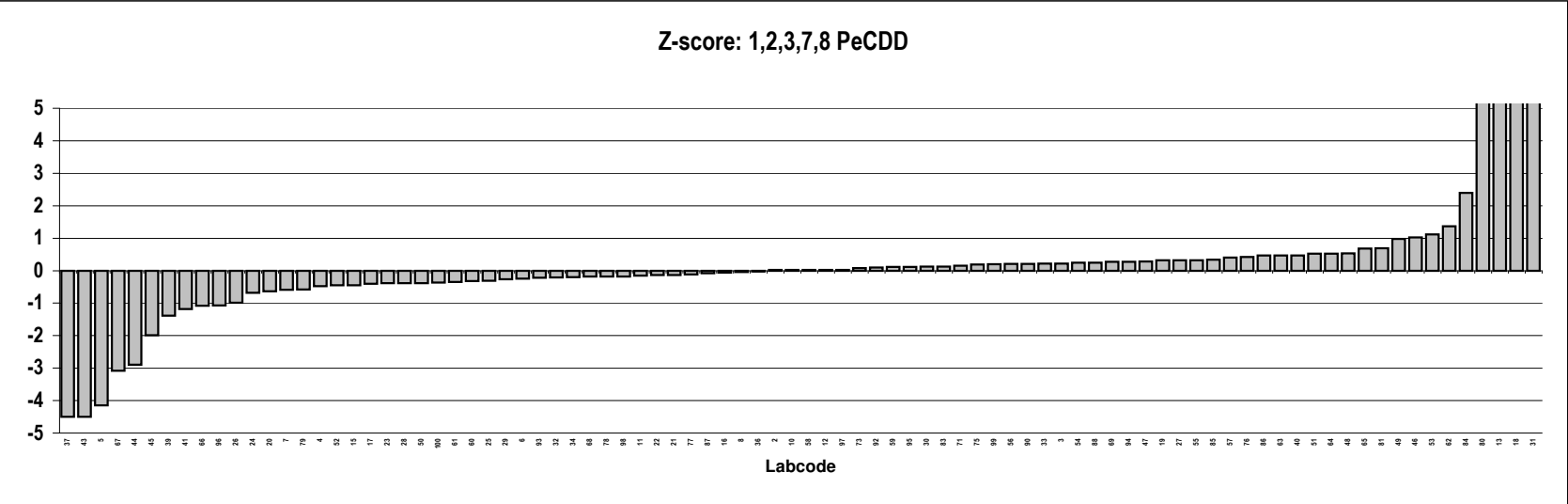
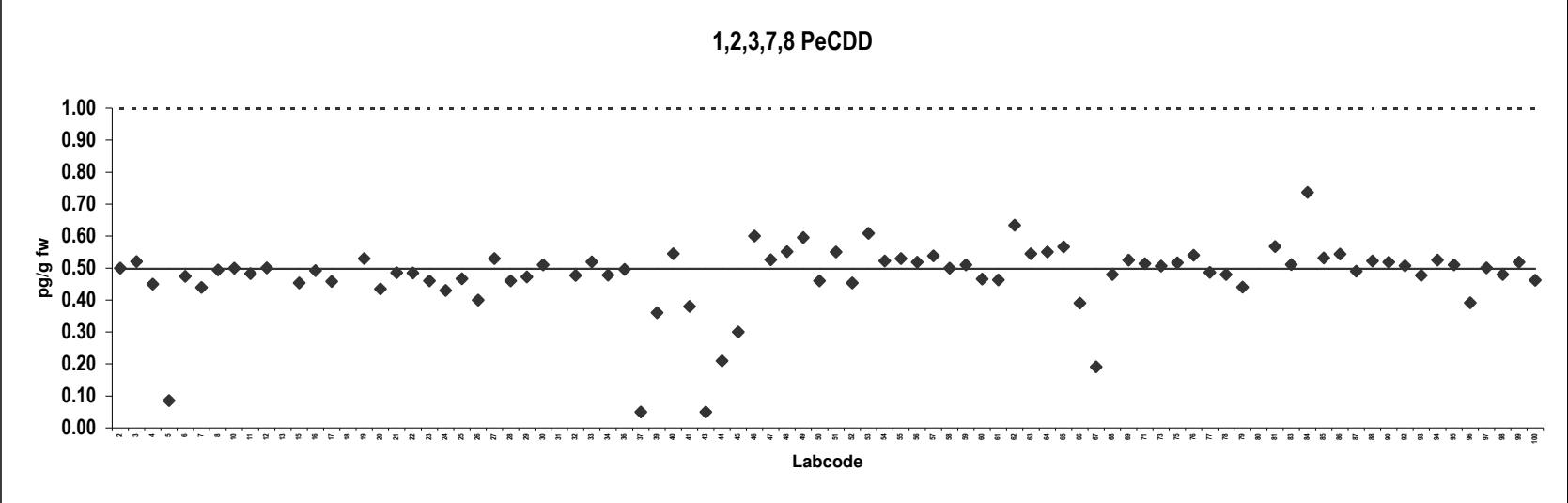
**Salmon**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.50		52	0.45	
3	0.52		53	0.61	
4	0.45		54	0.52	
5	0.085		55	0.53	
6	0.47		56	0.52	
7	0.44		57	0.54	
8	0.49		58	0.50	
10	0.50	ND	59	0.51	
11	0.48		60	0.47	
12	0.50		61	0.46	
13	3.5	Outlier	62	0.63	
15	0.45		63	0.54	
16	0.49		64	0.55	
17	0.46		65	0.57	
18	5.4	Outlier	66	0.39	
19	0.53		67	0.19	
20	0.43		68	0.48	
21	0.49		69	0.53	
22	0.48		71	0.51	
23	0.46		73	0.51	
24	0.43		75	0.52	
25	0.47		76	0.54	
26	0.40		77	0.49	
27	0.53		78	0.48	
28	0.46		79	0.44	
29	0.47		80	1.2	Outlier
30	0.51		81	0.57	
31	6.0	Outlier	83	0.51	
32	0.48		84	0.74	
33	0.52		85	0.53	
34	0.48		86	0.54	
36	0.50		87	0.49	
37	0.050	ND	88	0.52	
39	0.36		90	0.52	
40	0.54		92	0.51	
41	0.38		93	0.48	
43	0.050	ND	94	0.53	
44	0.21	ND	95	0.51	
45	0.30		96	0.39	
46	0.60	ND	97	0.50	
47	0.53		98	0.48	
48	0.55		99	0.52	
49	0.60		100	0.46	
50	0.46				
51	0.55				

**Consensus statistics**

Consensus median, pg/g	0.50
Median all values pg/g	0.50
Consensus mean, pg/g	0.48
Standard deviation, pg/g	0.11
Relative standard deviation, %	23
No. of values reported	88
No. of values removed	4
No. of reported non-detects	5



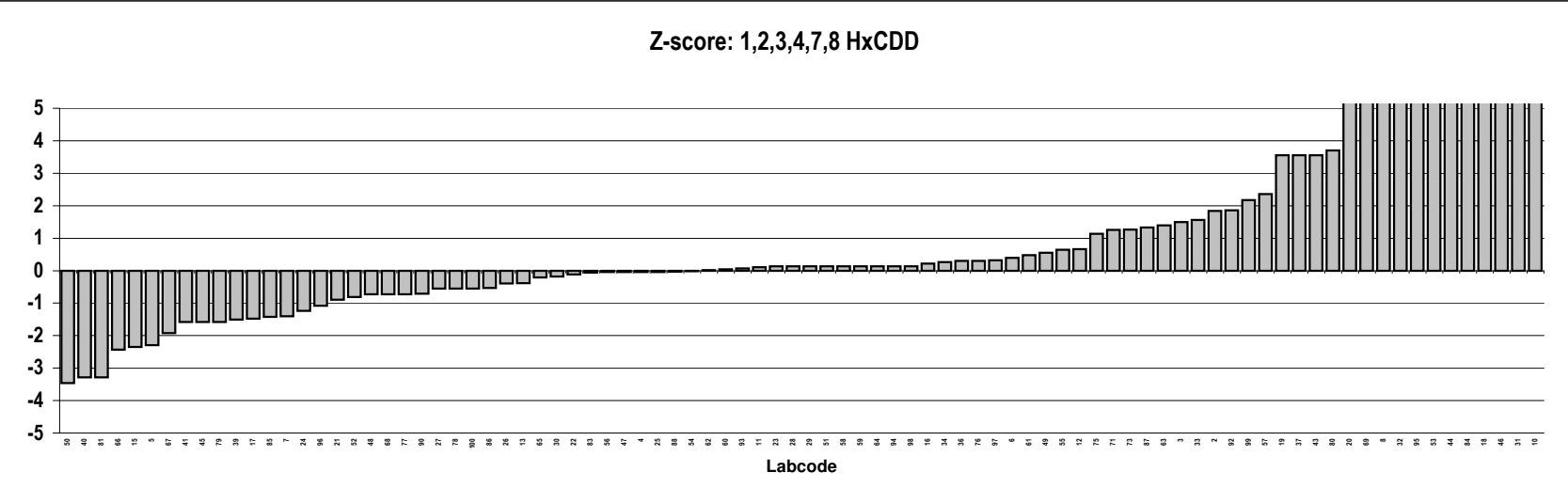
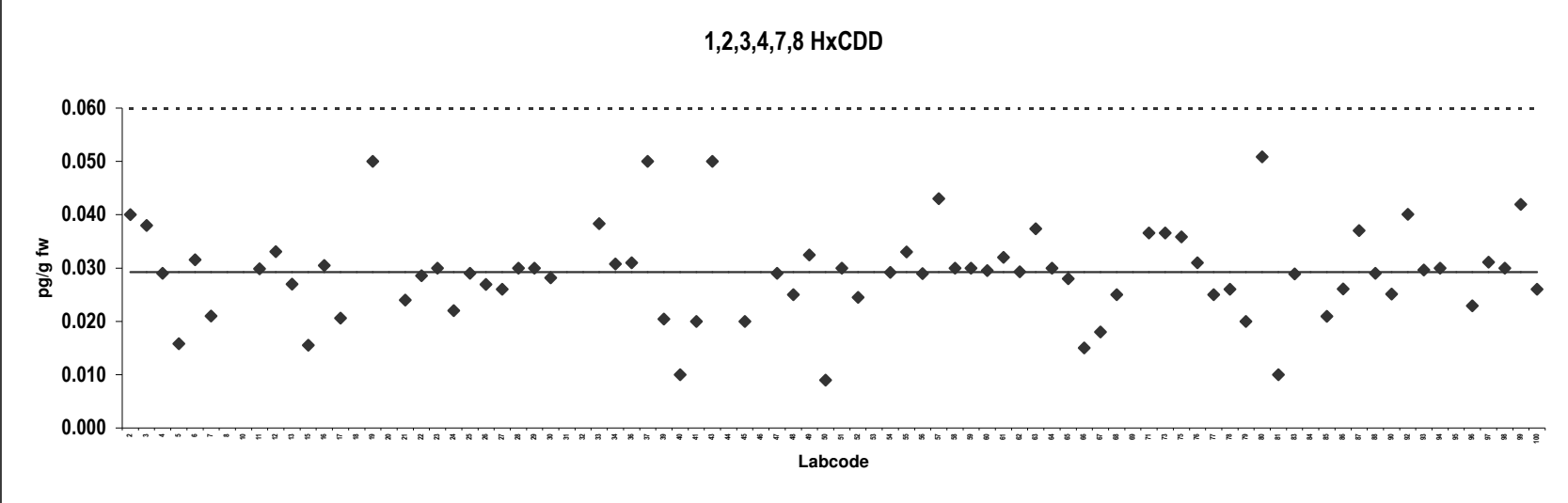


**Salmon**  
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.040		52	0.025	
3	0.038		53	0.097	Outlier
4	0.029		54	0.029	
5	0.016	ND	55	0.033	
6	0.032		56	0.029	
7	0.021		57	0.043	
8	0.074	Outlier	58	0.030	
10	1.0	Outlier,ND	59	0.030	
11	0.030		60	0.029	
12	0.033		61	0.032	
13	0.027	ND	62	0.029	
15	0.016		63	0.037	
16	0.031		64	0.030	
17	0.021		65	0.028	
18	0.16	Outlier,ND	66	0.015	
19	0.050	ND	67	0.018	
20	0.063	Outlier,ND	68	0.025	ND
21	0.024		69	0.066	Outlier,ND
22	0.029		71	0.037	
23	0.030		73	0.037	
24	0.022		75	0.036	
25	0.029		76	0.031	
26	0.027		77	0.025	
27	0.026		78	0.026	ND
28	0.030		79	0.020	
29	0.030		80	0.051	
30	0.028		81	0.010	
31	0.33	Outlier	83	0.029	
32	0.075	Outlier,ND	84	0.15	Outlier,ND
33	0.038		85	0.021	
34	0.031		86	0.026	
36	0.031		87	0.037	
37	0.050	ND	88	0.029	
39	0.020		90	0.025	
40	0.010	ND	92	0.040	
41	0.020		93	0.030	
43	0.050	ND	94	0.030	
44	0.10	Outlier,ND	95	0.079	Outlier,ND
45	0.020		96	0.023	
46	0.25	Outlier,ND	97	0.031	
47	0.029		98	0.030	
48	0.025		99	0.042	
49	0.032		100	0.026	
50	0.0090	ND			
51	0.030				

**Consensus statistics**

Consensus median, pg/g	0.029
Median all values pg/g	0.030
Consensus mean, pg/g	0.029
Standard deviation, pg/g	0.0086
Relative standard deviation, %	30
No. of values reported	88
No. of values removed	12
No. of reported non-detects	18



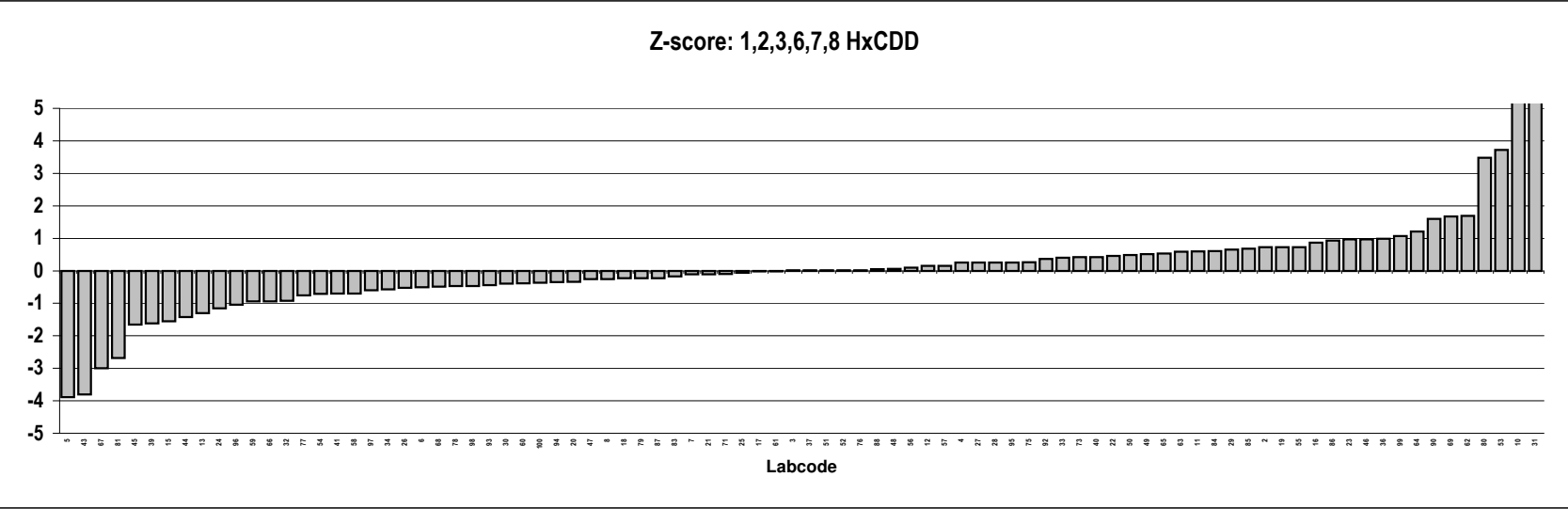
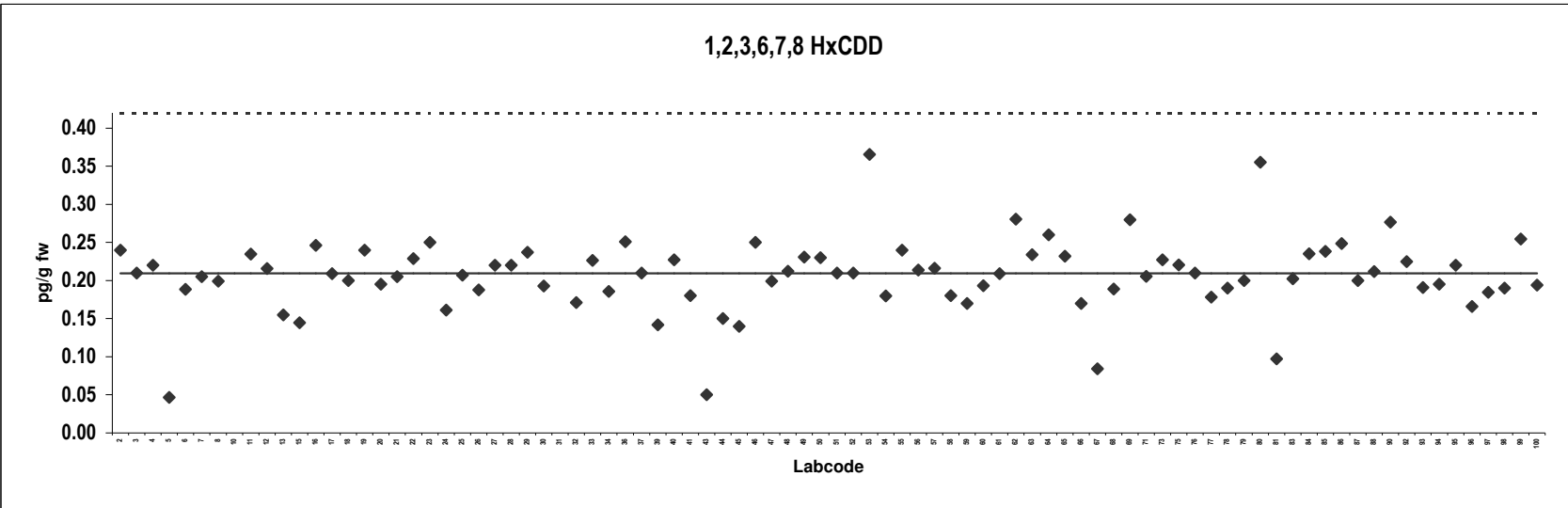
## Salmon

Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.24		52	0.21	
3	0.21		53	0.37	
4	0.22		54	0.18	
5	0.047		55	0.24	
6	0.19		56	0.21	
7	0.21		57	0.22	
8	0.20		58	0.18	
10	1.0	Outlier,ND	59	0.17	
11	0.23		60	0.19	
12	0.22		61	0.21	
13	0.16		62	0.28	
15	0.14		63	0.23	
16	0.25		64	0.26	
17	0.21		65	0.23	
18	0.20	ND	66	0.17	
19	0.24		67	0.084	
20	0.20		68	0.19	
21	0.21		69	0.28	
22	0.23		71	0.21	
23	0.25		73	0.23	
24	0.16		75	0.22	
25	0.21		76	0.21	
26	0.19		77	0.18	
27	0.22		78	0.19	
28	0.22		79	0.20	
29	0.24		80	0.36	
30	0.19		81	0.097	
31	3.2	Outlier	83	0.20	
32	0.17		84	0.24	
33	0.23		85	0.24	
34	0.19		86	0.25	
36	0.25		87	0.20	
37	0.21		88	0.21	
39	0.14		90	0.28	
40	0.23		92	0.22	
41	0.18		93	0.19	
43	0.050	ND	94	0.20	
44	0.15	ND	95	0.22	
45	0.14		96	0.17	
46	0.25	ND	97	0.18	
47	0.20		98	0.19	
48	0.21		99	0.25	
49	0.23		100	0.19	
50	0.23				
51	0.21				

### Consensus statistics

Consensus median, pg/g	0.21
Median all values pg/g	0.21
Consensus mean, pg/g	0.21
Standard deviation, pg/g	0.048
Relative standard deviation, %	23
No. of values reported	88
No. of values removed	2
No. of reported non-detects	5



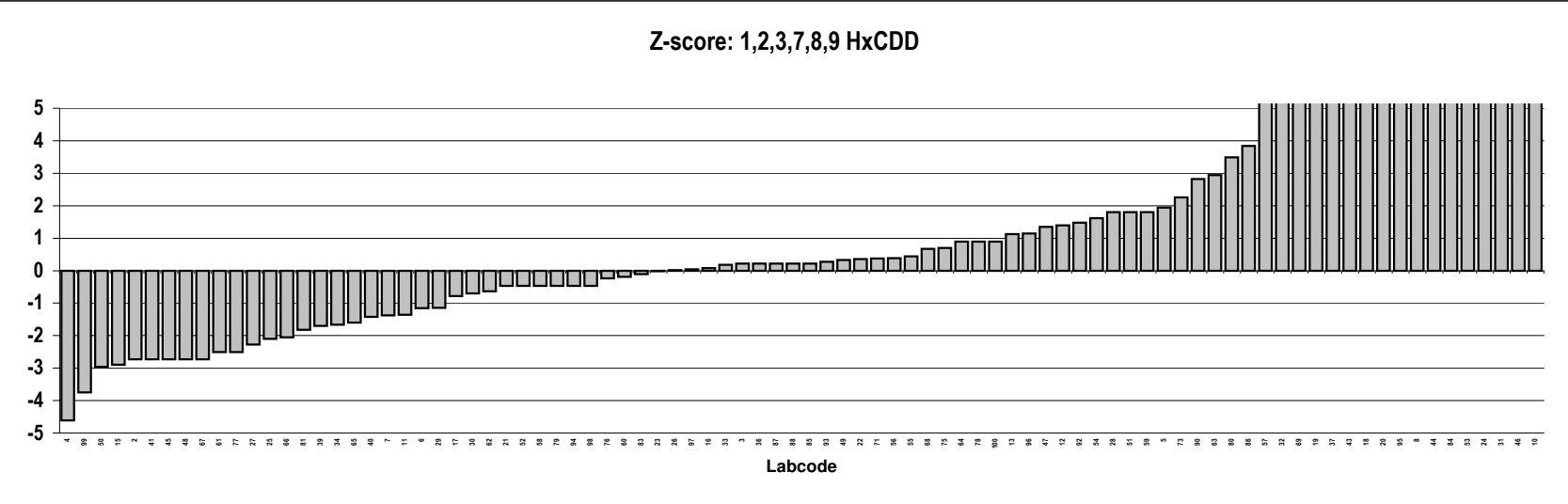
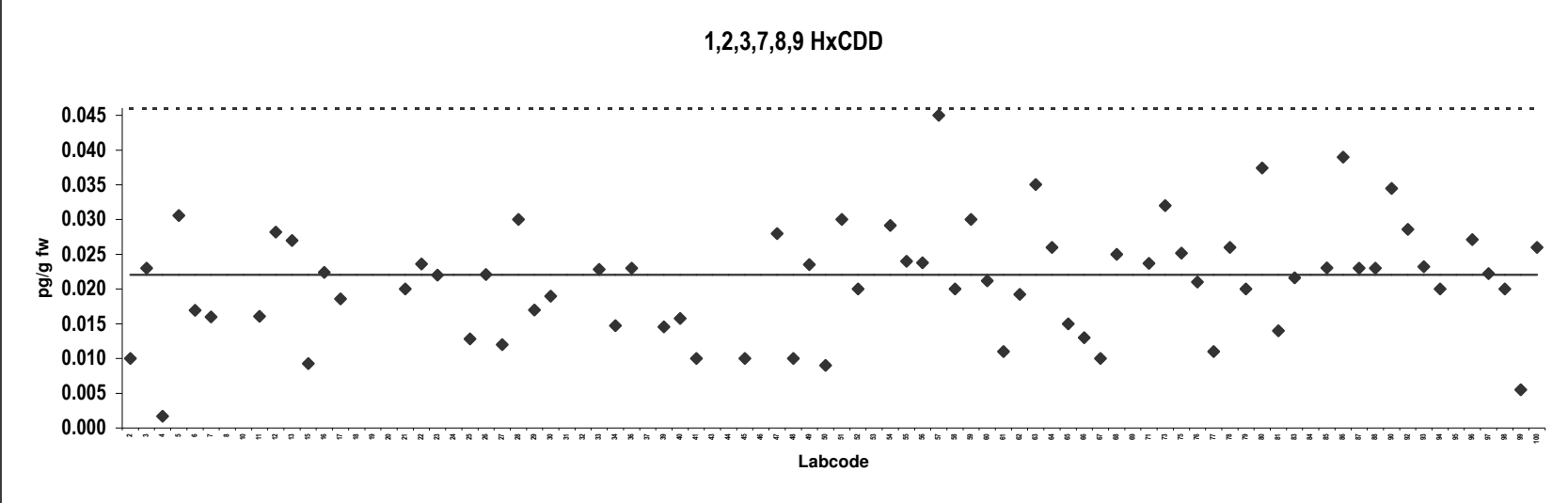
# Salmon

Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	52	0.020	
3	0.023		53	0.17	Outlier
4	0.0017	ND	54	0.029	
5	0.031	ND	55	0.024	
6	0.017		56	0.024	
7	0.016		57	0.045	
8	0.095	Outlier	58	0.020	
10	1.0	Outlier,ND	59	0.030	
11	0.016		60	0.021	
12	0.028		61	0.011	ND
13	0.027	ND	62	0.019	
15	0.0093		63	0.035	
16	0.022		64	0.026	
17	0.019		65	0.015	
18	0.059	Outlier,ND	66	0.013	
19	0.050	Outlier,ND	67	0.010	ND
20	0.063	Outlier,ND	68	0.025	ND
21	0.020		69	0.049	Outlier,ND
22	0.024		71	0.024	
23	0.022		73	0.032	
24	0.18	Outlier	75	0.025	
25	0.013		76	0.021	
26	0.022		77	0.011	
27	0.012		78	0.026	ND
28	0.030		79	0.020	
29	0.017		80	0.037	
30	0.019		81	0.014	
31	0.22	Outlier	83	0.022	
32	0.048	Outlier,ND	84	0.15	Outlier,ND
33	0.023		85	0.023	
34	0.015		86	0.039	
36	0.023		87	0.023	
37	0.050	Outlier,ND	88	0.023	
39	0.015		90	0.035	
40	0.016		92	0.029	
41	0.010	ND	93	0.023	
43	0.050	Outlier,ND	94	0.020	
44	0.10	Outlier,ND	95	0.070	Outlier,ND
45	0.010	ND	96	0.027	
46	0.25	Outlier,ND	97	0.022	
47	0.028		98	0.020	
48	0.010		99	0.0055	
49	0.024		100	0.026	
50	0.0090	ND			
51	0.030				

### Consensus statistics

Consensus median, pg/g	0.022
Median all values pg/g	0.023
Consensus mean, pg/g	0.021
Standard deviation, pg/g	0.0081
Relative standard deviation, %	38
No. of values reported	88
No. of values removed	16
No. of reported non-detects	23



**Salmon**  
**Congener: 1,2,3,4,6,7,8 HpCDD**

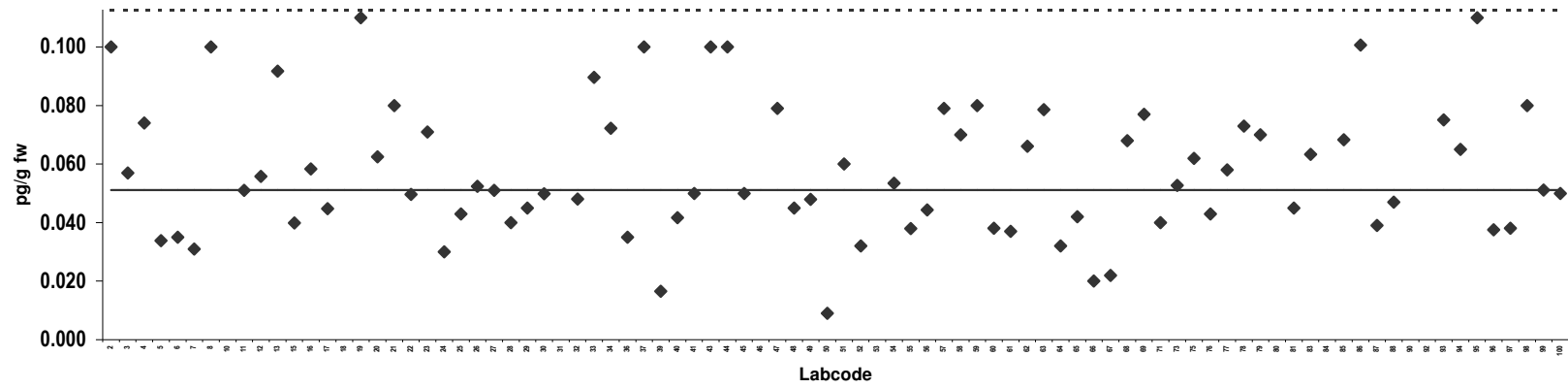
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.10		52	0.032	
3	0.057		53	0.56	Outlier
4	0.074		54	0.053	
5	0.034	ND	55	0.038	
6	0.035		56	0.044	
7	0.031		57	0.079	
8	0.10		58	0.070	ND
10	1.0	Outlier,ND	59	0.080	
11	0.051		60	0.038	
12	0.056		61	0.037	
13	0.092		62	0.066	
15	0.040		63	0.079	
16	0.058		64	0.032	ND
17	0.045		65	0.042	
18	11	Outlier	66	0.020	
19	0.11		67	0.022	
20	0.063	ND	68	0.068	
21	0.080		69	0.077	ND
22	0.050		71	0.040	
23	0.071		73	0.053	
24	0.030		75	0.062	
25	0.043		76	0.043	
26	0.052		77	0.058	
27	0.051		78	0.073	ND
28	0.040		79	0.070	
29	0.045		80	0.14	Outlier
30	0.050		81	0.045	
31	0.70	Outlier	83	0.063	
32	0.048	ND	84	0.23	Outlier,ND
33	0.090		85	0.068	
34	0.072		86	0.10	
36	0.035		87	0.039	
37	0.10	ND	88	0.047	
39	0.017		90	0.12	Outlier
40	0.042		92	0.32	Outlier
41	0.050	ND	93	0.075	
43	0.10	ND	94	0.065	
44	0.10	ND	95	0.11	ND
45	0.050	ND	96	0.038	
46	0.53	Outlier,ND	97	0.038	
47	0.079		98	0.080	ND
48	0.045		99	0.051	
49	0.048		100	0.050	
50	0.0090	ND			
51	0.060				

**Consensus statistics**

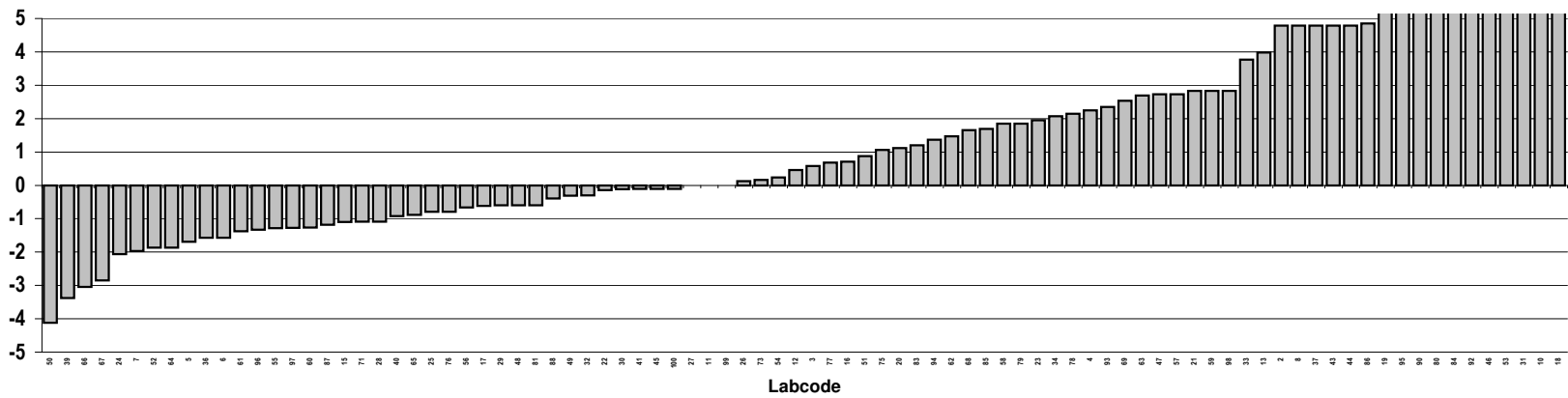
Consensus median, pg/g	0.051
Median all values pg/g	0.056
Consensus mean, pg/g	0.058
Standard deviation, pg/g	0.023
Relative standard deviation, %	40
No. of values reported	88
No. of values removed	9
No. of reported non-detects	18



1,2,3,4,6,7,8 HpCDD



Z-score: 1,2,3,4,6,7,8 HpCDD

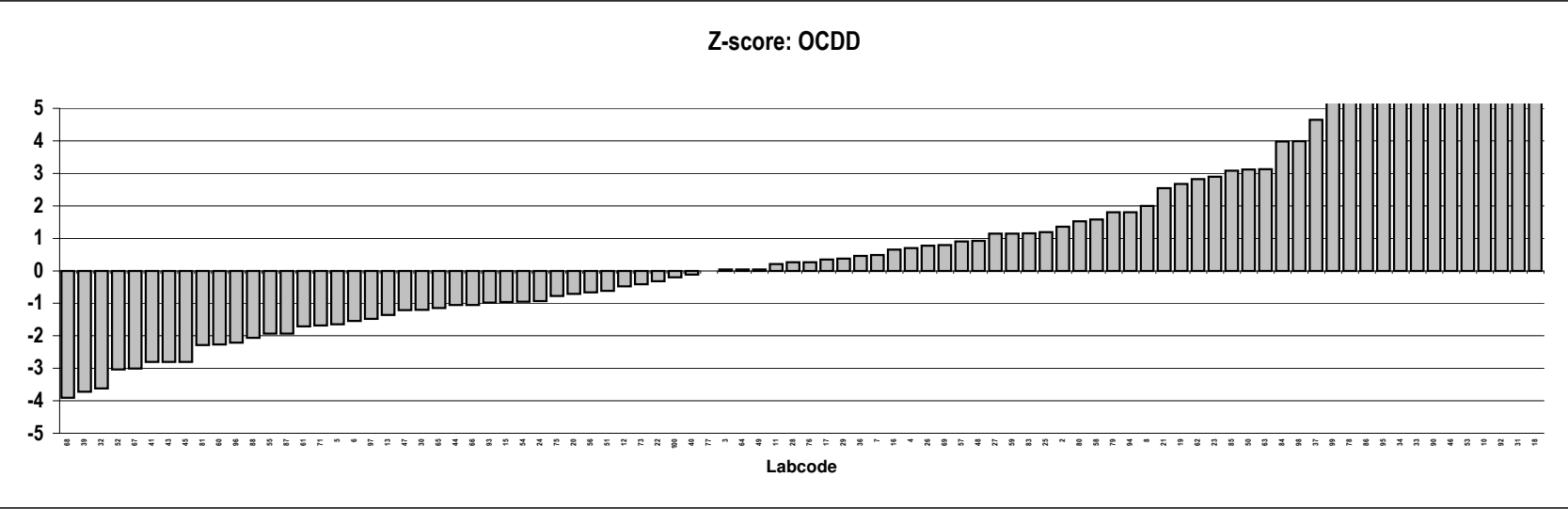
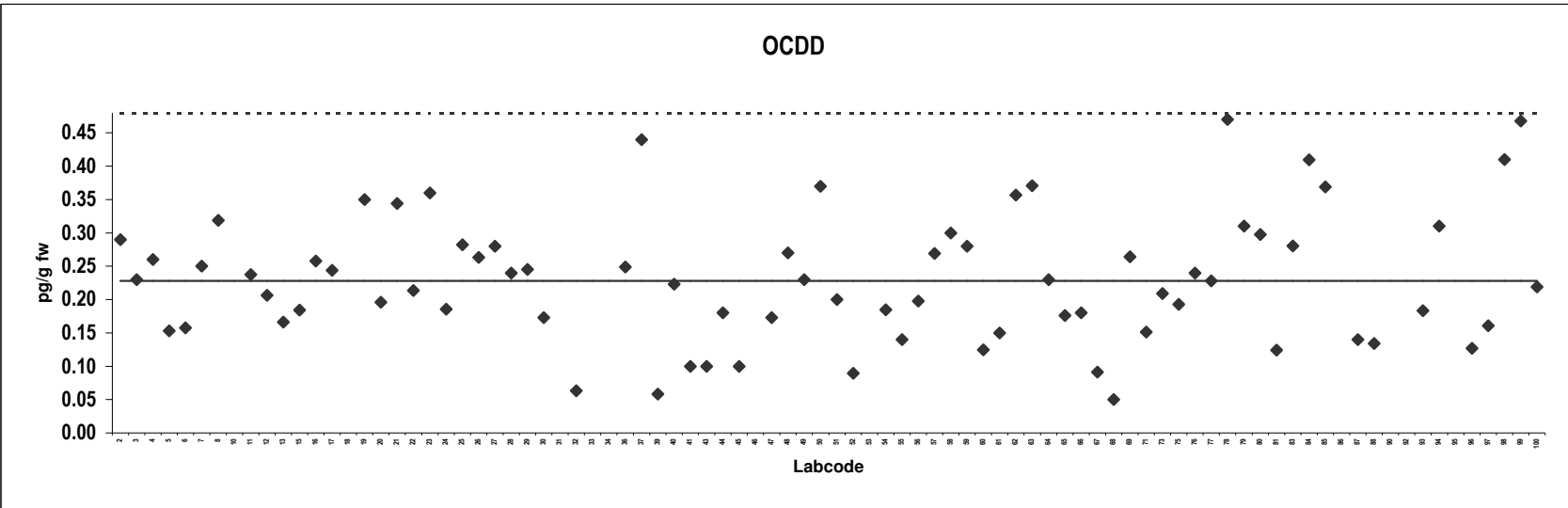


**Salmon**  
Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.29		52	0.089	
3	0.23		53	1.6	Outlier
4	0.26		54	0.18	
5	0.15		55	0.14	
6	0.16		56	0.20	
7	0.25		57	0.27	
8	0.32		58	0.30	ND
10	2.0	Outlier,ND	59	0.28	
11	0.24		60	0.12	
12	0.21		61	0.15	
13	0.17		62	0.36	
15	0.18		63	0.37	
16	0.26		64	0.23	ND
17	0.24		65	0.18	
18	6.1	Outlier	66	0.18	
19	0.35		67	0.091	
20	0.20		68	0.050	ND
21	0.34		69	0.26	
22	0.21		71	0.15	
23	0.36		73	0.21	
24	0.19		75	0.19	
25	0.28		76	0.24	
26	0.26		77	0.23	
27	0.28		78	0.47	
28	0.24		79	0.31	
29	0.25		80	0.30	
30	0.17		81	0.12	
31	3.4	Outlier	83	0.28	
32	0.063	ND	84	0.41	ND
33	0.63	Outlier	85	0.37	
34	0.60	Outlier	86	0.50	Outlier
36	0.25		87	0.14	
37	0.44		88	0.13	
39	0.058		90	0.76	Outlier
40	0.22		92	2.9	Outlier
41	0.10	ND	93	0.18	
43	0.10	ND	94	0.31	
44	0.18	ND	95	0.52	Outlier
45	0.10	ND	96	0.13	
46	1.0	Outlier	97	0.16	
47	0.17		98	0.41	
48	0.27		99	0.47	
49	0.23		100	0.22	
50	0.37				
51	0.20				

**Consensus statistics**

Consensus median, pg/g	0.23
Median all values pg/g	0.24
Consensus mean, pg/g	0.23
Standard deviation, pg/g	0.096
Relative standard deviation, %	41
No. of values reported	88
No. of values removed	11
No. of reported non-detects	10



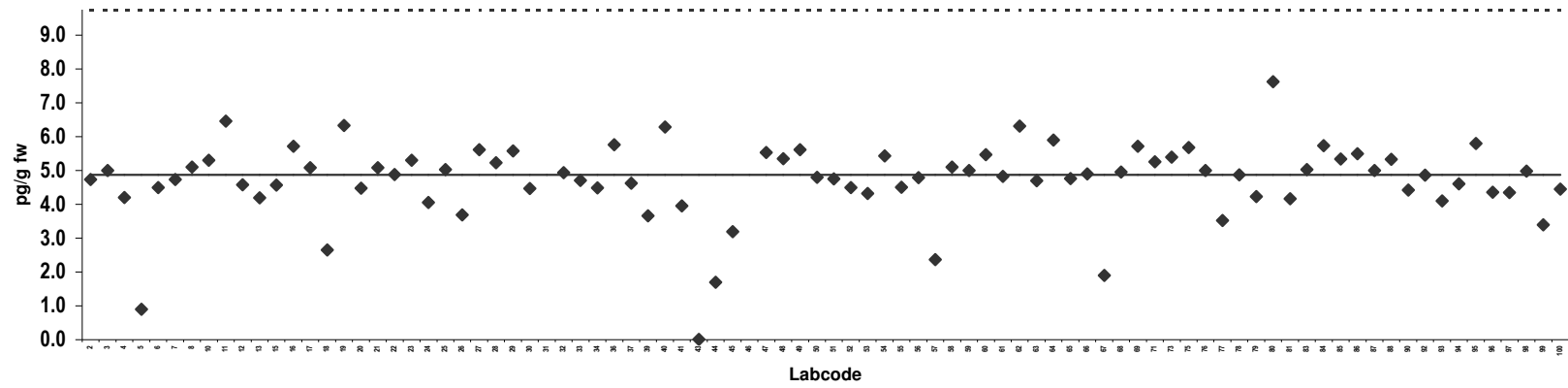
**Salmon**  
Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4.7		52	4.5	
3	5.0		53	4.3	
4	4.2		54	5.4	
5	0.90		55	4.5	
6	4.5		56	4.8	
7	4.7		57	2.4	
8	5.1		58	5.1	
10	5.3		59	5.0	
11	6.5		60	5.5	
12	4.6		61	4.8	
13	4.2		62	6.3	
15	4.6		63	4.7	
16	5.7		64	5.9	
17	5.1		65	4.8	
18	2.7		66	4.9	
19	6.3		67	1.9	
20	4.5		68	5.0	
21	5.1		69	5.7	
22	4.9		71	5.3	
23	5.3		73	5.4	
24	4.1		75	5.7	
25	5.0		76	5.0	
26	3.7		77	3.5	
27	5.6		78	4.9	
28	5.2		79	4.2	
29	5.6		80	7.6	
30	4.5		81	4.2	
31	69	Outlier	83	5.0	
32	4.9		84	5.7	
33	4.7		85	5.3	
34	4.5		86	5.5	
36	5.8		87	5.0	
37	4.6		88	5.3	
39	3.7		90	4.4	
40	6.3		92	4.9	
41	4.0		93	4.1	
43	0.010	ND	94	4.6	
44	1.7		95	5.8	
45	3.2		96	4.4	
46	10	Outlier	97	4.3	
47	5.5		98	5.0	
48	5.3		99	3.4	
49	5.6		100	4.4	
50	4.8				
51	4.8				

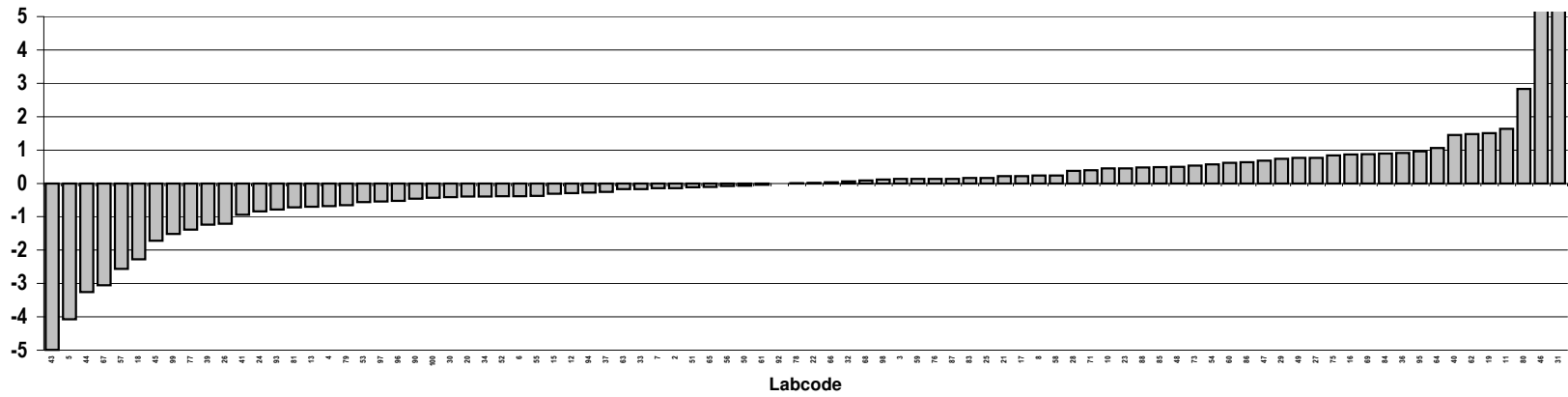
**Consensus statistics**

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.7
Standard deviation, pg/g	1.1
Relative standard deviation, %	24
No. of values reported	88
No. of values removed	2
No. of reported non-detects	1

### 2,3,7,8 TCDF



### Z-score: 2,3,7,8 TCDF

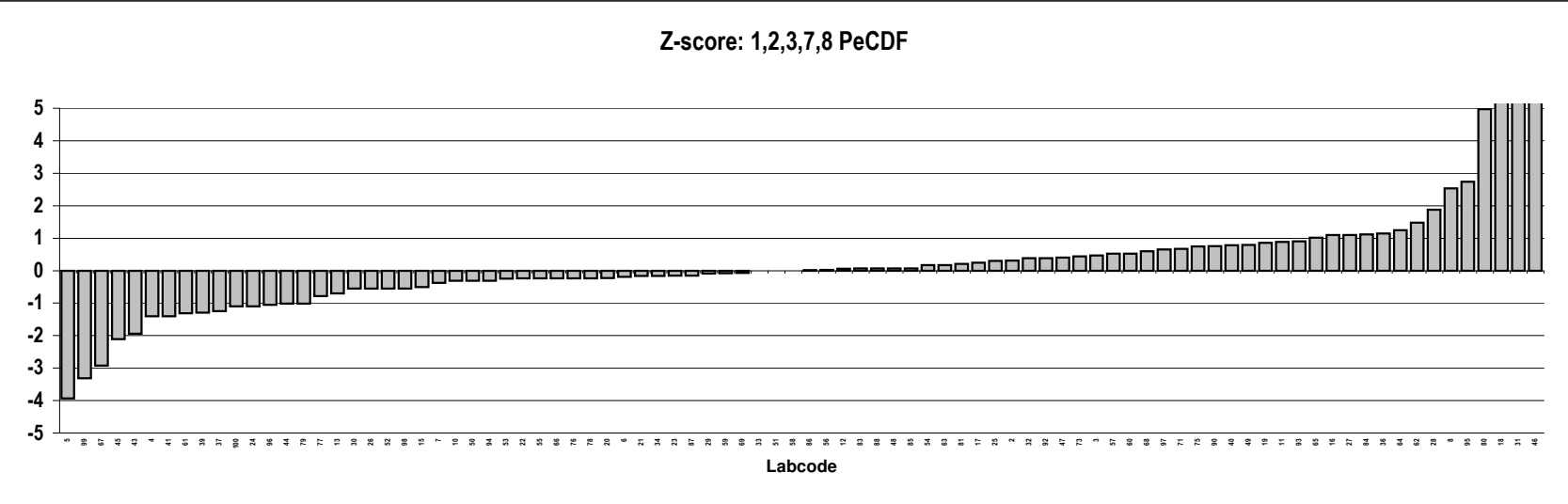
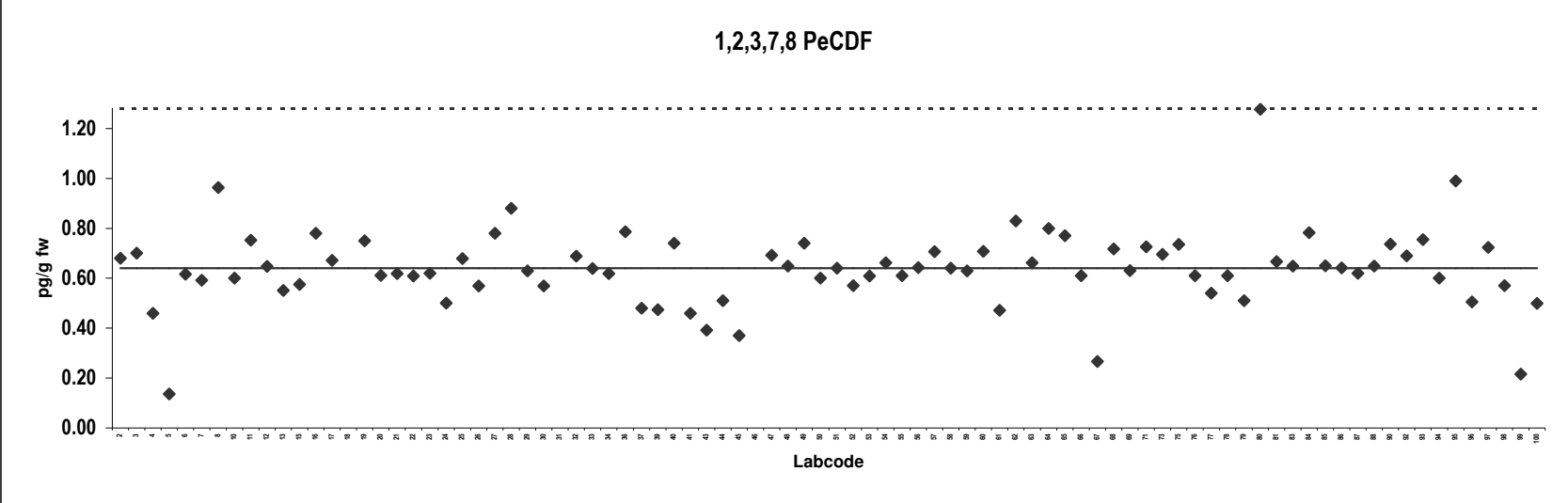


**Salmon**  
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.68		52	0.57	
3	0.70		53	0.61	
4	0.46		54	0.66	
5	0.14		55	0.61	
6	0.62		56	0.64	
7	0.59		57	0.71	
8	0.96		58	0.64	
10	0.60		59	0.63	
11	0.75		60	0.71	
12	0.65		61	0.47	
13	0.55		62	0.83	
15	0.58		63	0.66	
16	0.78		64	0.80	
17	0.67		65	0.77	
18	2.0	Outlier	66	0.61	
19	0.75		67	0.27	
20	0.61		68	0.72	
21	0.62		69	0.63	
22	0.61		71	0.73	
23	0.62		73	0.70	
24	0.50		75	0.74	
25	0.68		76	0.61	
26	0.57		77	0.54	
27	0.78		78	0.61	
28	0.88		79	0.51	
29	0.63		80	1.3	
30	0.57		81	0.67	
31	8.6	Outlier	83	0.65	
32	0.69		84	0.78	
33	0.64		85	0.65	
34	0.62		86	0.64	
36	0.79		87	0.62	
37	0.48		88	0.65	
39	0.47		90	0.74	
40	0.74		92	0.69	
41	0.46		93	0.76	
43	0.39		94	0.60	
44	0.51		95	0.99	
45	0.37		96	0.51	
46	24	Outlier	97	0.72	
47	0.69		98	0.57	
48	0.65		99	0.22	
49	0.74		100	0.50	
50	0.60				
51	0.64				

**Consensus statistics**

Consensus median, pg/g	0.64
Median all values pg/g	0.64
Consensus mean, pg/g	0.64
Standard deviation, pg/g	0.15
Relative standard deviation, %	24
No. of values reported	88
No. of values removed	3
No. of reported non-detects	0



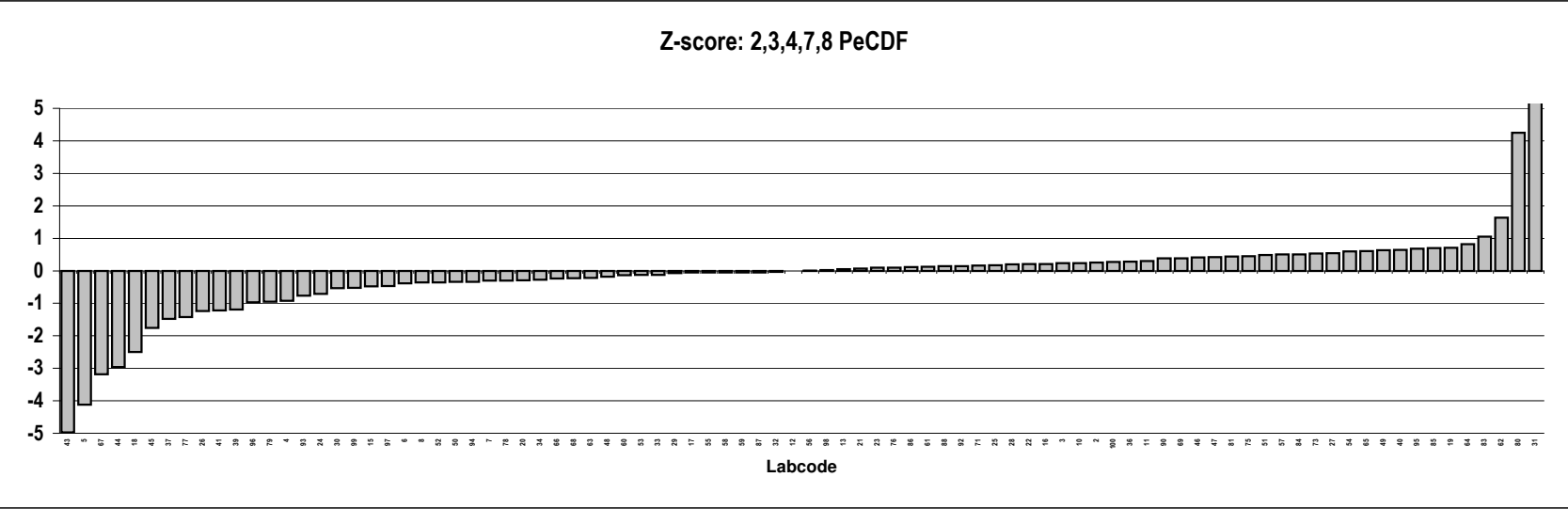
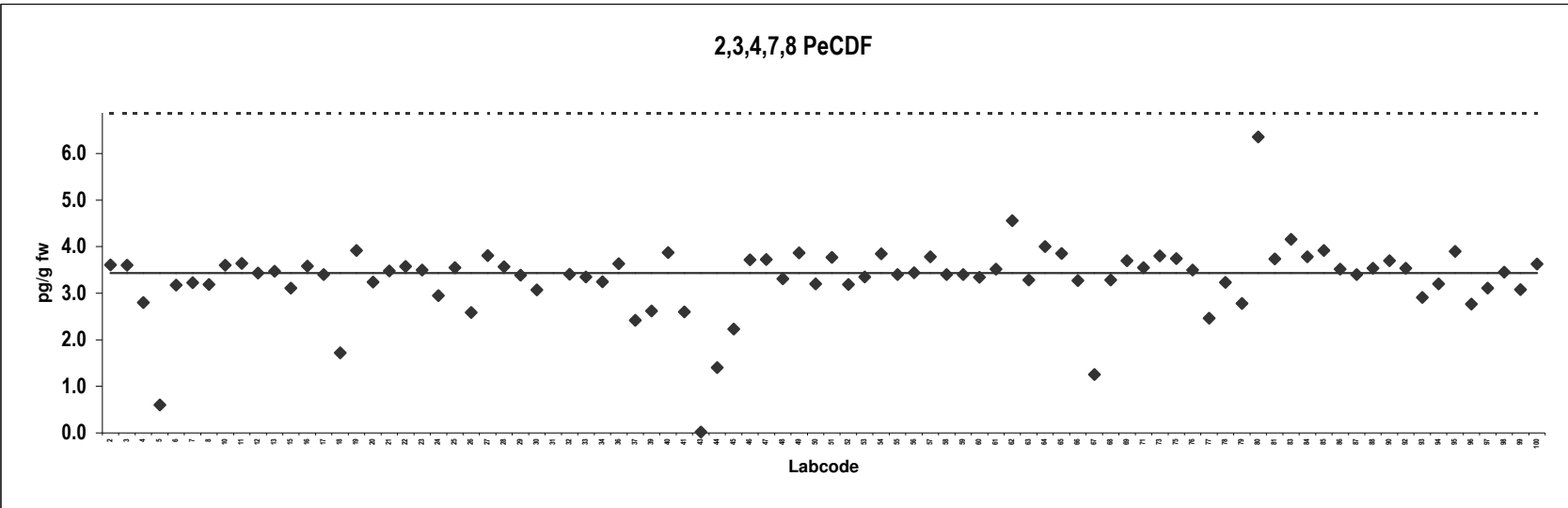
**Salmon**  
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	3.6		52	3.2	
3	3.6		53	3.3	
4	2.8		54	3.8	
5	0.60		55	3.4	
6	3.2		56	3.4	
7	3.2		57	3.8	
8	3.2		58	3.4	
10	3.6		59	3.4	
11	3.6		60	3.3	
12	3.4		61	3.5	
13	3.5		62	4.6	
15	3.1		63	3.3	
16	3.6		64	4.0	
17	3.4		65	3.9	
18	1.7		66	3.3	
19	3.9		67	1.3	
20	3.2		68	3.3	
21	3.5		69	3.7	
22	3.6		71	3.5	
23	3.5		73	3.8	
24	2.9		75	3.7	
25	3.6		76	3.5	
26	2.6		77	2.5	
27	3.8		78	3.2	
28	3.6		79	2.8	
29	3.4		80	6.4	
30	3.1		81	3.7	
31	4.0	Outlier	83	4.2	
32	3.4		84	3.8	
33	3.4		85	3.9	
34	3.2		86	3.5	
36	3.6		87	3.4	
37	2.4		88	3.5	
39	2.6		90	3.7	
40	3.9		92	3.5	
41	2.6		93	2.9	
43	0.020	ND	94	3.2	
44	1.4		95	3.9	
45	2.2		96	2.8	
46	3.7		97	3.1	
47	3.7		98	3.5	
48	3.3		99	3.1	
49	3.9		100	3.6	
50	3.2				
51	3.8				

**Consensus statistics**

Consensus median, pg/g	3.4
Median all values pg/g	3.4
Consensus mean, pg/g	3.3
Standard deviation, pg/g	0.78
Relative standard deviation, %	24
No. of values reported	88
No. of values removed	1
No. of reported non-detects	1





## Salmon

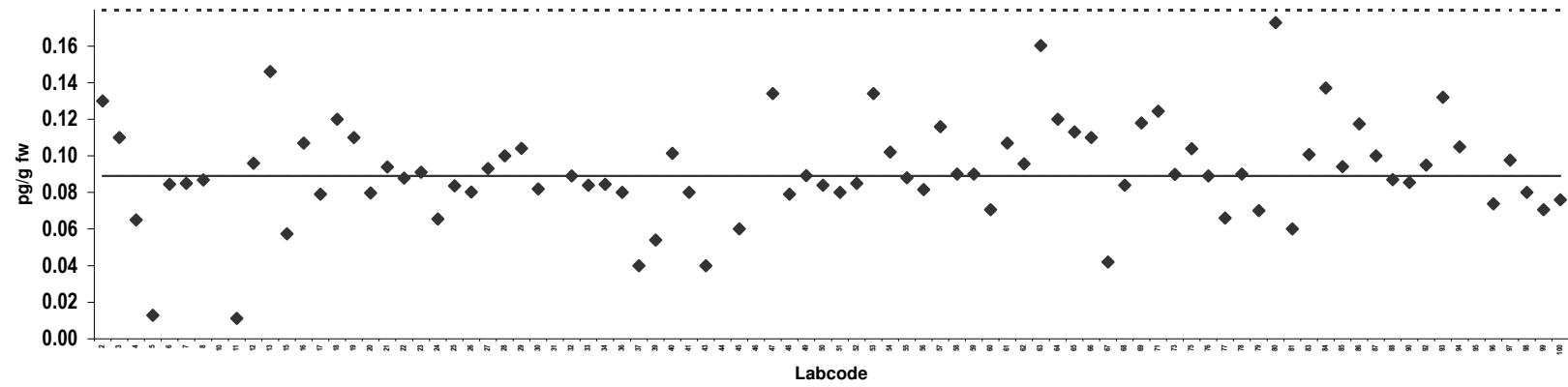
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.13		52	0.085	
3	0.11		53	0.13	
4	0.065		54	0.10	
5	0.013		55	0.088	
6	0.085		56	0.081	
7	0.085		57	0.12	
8	0.087		58	0.090	
10	1.0	Outlier,ND	59	0.090	
11	0.011	ND	60	0.071	
12	0.096		61	0.11	
13	0.15		62	0.096	
15	0.057		63	0.16	
16	0.11		64	0.12	
17	0.079		65	0.11	
18	0.12	ND	66	0.11	
19	0.11		67	0.042	
20	0.080		68	0.084	
21	0.094		69	0.12	
22	0.088		71	0.12	
23	0.091		73	0.090	
24	0.065		75	0.10	
25	0.084		76	0.089	
26	0.080		77	0.066	
27	0.093		78	0.090	
28	0.10		79	0.070	
29	0.10		80	0.17	
30	0.082		81	0.060	
31	1.1	Outlier	83	0.10	
32	0.089		84	0.14	
33	0.084		85	0.094	
34	0.084		86	0.12	
36	0.080		87	0.10	
37	0.040	ND	88	0.087	
39	0.054		90	0.085	
40	0.10		92	0.095	
41	0.080		93	0.13	
43	0.040	ND	94	0.11	
44	1.8	Outlier	95	0.32	Outlier
45	0.060		96	0.074	
46	2.6	Outlier	97	0.098	
47	0.13		98	0.080	
48	0.079		99	0.070	
49	0.089		100	0.076	
50	0.084				
51	0.080				

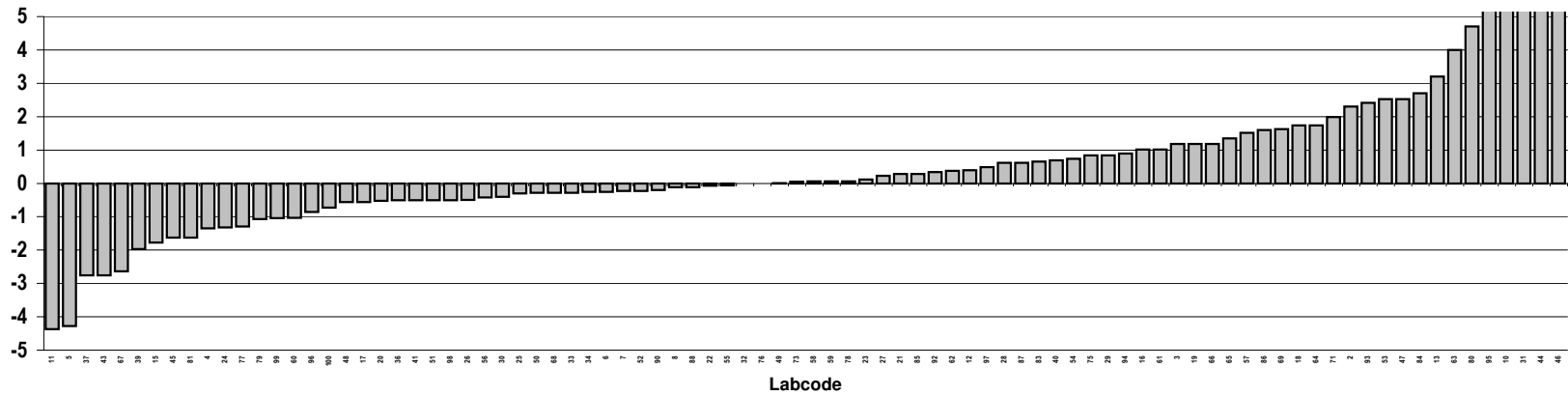
### Consensus statistics

Consensus median, pg/g	0.089
Median all values pg/g	0.090
Consensus mean, pg/g	0.091
Standard deviation, pg/g	0.027
Relative standard deviation, %	30
No. of values reported	88
No. of values removed	5
No. of reported non-detects	5

1,2,3,4,7,8 HxCDF



Z-score: 1,2,3,4,7,8 HxCDF



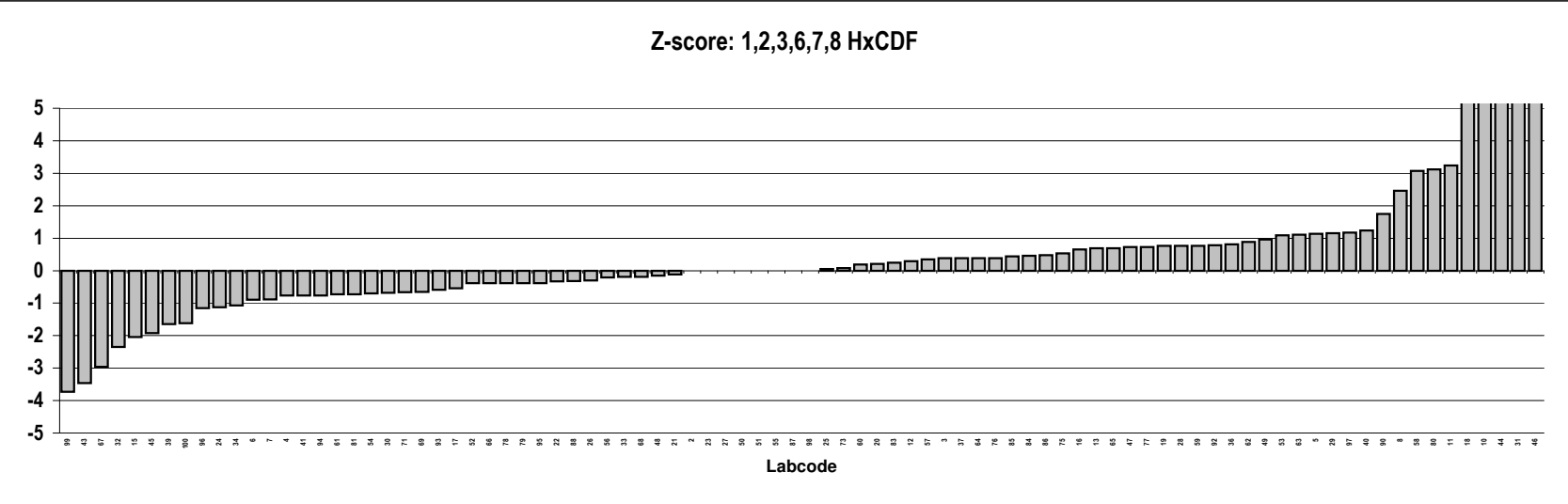
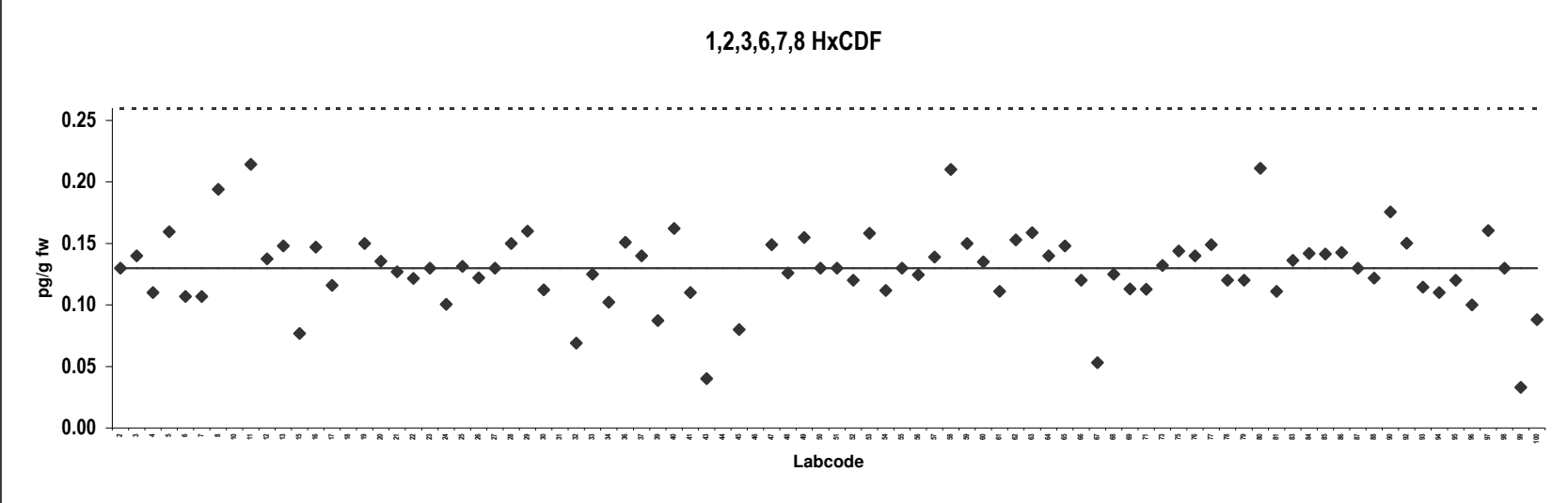
## Salmon

Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.13		52	0.12	
3	0.14		53	0.16	
4	0.11		54	0.11	
5	0.16		55	0.13	
6	0.11		56	0.12	
7	0.11		57	0.14	
8	0.19		58	0.21	
10	1.0	Outlier,ND	59	0.15	
11	0.21		60	0.13	
12	0.14		61	0.11	
13	0.15		62	0.15	
15	0.077		63	0.16	
16	0.15		64	0.14	
17	0.12		65	0.15	
18	0.89	Outlier	66	0.12	
19	0.15		67	0.053	
20	0.14		68	0.13	
21	0.13		69	0.11	
22	0.12		71	0.11	
23	0.13		73	0.13	
24	0.10		75	0.14	
25	0.13		76	0.14	
26	0.12		77	0.15	
27	0.13		78	0.12	
28	0.15		79	0.12	
29	0.16		80	0.21	
30	0.11		81	0.11	
31	1.7	Outlier	83	0.14	
32	0.069		84	0.14	
33	0.12		85	0.14	
34	0.10		86	0.14	
36	0.15		87	0.13	
37	0.14		88	0.12	
39	0.087		90	0.18	
40	0.16		92	0.15	
41	0.11		93	0.11	
43	0.040	ND	94	0.11	
44	1.0	Outlier	95	0.12	
45	0.080		96	0.10	
46	2.0	Outlier	97	0.16	
47	0.15		98	0.13	
48	0.13		99	0.033	
49	0.15		100	0.088	
50	0.13				
51	0.13				

### Consensus statistics

Consensus median, pg/g	0.13
Median all values pg/g	0.13
Consensus mean, pg/g	0.13
Standard deviation, pg/g	0.032
Relative standard deviation, %	24
No. of values reported	88
No. of values removed	5
No. of reported non-detects	2

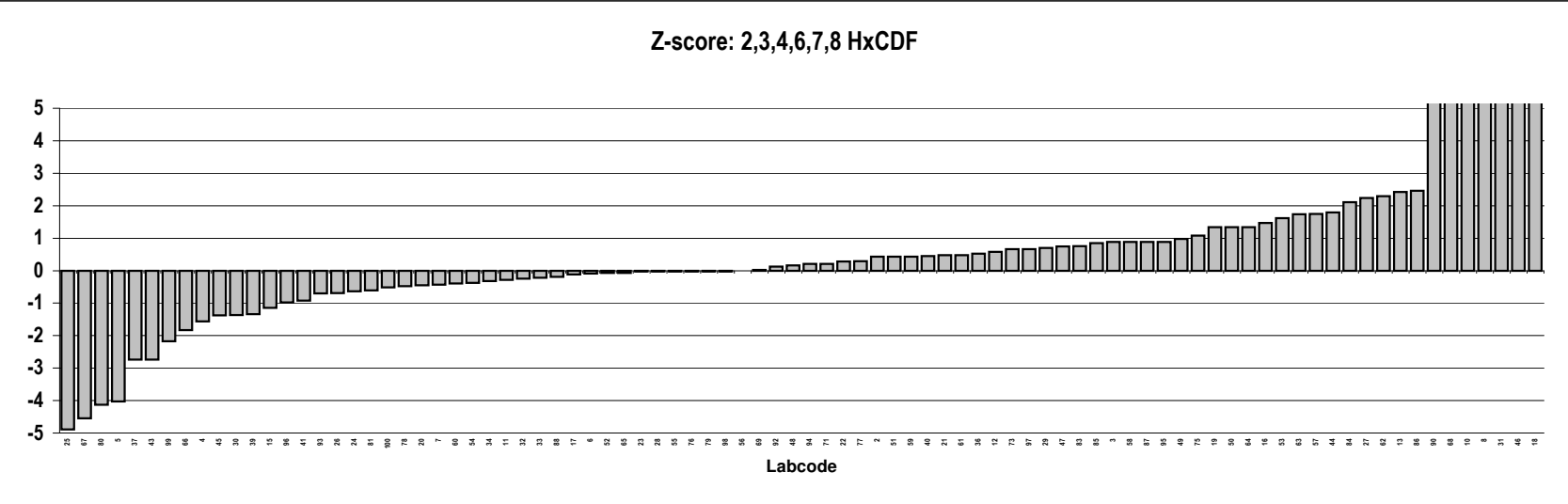
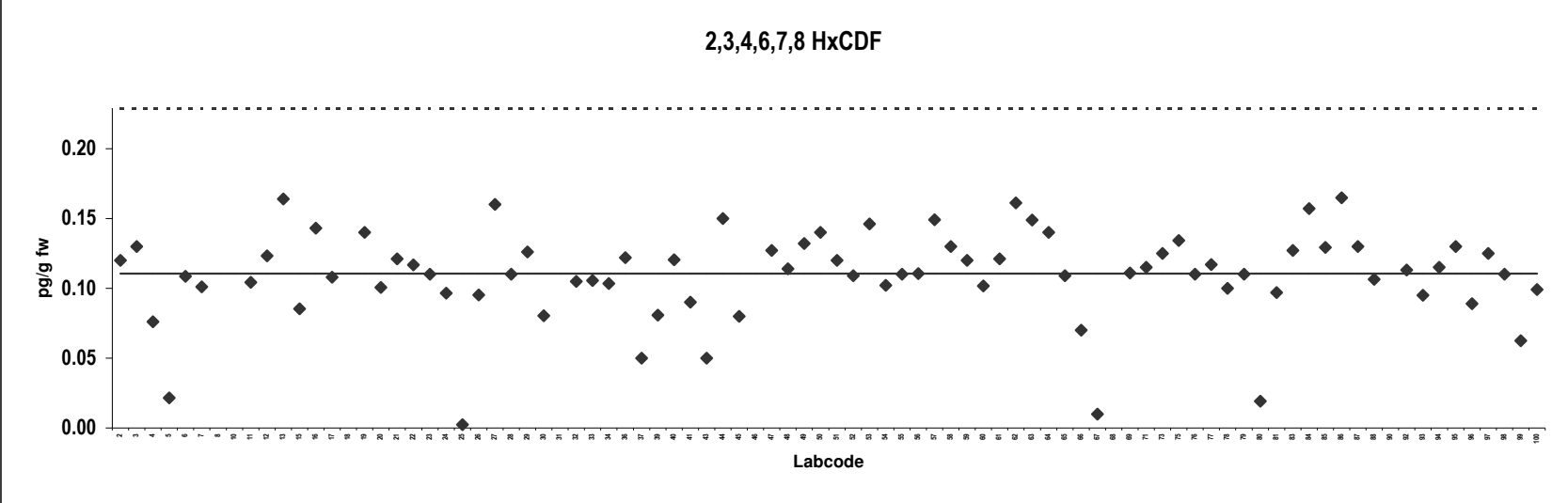


**Salmon**  
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.12		52	0.11	
3	0.13		53	0.15	
4	0.076		54	0.10	
5	0.022		55	0.11	
6	0.11		56	0.11	
7	0.10		57	0.15	
8	1.0	Outlier	58	0.13	
10	1.0	Outlier,ND	59	0.12	
11	0.10		60	0.10	
12	0.12		61	0.12	
13	0.16		62	0.16	
15	0.085		63	0.15	
16	0.14		64	0.14	ND
17	0.11		65	0.11	
18	49	Outlier	66	0.070	
19	0.14		67	0.010	ND
20	0.10		68	0.37	Outlier
21	0.12		69	0.11	
22	0.12		71	0.12	
23	0.11		73	0.13	
24	0.096		75	0.13	
25	0.0024	ND	76	0.11	
26	0.095		77	0.12	
27	0.16		78	0.10	
28	0.11		79	0.11	
29	0.13		80	0.019	
30	0.080		81	0.097	
31	1.5	Outlier	83	0.13	
32	0.11		84	0.16	
33	0.11		85	0.13	
34	0.10		86	0.16	
36	0.12		87	0.13	
37	0.050	ND	88	0.11	
39	0.081		90	0.28	Outlier
40	0.12		92	0.11	
41	0.090		93	0.095	
43	0.050	ND	94	0.12	
44	0.15	ND	95	0.13	
45	0.080		96	0.089	
46	1.6	Outlier	97	0.13	
47	0.13		98	0.11	
48	0.11		99	0.063	
49	0.13		100	0.099	
50	0.14				
51	0.12				

**Consensus statistics**

Consensus median, pg/g	0.11
Median all values pg/g	0.11
Consensus mean, pg/g	0.11
Standard deviation, pg/g	0.032
Relative standard deviation, %	30
No. of values reported	88
No. of values removed	7
No. of reported non-detects	7



# Salmon

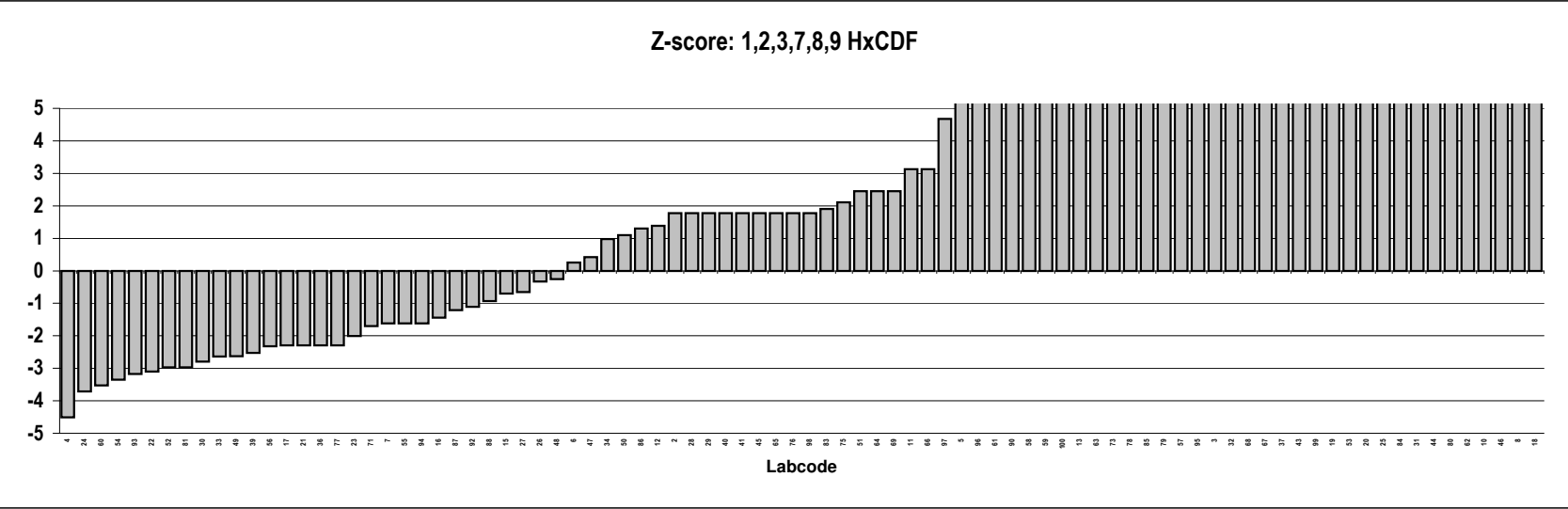
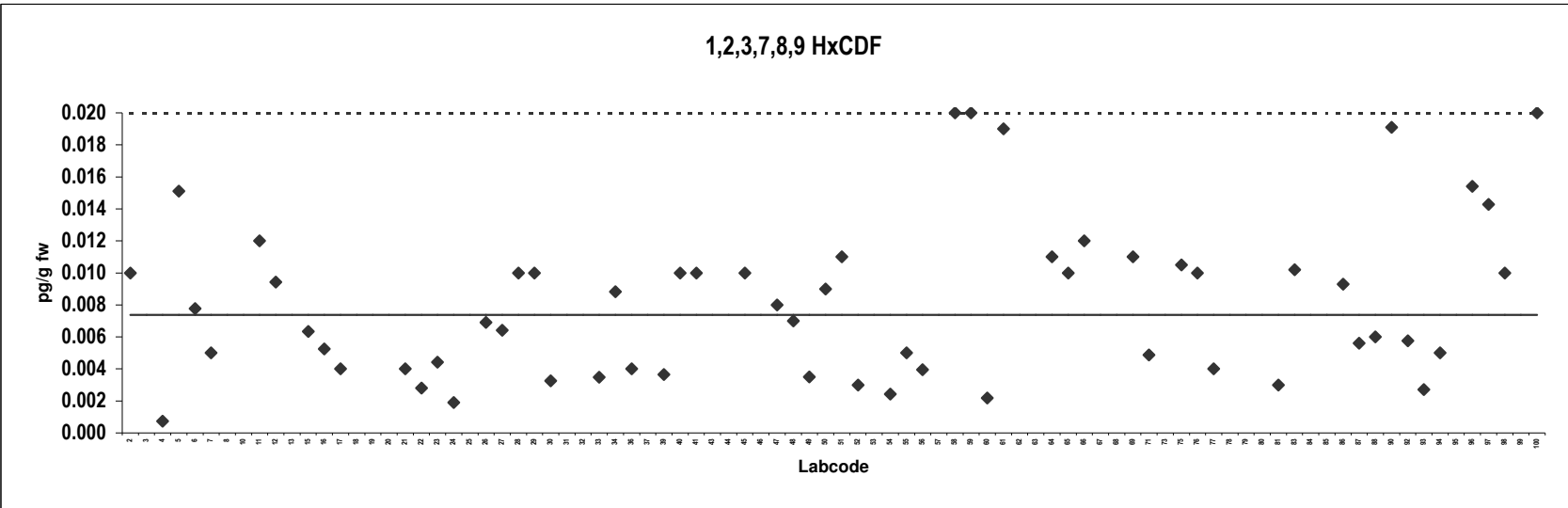
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	52	0.0030	ND
3	0.037	Outlier	53	0.061	Outlier
4	0.00073	ND	54	0.0024	
5	0.015	ND	55	0.0050	ND
6	0.0078		56	0.0040	
7	0.0050	ND	57	0.034	Outlier,ND
8	1.8	Outlier	58	0.020	ND
10	1.0	Outlier,ND	59	0.020	ND
11	0.012	ND	60	0.0022	
12	0.0094		61	0.019	ND
13	0.022	Outlier,ND	62	0.34	Outlier
15	0.0063		63	0.025	Outlier
16	0.0053		64	0.011	
17	0.0040	ND	65	0.010	ND
18	30	Outlier	66	0.012	
19	0.060	Outlier	67	0.048	Outlier
20	0.063	Outlier,ND	68	0.047	Outlier
21	0.0040	ND	69	0.011	ND
22	0.0028		71	0.0049	
23	0.0044		73	0.025	Outlier,ND
24	0.0019		75	0.011	
25	0.10	Outlier	76	0.010	ND
26	0.0069	ND	77	0.0040	
27	0.0064	ND	78	0.026	Outlier,ND
28	0.010	ND	79	0.030	Outlier
29	0.010	ND	80	0.20	Outlier
30	0.0033	ND	81	0.0030	
31	0.19	Outlier	83	0.010	
32	0.045	Outlier,ND	84	0.14	Outlier,ND
33	0.0035		85	0.029	Outlier,ND
34	0.0088	ND	86	0.0093	
36	0.0040	ND	87	0.0056	
37	0.050	Outlier,ND	88	0.0060	ND
39	0.0037	ND	90	0.019	ND
40	0.010	ND	92	0.0058	ND
41	0.010	ND	93	0.0027	ND
43	0.050	Outlier,ND	94	0.0050	ND
44	0.20	Outlier,ND	95	0.035	Outlier,ND
45	0.010	ND	96	0.015	ND
46	1.1	Outlier	97	0.014	ND
47	0.0080		98	0.010	ND
48	0.0070	ND	99	0.055	Outlier
49	0.0035		100	0.020	ND
50	0.0090	ND			
51	0.011	ND			

## Consensus statistics

Consensus median, pg/g	0.0074
Median all values pg/g	0.010
Consensus mean, pg/g	0.0082
Standard deviation, pg/g	0.0049
Relative standard deviation, %	60
No. of values reported	88
No. of values removed	28
No. of reported non-detects	51





# Salmon

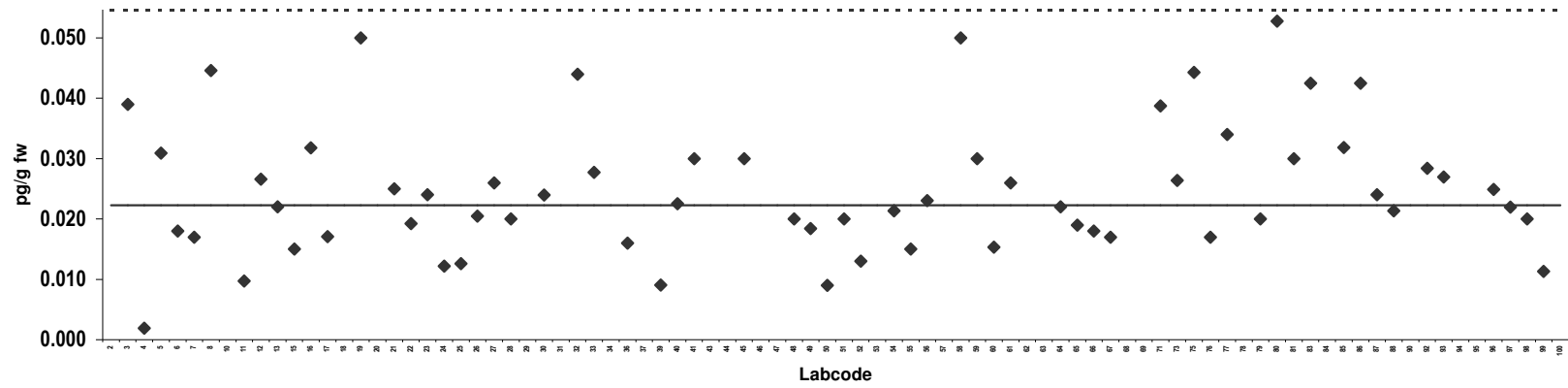
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.10	Outlier	52	0.013	
3	0.039		53	0.12	Outlier
4	0.0019	ND	54	0.021	
5	0.031		55	0.015	
6	0.018		56	0.023	
7	0.017		57	0.11	Outlier
8	0.045		58	0.050	ND
10	1.0	Outlier,ND	59	0.030	
11	0.0097	ND	60	0.015	
12	0.027		61	0.026	ND
13	0.022	ND	62	0.058	Outlier
15	0.015		63	0.086	Outlier
16	0.032		64	0.022	ND
17	0.017		65	0.019	
18	13	Outlier	66	0.018	
19	0.050		67	0.017	
20	0.063	Outlier,ND	68	0.18	Outlier
21	0.025		69	0.14	Outlier,ND
22	0.019		71	0.039	
23	0.024		73	0.026	
24	0.012		75	0.044	
25	0.013		76	0.017	
26	0.021		77	0.034	
27	0.026		78	0.073	Outlier,ND
28	0.020		79	0.020	
29	0.077	Outlier	80	0.053	
30	0.024		81	0.030	
31	0.46	Outlier	83	0.043	
32	0.044		84	0.12	Outlier
33	0.028		85	0.032	
34	0.069	Outlier	86	0.043	
36	0.016		87	0.024	
37	0.20	Outlier,ND	88	0.021	
39	0.0090		90	0.12	Outlier
40	0.023		92	0.028	
41	0.030	ND	93	0.027	
43	0.070	Outlier,ND	94	0.11	Outlier
44	0.12	Outlier,ND	95	0.092	Outlier,ND
45	0.030	ND	96	0.025	
46	1.8	Outlier	97	0.022	
47	0.068	Outlier	98	0.020	
48	0.020		99	0.011	
49	0.018		100	0.056	Outlier
50	0.0090	ND			
51	0.020				

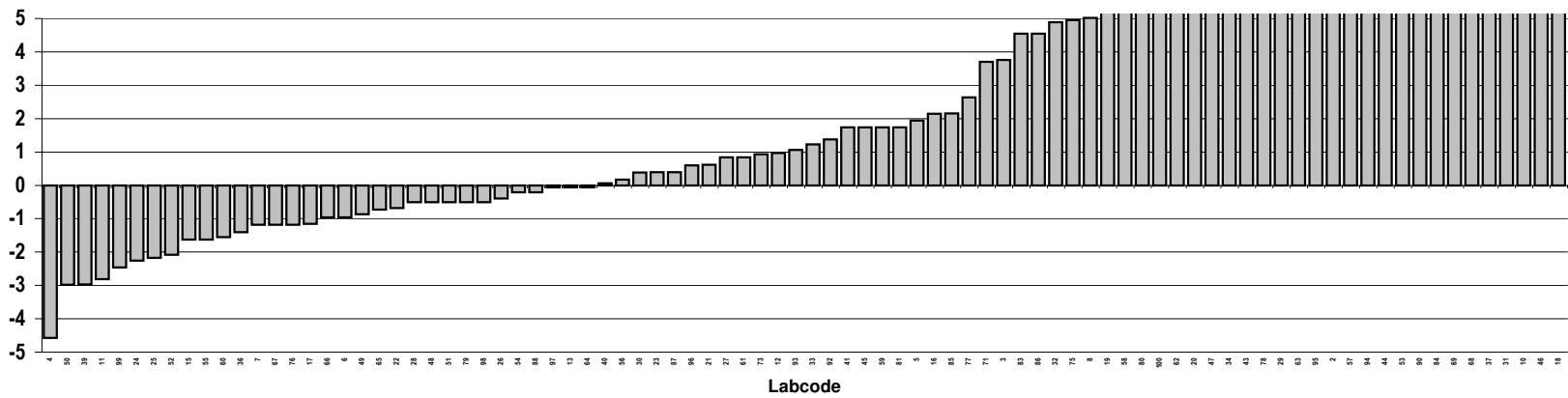
## Consensus statistics

Consensus median, pg/g	0.022
Median all values pg/g	0.027
Consensus mean, pg/g	0.025
Standard deviation, pg/g	0.011
Relative standard deviation, %	44
No. of values reported	88
No. of values removed	24
No. of reported non-detects	17

1,2,3,4,6,7,8 HpCDF



Z-score: 1,2,3,4,6,7,8 HpCDF



# Salmon

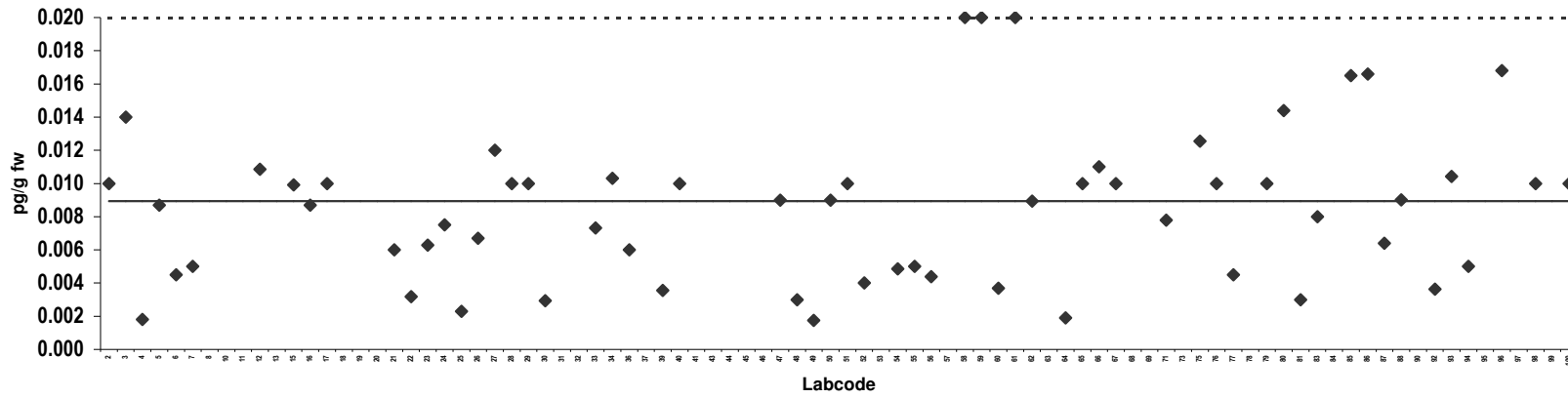
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	52	0.0040	ND
3	0.014	ND	53	0.049	Outlier
4	0.0018	ND	54	0.0049	
5	0.0087		55	0.0050	ND
6	0.0045	ND	56	0.0044	
7	0.0050	ND	57	0.055	Outlier
8	0.021	Outlier,ND	58	0.020	ND
10	1.0	Outlier,ND	59	0.020	ND
11	0.036	Outlier	60	0.0037	
12	0.011		61	0.020	ND
13	0.029	Outlier,ND	62	0.0089	
15	0.0099		63	0.033	Outlier
16	0.0087		64	0.0019	ND
17	0.010	ND	65	0.010	ND
18	5.7	Outlier	66	0.011	
19	0.050	Outlier,ND	67	0.010	ND
20	0.063	Outlier,ND	68	0.030	Outlier,ND
21	0.0060	ND	69	0.068	Outlier,ND
22	0.0032		71	0.0078	
23	0.0063		73	0.025	Outlier,ND
24	0.0075		75	0.013	
25	0.0023		76	0.010	ND
26	0.0067		77	0.0045	
27	0.012		78	0.073	Outlier,ND
28	0.010	ND	79	0.010	ND
29	0.010	ND	80	0.014	
30	0.0029	ND	81	0.0030	
31	0.10	Outlier	83	0.0080	
32	0.045	Outlier,ND	84	0.18	Outlier,ND
33	0.0073		85	0.017	ND
34	0.010	ND	86	0.017	
36	0.0060	ND	87	0.0064	
37	0.20	Outlier,ND	88	0.0090	ND
39	0.0036	ND	90	0.020	Outlier
40	0.010	ND	92	0.0036	ND
41	0.030	Outlier,ND	93	0.010	
43	0.10	Outlier,ND	94	0.0050	ND
44	0.12	Outlier,ND	95	0.11	Outlier,ND
45	0.030	Outlier,ND	96	0.017	ND
46	0.27	Outlier,ND	97	0.026	Outlier,ND
47	0.0090		98	0.010	ND
48	0.0030	ND	99	0.040	Outlier
49	0.0018		100	0.010	ND
50	0.0090	ND			
51	0.010	ND			

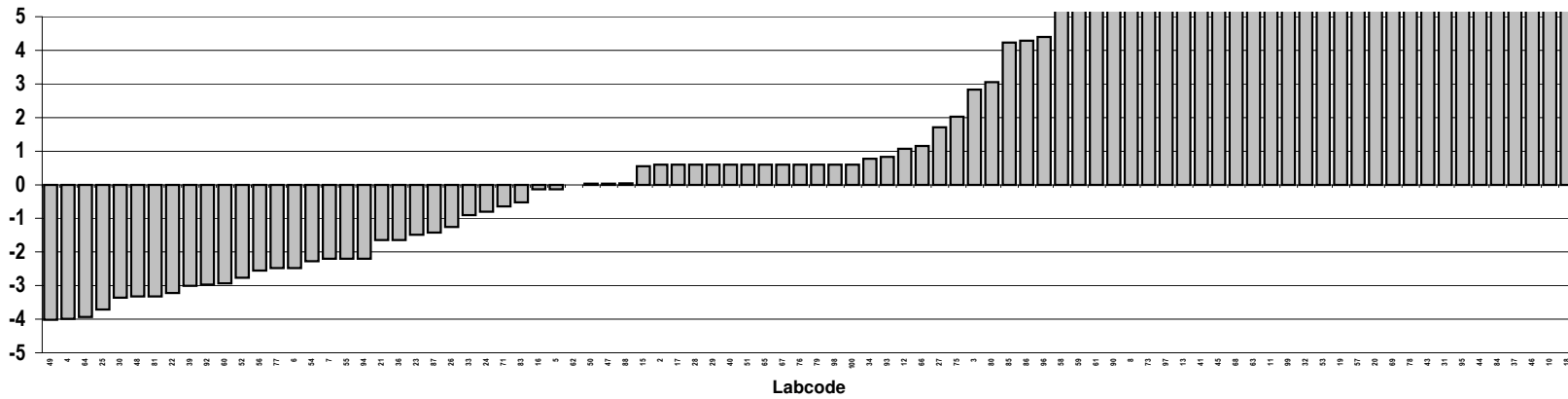
## Consensus statistics

Consensus median, pg/g	0.0089
Median all values pg/g	0.010
Consensus mean, pg/g	0.0085
Standard deviation, pg/g	0.0046
Relative standard deviation, %	54
No. of values reported	88
No. of values removed	27
No. of reported non-detects	53

1,2,3,4,7,8,9 HpCDF



Z-score: 1,2,3,4,7,8,9 HpCDF

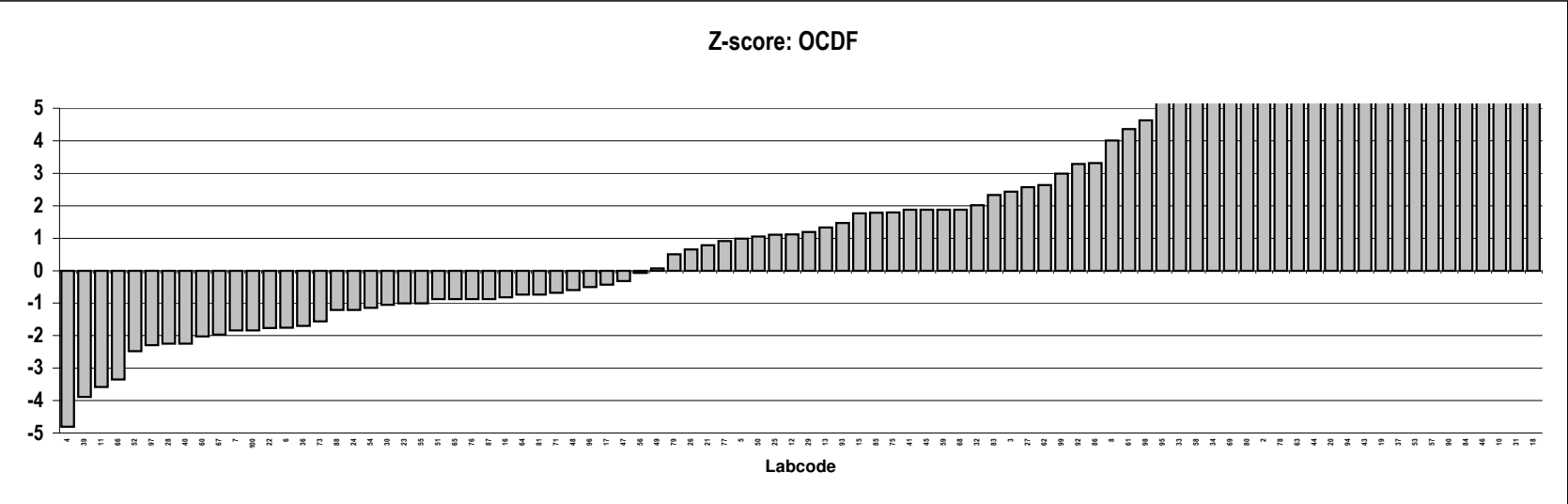
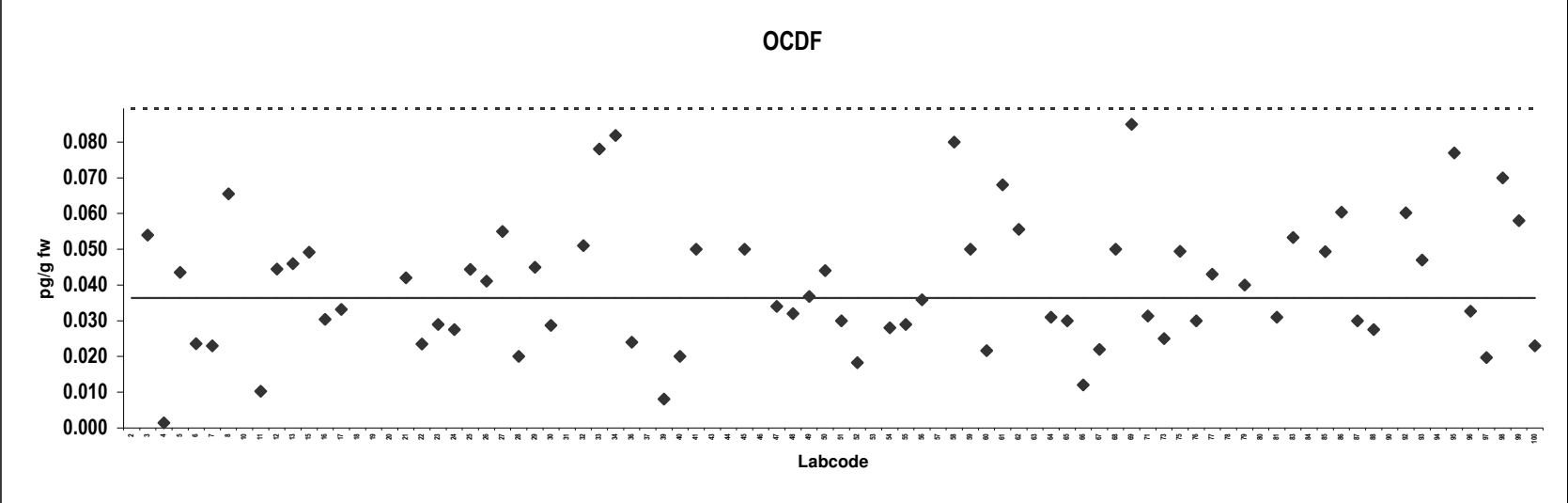


**Salmon**  
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.10	Outlier	52	0.018	
3	0.054		53	0.21	Outlier
4	0.0014	ND	54	0.028	
5	0.044		55	0.029	
6	0.024		56	0.036	
7	0.023		57	0.22	Outlier
8	0.066		58	0.080	ND
10	2.0	Outlier,ND	59	0.050	
11	0.010	ND	60	0.022	
12	0.044		61	0.068	ND
13	0.046	ND	62	0.056	
15	0.049		63	0.12	Outlier
16	0.030		64	0.031	ND
17	0.033		65	0.030	
18	21	Outlier	66	0.012	
19	0.20	Outlier,ND	67	0.022	
20	0.13	Outlier,ND	68	0.050	ND
21	0.042		69	0.085	ND
22	0.023		71	0.031	
23	0.029		73	0.025	ND
24	0.028		75	0.049	
25	0.044		76	0.030	ND
26	0.041		77	0.043	
27	0.055		78	0.12	Outlier,ND
28	0.020		79	0.040	
29	0.045		80	0.091	Outlier
30	0.029		81	0.031	
31	2.7	Outlier	83	0.053	
32	0.051	ND	84	0.37	Outlier,ND
33	0.078		85	0.049	
34	0.082		86	0.060	
36	0.024		87	0.030	
37	0.20	Outlier,ND	88	0.028	
39	0.0081		90	0.30	Outlier
40	0.020	ND	92	0.060	
41	0.050	ND	93	0.047	
43	0.15	Outlier,ND	94	0.15	Outlier
44	0.12	Outlier,ND	95	0.077	ND
45	0.050	ND	96	0.033	
46	0.80	Outlier	97	0.020	ND
47	0.034		98	0.070	ND
48	0.032		99	0.058	
49	0.037		100	0.023	
50	0.044	ND			
51	0.030				

**Consensus statistics**

Consensus median, pg/g	0.036
Median all values pg/g	0.045
Consensus mean, pg/g	0.040
Standard deviation, pg/g	0.018
Relative standard deviation, %	46
No. of values reported	88
No. of values removed	18
No. of reported non-detects	26



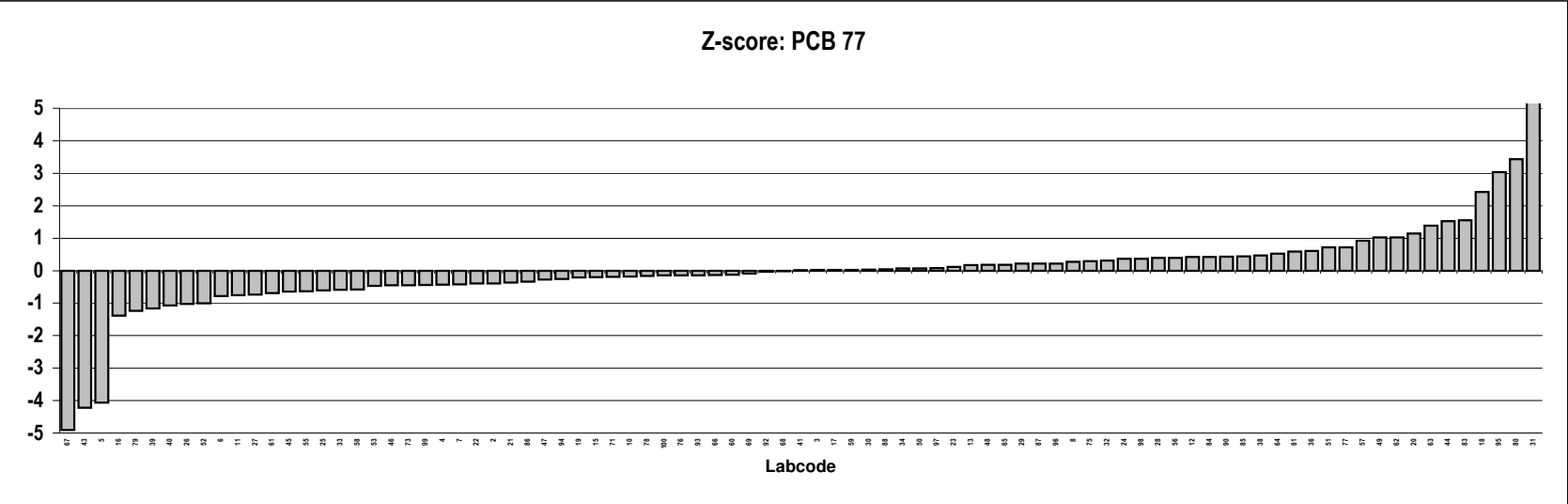
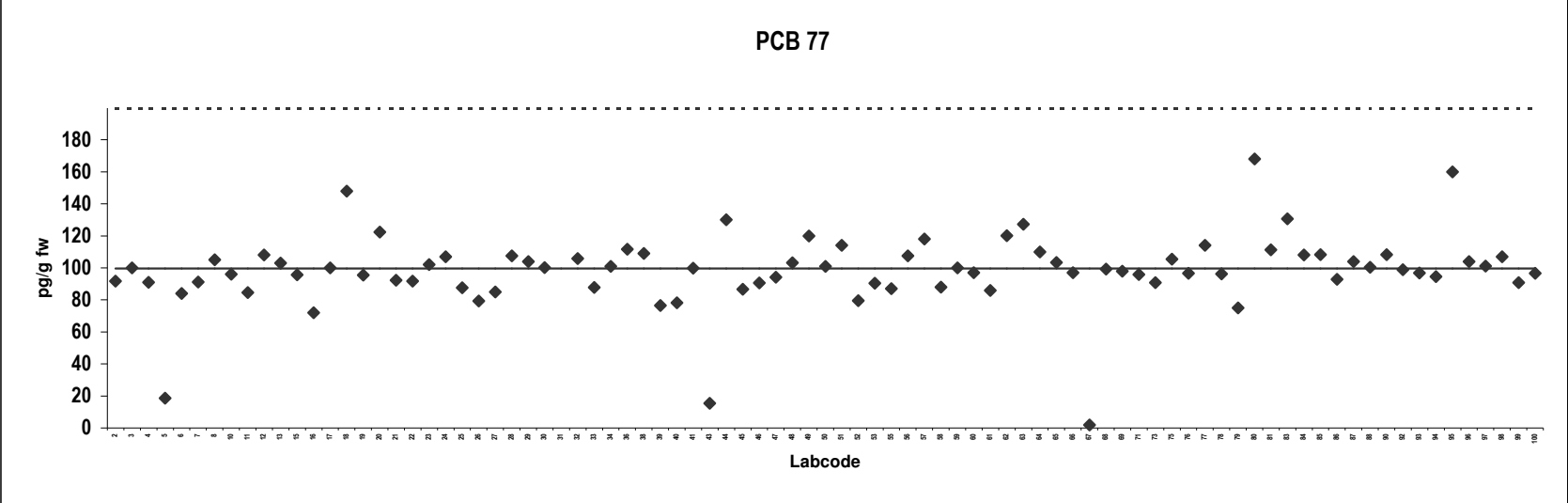
**Salmon**  
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	92		52	80	
3	100		53	90	
4	91		55	87	
5	19		56	108	
6	84		57	118	
7	91		58	88	
8	105		59	100	
10	96		60	97	
11	84		61	86	
12	108		62	120	
13	103		63	127	
15	96		64	110	
16	72		65	103	
17	100		66	97	
18	148		67	1.8	
19	95		68	99	
20	122		69	98	
21	92		71	96	
22	92		73	91	
23	102		75	105	
24	107		76	97	
25	88		77	114	
26	79		78	96	
27	85		79	75	
28	107		80	168	
29	104		81	111	
30	100		83	131	
31	1050	Outlier	84	108	
32	106		85	108	
33	88		86	93	
34	101		87	104	
36	112		88	100	
38	109		90	108	
39	76		92	99	
40	78		93	97	
41	100		94	95	
43	16		95	160	
44	130	ND	96	104	
45	87		97	101	
46	91		98	107	
47	94		99	91	
48	103		100	97	
49	120				
50	101				
51	114				

**Consensus statistics**

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	98
Standard deviation, pg/g	23
Relative standard deviation, %	23
No. of values reported	87
No. of values removed	1
No. of reported non-detects	1



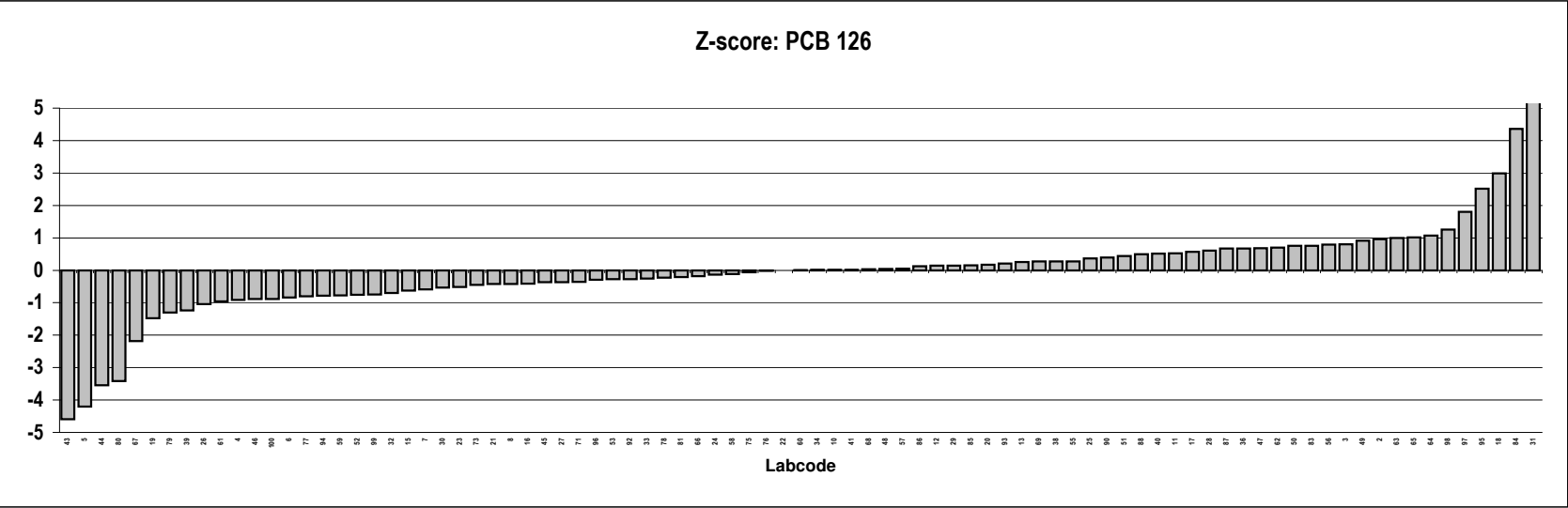
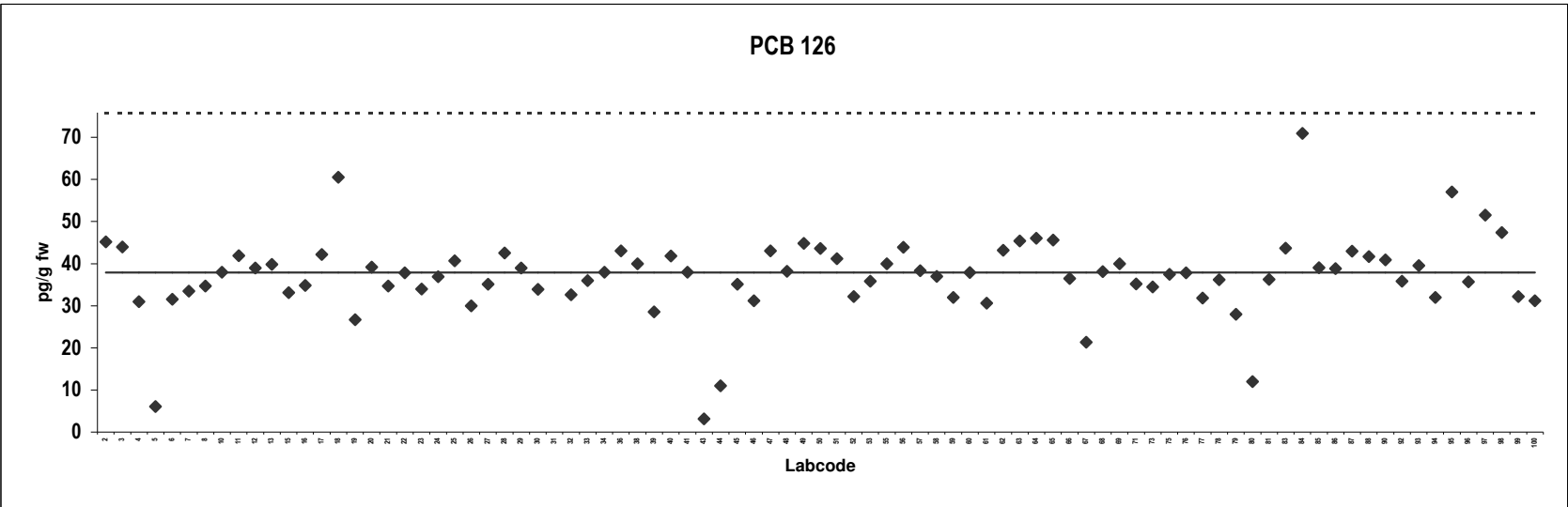


**Salmon**  
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	45		52	32	
3	44		53	36	
4	31		55	40	
5	6.1		56	44	
6	32		57	38	
7	33		58	37	
8	35		59	32	
10	38		60	38	
11	42		61	31	
12	39		62	43	
13	40		63	45	
15	33		64	46	
16	35		65	46	
17	42		66	37	
18	61		67	21	
19	27		68	38	
20	39		69	40	
21	35		71	35	
22	38		73	35	
23	34		75	37	
24	37		76	38	
25	41		77	32	
26	30		78	36	
27	35		79	28	
28	43		80	12	
29	39		81	36	
30	34		83	44	
31	386	Outlier	84	71	
32	33		85	39	
33	36		86	39	
34	38		87	43	
36	43		88	42	
38	40		90	41	
39	29		92	36	
40	42		93	40	
41	38		94	32	
43	3.1		95	57	
44	11	ND	96	36	
45	35		97	52	
46	31		98	47	
47	43		99	32	
48	38		100	31	
49	45				
50	44				
51	41				

**Consensus statistics**

Consensus median, pg/g	38
Median all values pg/g	38
Consensus mean, pg/g	37
Standard deviation, pg/g	9.5
Relative standard deviation, %	26
No. of values reported	87
No. of values removed	1
No. of reported non-detects	1

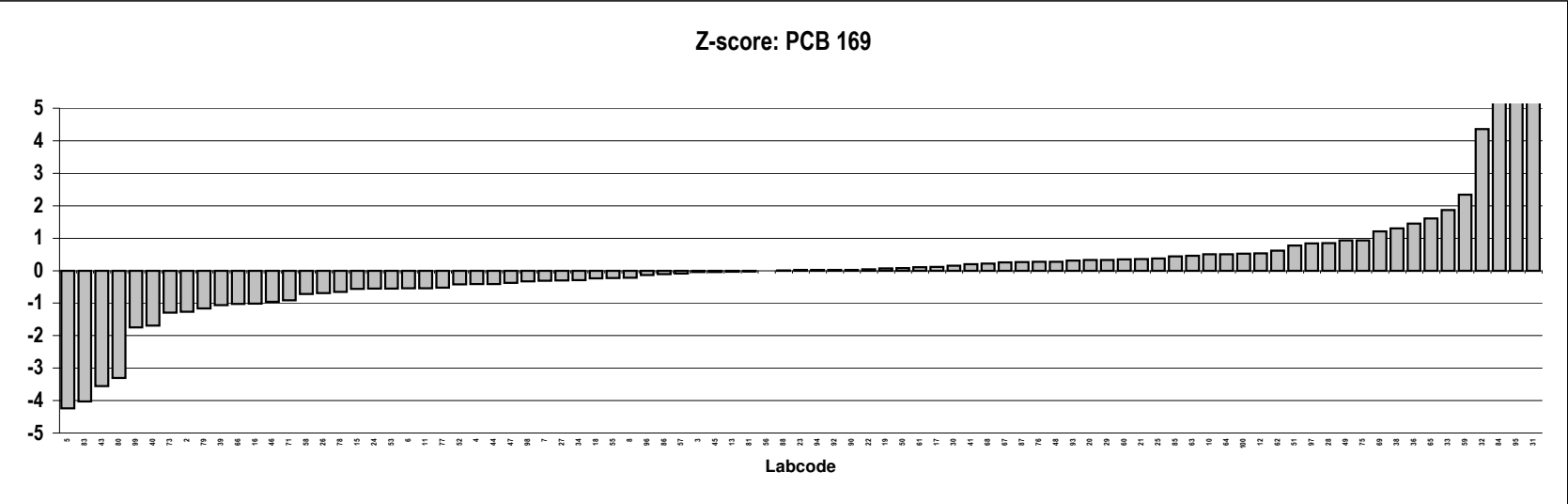
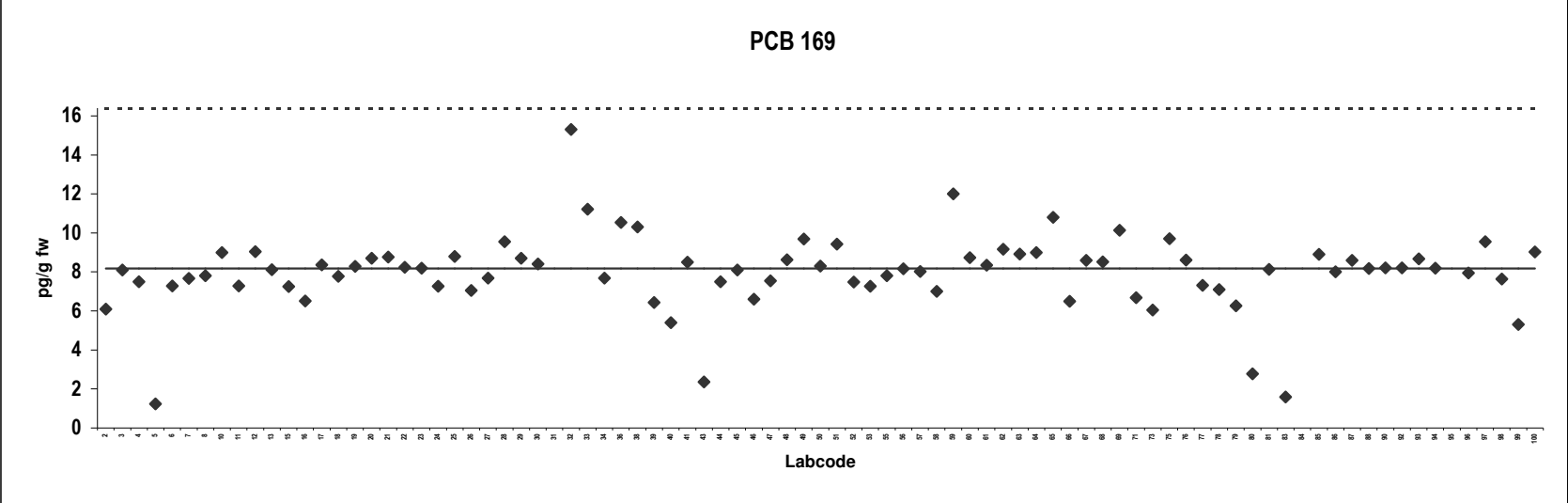


**Salmon**  
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	6.1		52	7.5	
3	8.1		53	7.3	
4	7.5		55	7.8	
5	1.2		56	8.2	
6	7.3		57	8.0	
7	7.7		58	7.0	
8	7.8		59	12	
10	9.0		60	8.7	
11	7.3		61	8.3	
12	9.0		62	9.2	
13	8.1		63	8.9	
15	7.3		64	9.0	
16	6.5		65	11	
17	8.4		66	6.5	
18	7.8		67	8.6	
19	8.3		68	8.5	
20	8.7		69	10	
21	8.8		71	6.7	
22	8.2		73	6.1	
23	8.2		75	9.7	
24	7.3		76	8.6	
25	8.8		77	7.3	
26	7.0		78	7.1	
27	7.7		79	6.3	
28	9.6		80	2.8	
29	8.7		81	8.1	
30	8.4		83	1.6	ND
31	101	Outlier	84	22	Outlier
32	15		85	8.9	
33	11		86	8.0	
34	7.7		87	8.6	
36	11		88	8.2	
38	10		90	8.2	
39	6.4		92	8.2	
40	5.4		93	8.7	
41	8.5		94	8.2	
43	2.4		95	23	Outlier
44	7.5	ND	96	8.0	
45	8.1		97	9.5	
46	6.6		98	7.6	
47	7.6		99	5.3	
48	8.6		100	9.0	
49	9.7				
50	8.3				
51	9.4				

**Consensus statistics**

Consensus median, pg/g	8.2
Median all values pg/g	8.2
Consensus mean, pg/g	8.0
Standard deviation, pg/g	2.0
Relative standard deviation, %	25
No. of values reported	87
No. of values removed	3
No. of reported non-detects	2



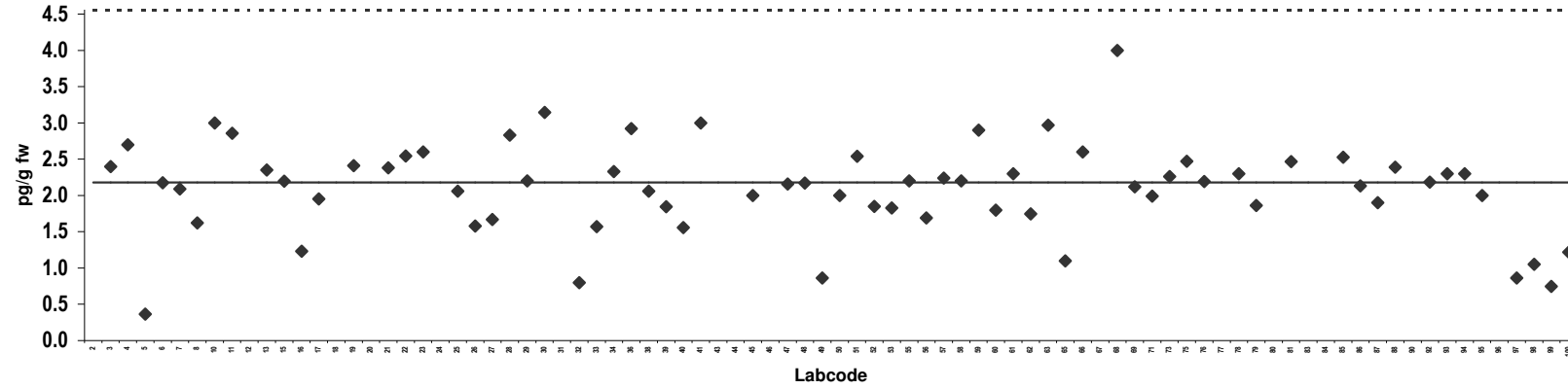
**Salmon**  
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	2.2	Outlier	52	1.9	
3	2.4		53	1.8	
4	2.7		55	2.2	
5	0.37		56	1.7	
6	2.2		57	2.2	
7	2.1		58	2.2	
8	1.6		59	2.9	
10	3.0		60	1.8	
11	2.9		61	2.3	
12	5.9	Outlier	62	1.7	
13	2.4		63	3.0	
15	2.2		65	1.1	
16	1.2		66	2.6	
17	2.0		67	74	Outlier ND
18	81	Outlier	68	4.0	
19	2.4		69	2.1	
20	5.0	Outlier,ND	71	2.0	
21	2.4		73	2.3	
22	2.5		75	2.5	
23	2.6		76	2.2	
24	5.5	Outlier	77	6.3	Outlier
25	2.1		78	2.3	
26	1.6		79	1.9	
27	1.7		80	68	Outlier
28	2.8		81	2.5	
29	2.2		83	17	Outlier,ND
30	3.1		84	18	Outlier,ND
31	2.2	Outlier	85	2.5	
32	0.80		86	2.1	
33	1.6		87	1.9	
34	2.3		88	2.4	
36	2.9		90	13	Outlier
38	2.1		92	2.2	
39	1.8		93	2.3	
40	1.6		94	2.3	
41	3.0		95	2.0	ND
43	5.6	Outlier	96	7.7	Outlier
44	30	Outlier,ND	97	0.86	ND
45	2.0		98	1.1	
46	21	Outlier	99	0.75	
47	2.2		100	1.2	
48	2.2				
49	0.86				
50	2.0				
51	2.5				

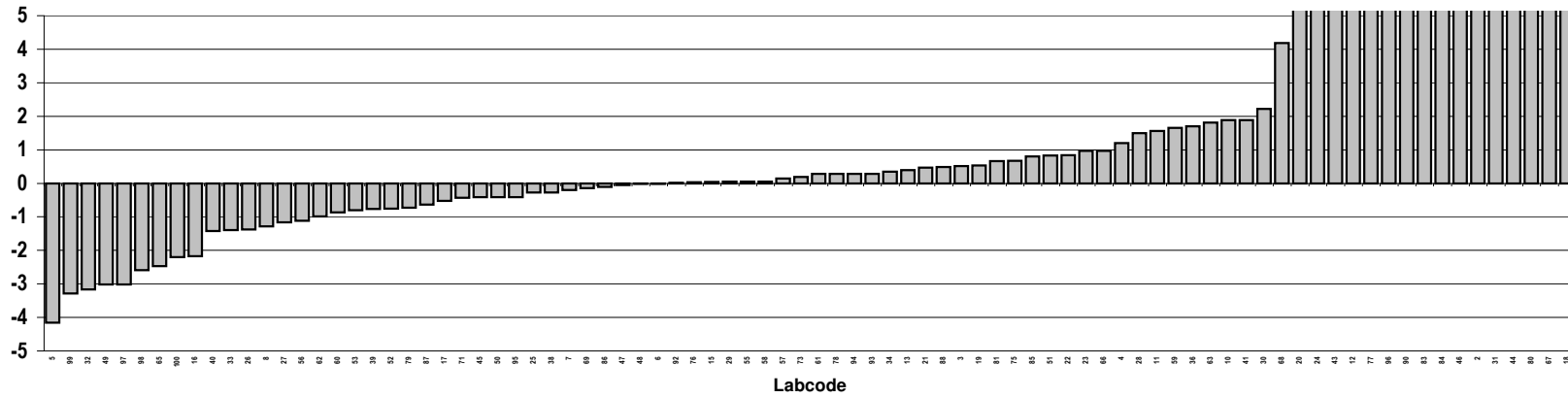
**Consensus statistics**

Consensus median, pg/g	2.2
Median all values pg/g	2.3
Consensus mean, pg/g	2.1
Standard deviation, pg/g	0.63
Relative standard deviation, %	30
No. of values reported	86
No. of values removed	16
No. of reported non-detects	7

### PCB 81



### Z-score: PCB 81



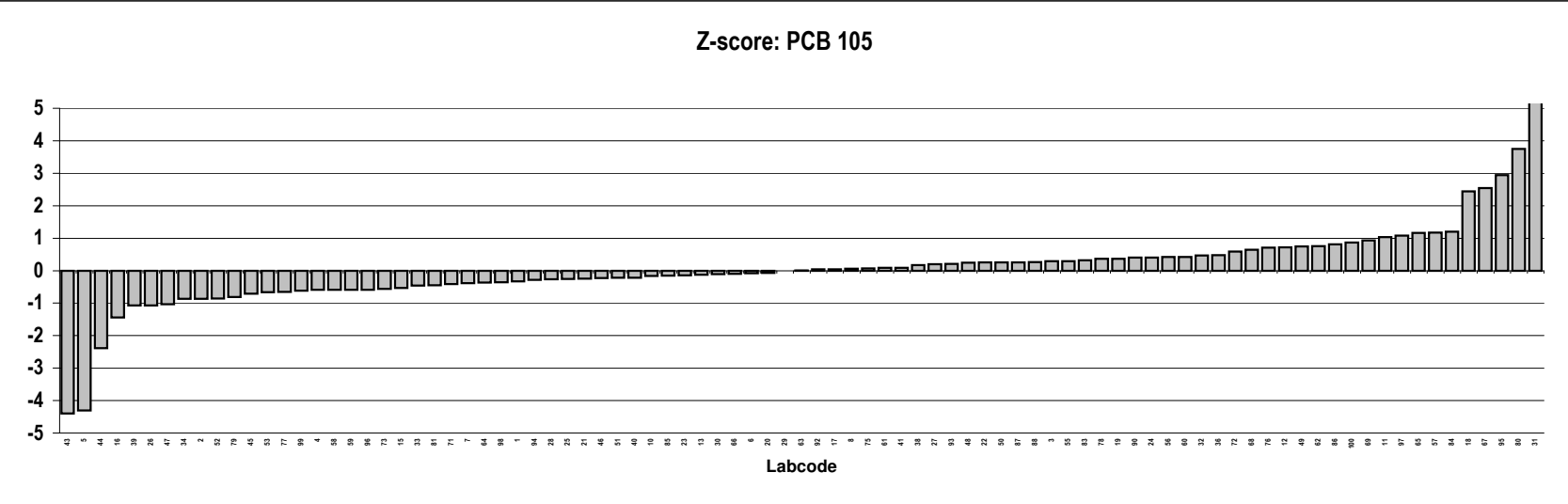
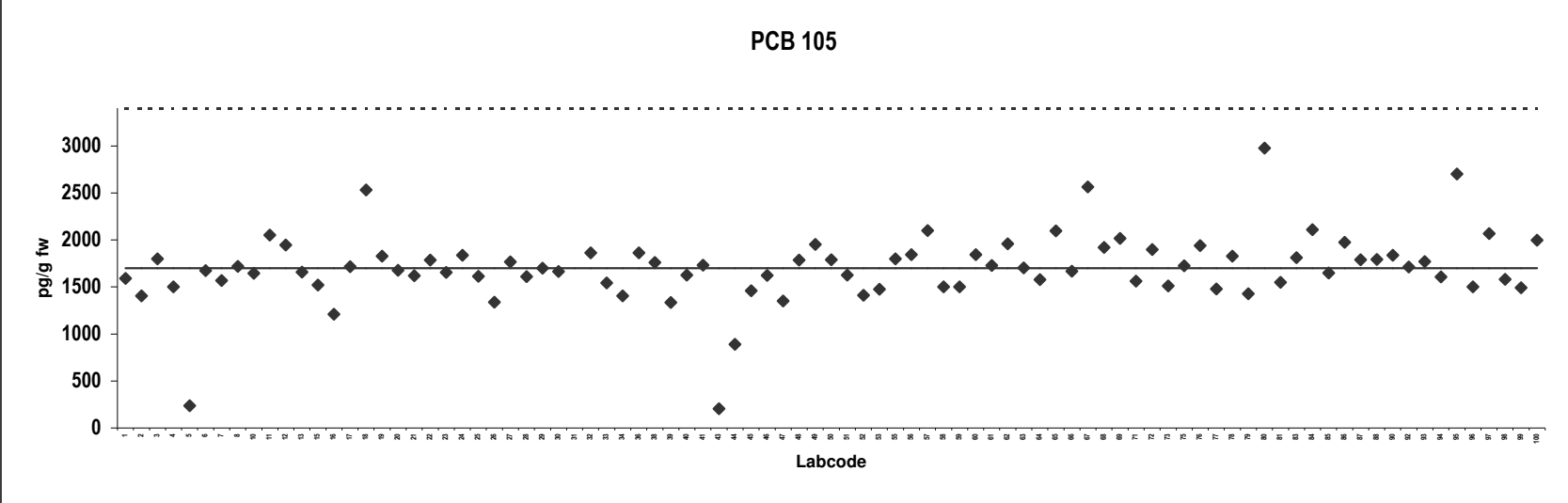
**Salmon**  
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1590		51	1626	
2	1406		52	1410	
3	1800		53	1477	
4	1500		55	1800	
5	236		56	1844	
6	1675		57	2100	
7	1570		58	1500	
8	1720		59	1500	
10	1646		60	1845	
11	2051		61	1729	
12	1946		62	1959	
13	1658		63	1701	
15	1520		64	1577	
16	1209		65	2097	
17	1716		66	1668	
18	2530		67	2565	
19	1826		68	1920	
20	1676		69	2017	
21	1618		71	1562	
22	1786		72	1899	
23	1653		73	1510	
24	1838		75	1724	
25	1614		76	1940	
26	1337		77	1479	
27	1768		78	1826	
28	1610		79	1426	
29	1700		80	2977	
30	1663		81	1548	
31	19700	Outlier	83	1810	
32	1861		84	2108	
33	1543		85	1647	
34	1405		86	1975	
36	1862		87	1788	
38	1760		88	1791	
39	1335		90	1836	
40	1627		92	1713	
41	1730		93	1770	
43	204		94	1605	
44	890		95	2700	
45	1460		96	1500	
46	1624		97	2068	
47	1350		98	1580	
48	1784		99	1491	
49	1953		100	1996	
50	1788				

**Consensus statistics**

Consensus median, pg/g	1700
Median all values pg/g	1701
Consensus mean, pg/g	1700
Standard deviation, pg/g	376
Relative standard deviation, %	22
No. of values reported	89
No. of values removed	1
No. of reported non-detects	0



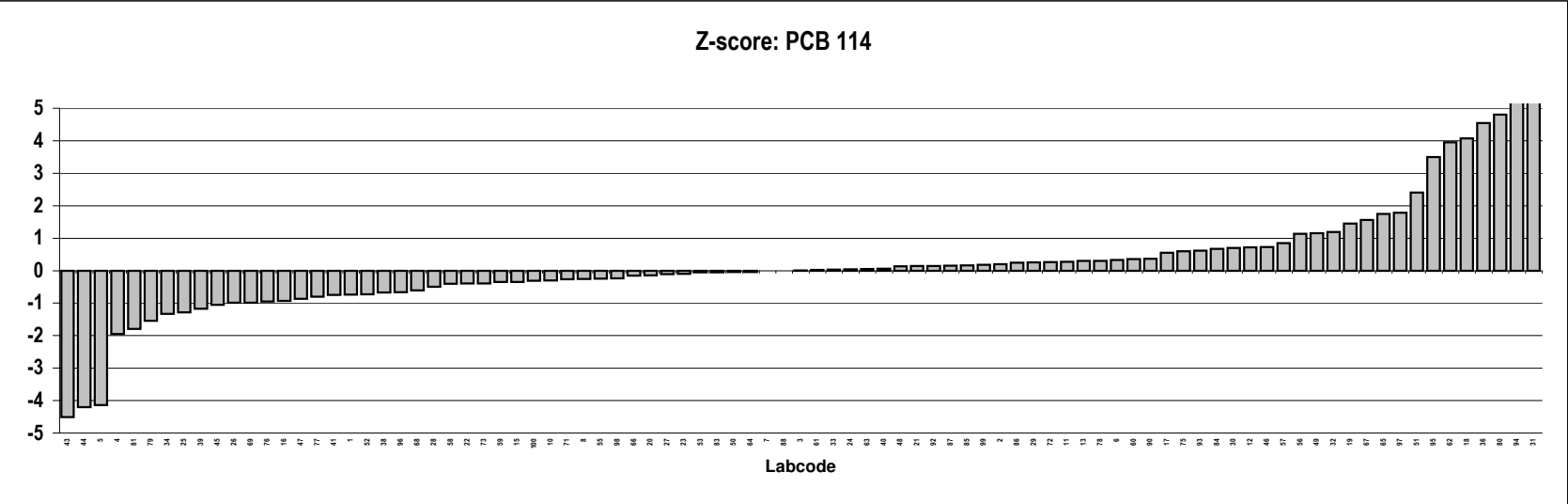
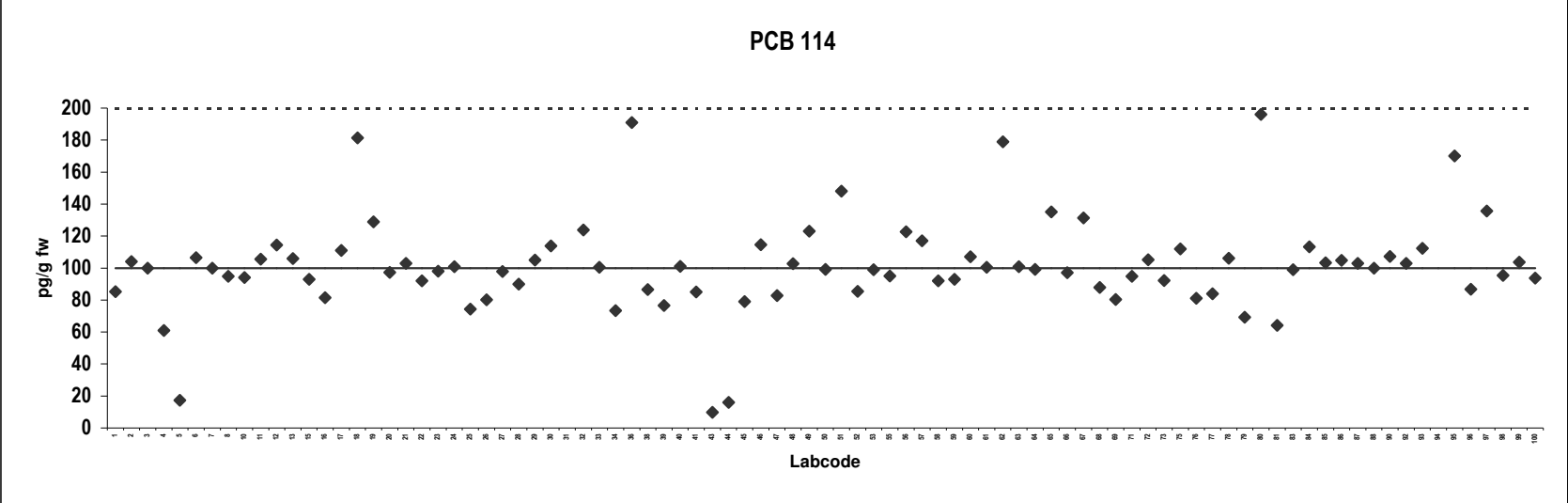


**Salmon**  
Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	85		51	148	
2	104		52	85	
3	100		53	99	
4	61		55	95	
5	17		56	123	
6	107		57	117	
7	100		58	92	
8	95		59	93	
10	94		60	107	
11	106		61	100	
12	114		62	179	
13	106		63	101	
15	93		64	99	
16	81		65	135	
17	111		66	97	
18	181		67	131	
19	129		68	88	
20	97		69	80	
21	103		71	95	
22	92		72	105	
23	98		73	92	
24	101		75	112	
25	74		76	81	
26	80		77	84	
27	98		78	106	
28	90		79	69	
29	105		80	196	
30	114		81	64	
31	1200	Outlier	83	99	
32	124		84	113	
33	101		85	103	
34	73		86	105	
36	191		87	103	
38	87		88	100	
39	77		90	107	
40	101		92	103	
41	85		93	112	
43	9.9		94	215	Outlier
44	16	ND	95	170	
45	79		96	87	
46	115		97	136	
47	83		98	95	
48	103		99	104	
49	123		100	94	
50	99				

**Consensus statistics**

Consensus median, pg/g	100
Median all values pg/g	100
Consensus mean, pg/g	101
Standard deviation, pg/g	30
Relative standard deviation, %	30
No. of values reported	89
No. of values removed	2
No. of reported non-detects	1

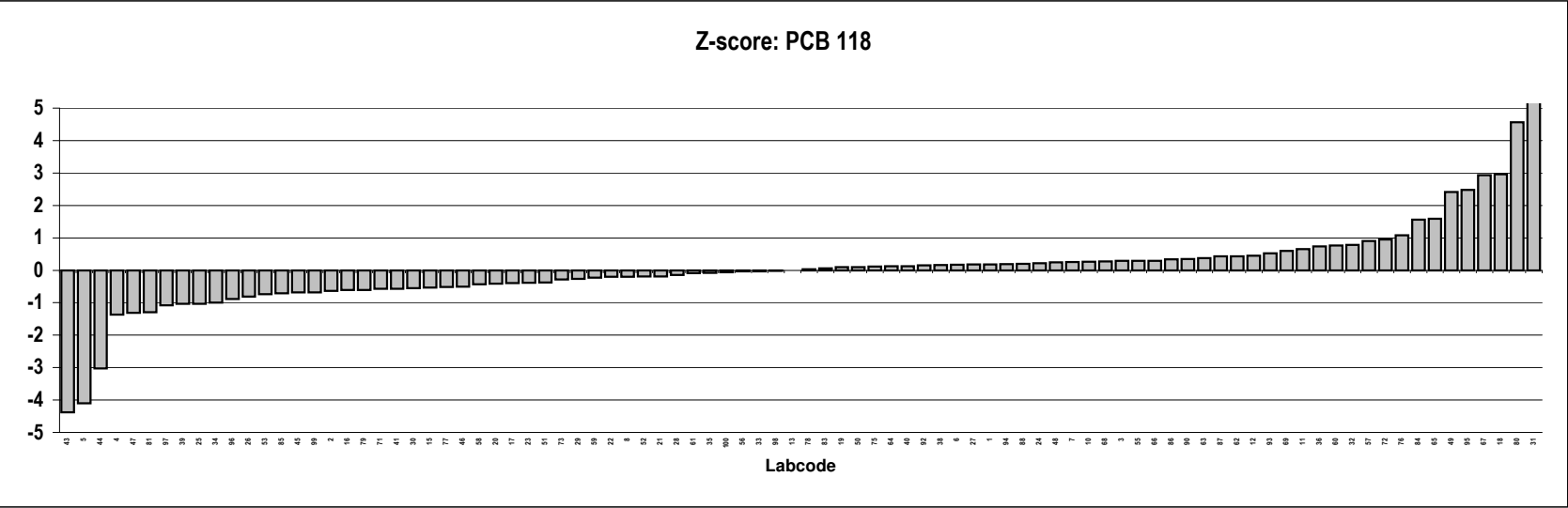
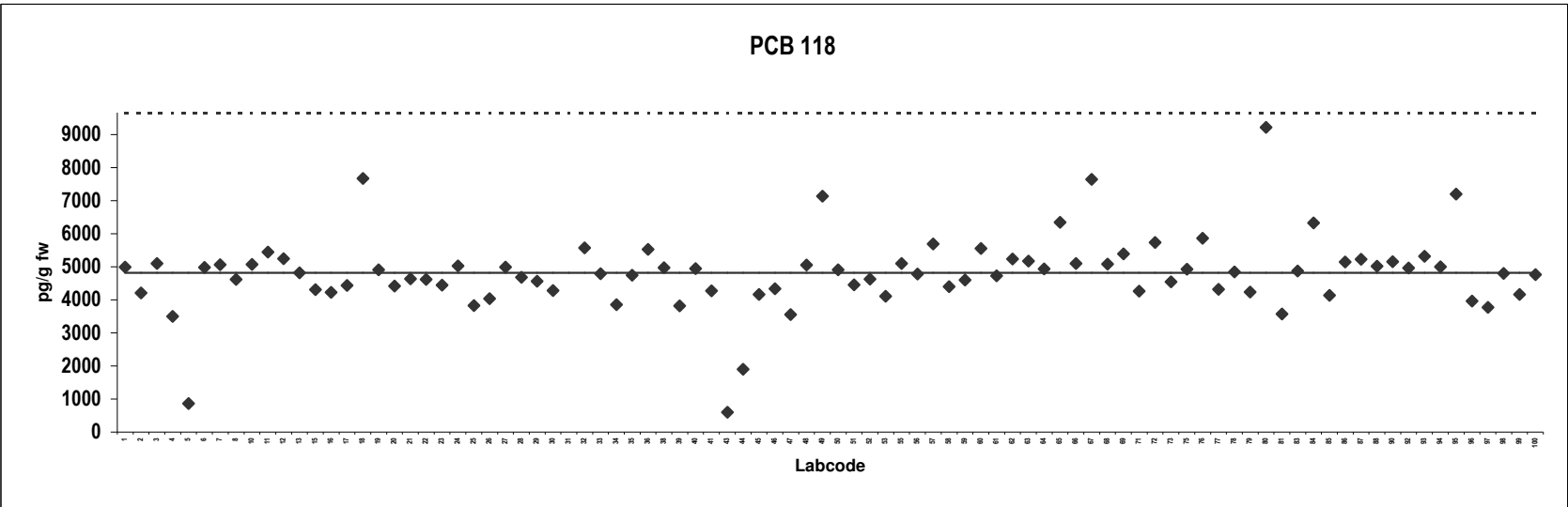


**Salmon**  
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4990		50	4909	
2	4205		51	4454	
3	5100		52	4630	
4	3500		53	4104	
5	867		55	5100	
6	4980		56	4783	
7	5059		57	5690	
8	4620		58	4400	
10	5067		59	4600	
11	5445		60	5549	
12	5247		61	4730	
13	4816		62	5232	
15	4304		63	5174	
16	4230		64	4935	
17	4434		65	6343	
18	7666		66	5100	
19	4907		67	7644	
20	4420		68	5076	
21	4635		69	5393	
22	4620		71	4266	
23	4443		72	5732	
24	5027		73	4540	
25	3825		75	4924	
26	4039		76	5860	
27	4986		77	4317	
28	4680		78	4844	
29	4560		79	4231	
30	4283		80	9217	
31	57000	Outlier	81	3572	
32	5571		83	4871	
33	4789		84	6324	
34	3855		85	4135	
35	4741		86	5142	
36	5522		87	5228	
38	4970		88	5012	
39	3819		90	5148	
40	4940		92	4963	
41	4270		93	5319	
43	599		94	4995	
44	1900		95	7200	
45	4160		96	3960	
46	4332		97	3775	
47	3551		98	4800	
48	5054		99	4160	
49	7138		100	4762	

**Consensus statistics**

Consensus median, pg/g	4816
Median all values pg/g	4830
Consensus mean, pg/g	4801
Standard deviation, pg/g	1147
Relative standard deviation, %	24
No. of values reported	90
No. of values removed	1
No. of reported non-detects	0

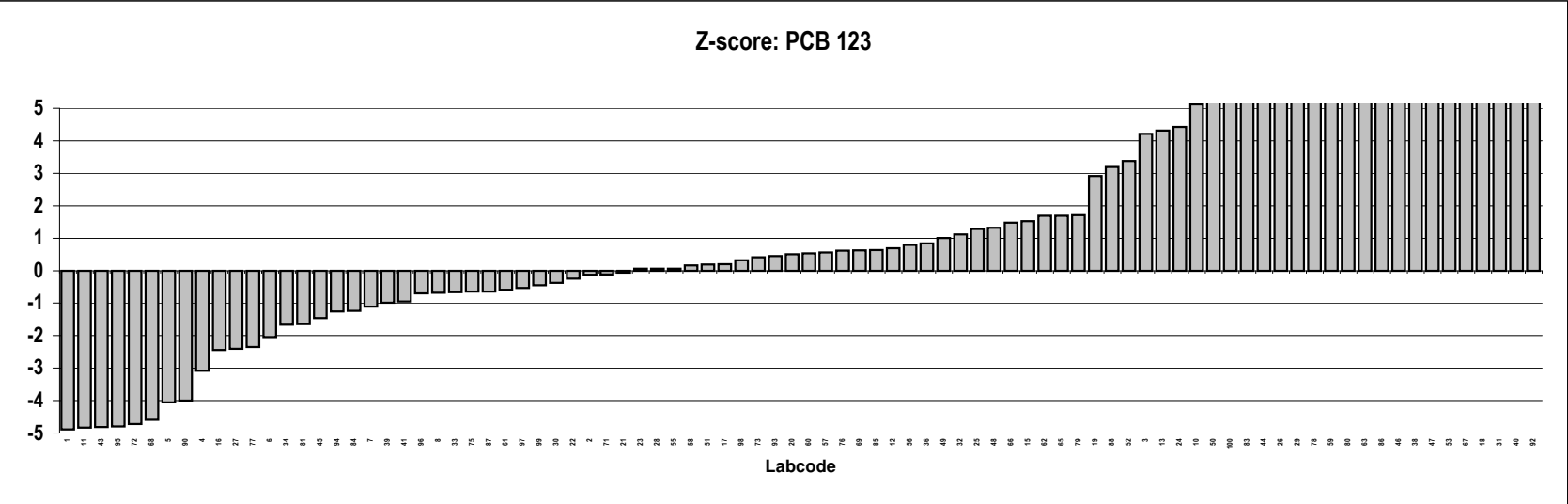
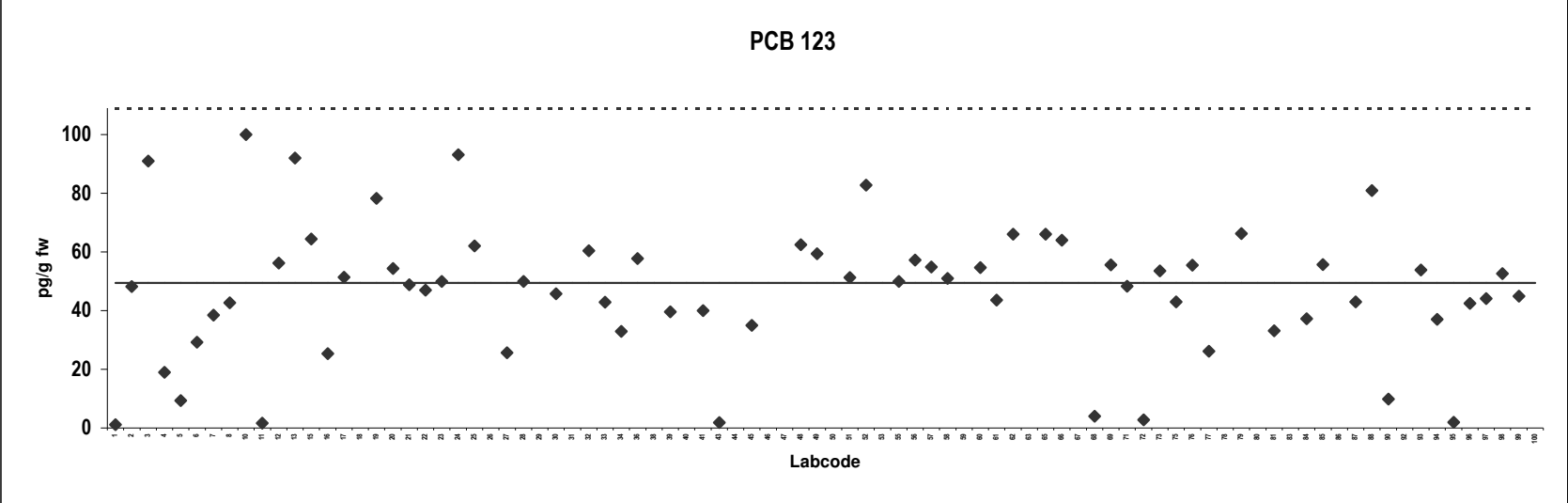


**Salmon**  
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.1	ND	51	51	
2	48		52	83	
3	91		53	666	Outlier
4	19		55	50	
5	9.4	ND	56	57	
6	29		57	55	
7	38		58	51	
8	43		59	190	Outlier
10	100		60	55	
11	1.7	ND	61	44	
12	56		62	66	
13	92		63	224	Outlier
15	64		65	66	
16	25		66	64	
17	51		67	743	Outlier
18	1063	Outlier	68	4.0	ND
19	78		69	56	
20	54		71	48	
21	49		72	2.7	ND
22	47		73	54	
23	50		75	43	
24	93		76	56	
25	62		77	26	
26	142	Outlier	78	178	Outlier
27	26		79	66	
28	50		80	219	Outlier
29	156	Outlier	81	33	
30	46		83	125	Outlier
31	1530	Outlier	84	37	
32	60		85	56	
33	43		86	250	Outlier
34	33		87	43	
36	58		88	81	
38	621	Outlier	90	9.9	
39	40		92	4553	Outlier
40	3334	Outlier	93	54	
41	40		94	37	
43	1.8		95	2.0	ND
44	130	Outlier,ND	96	43	
45	35		97	44	
46	476	Outlier	98	53	
47	664	Outlier	99	45	
48	62		100	113	Outlier
49	59				
50	112	Outlier			

**Consensus statistics**

Consensus median, pg/g	49
Median all values pg/g	55
Consensus mean, pg/g	47
Standard deviation, pg/g	23
Relative standard deviation, %	48
No. of values reported	88
No. of values removed	20
No. of reported non-detects	7



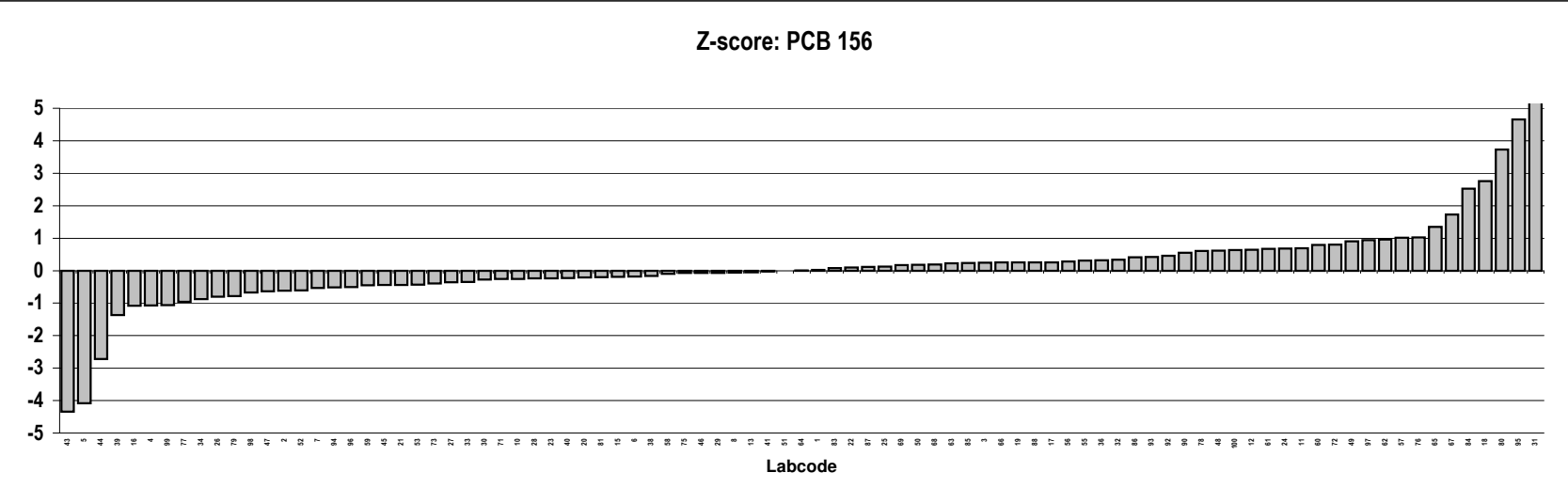
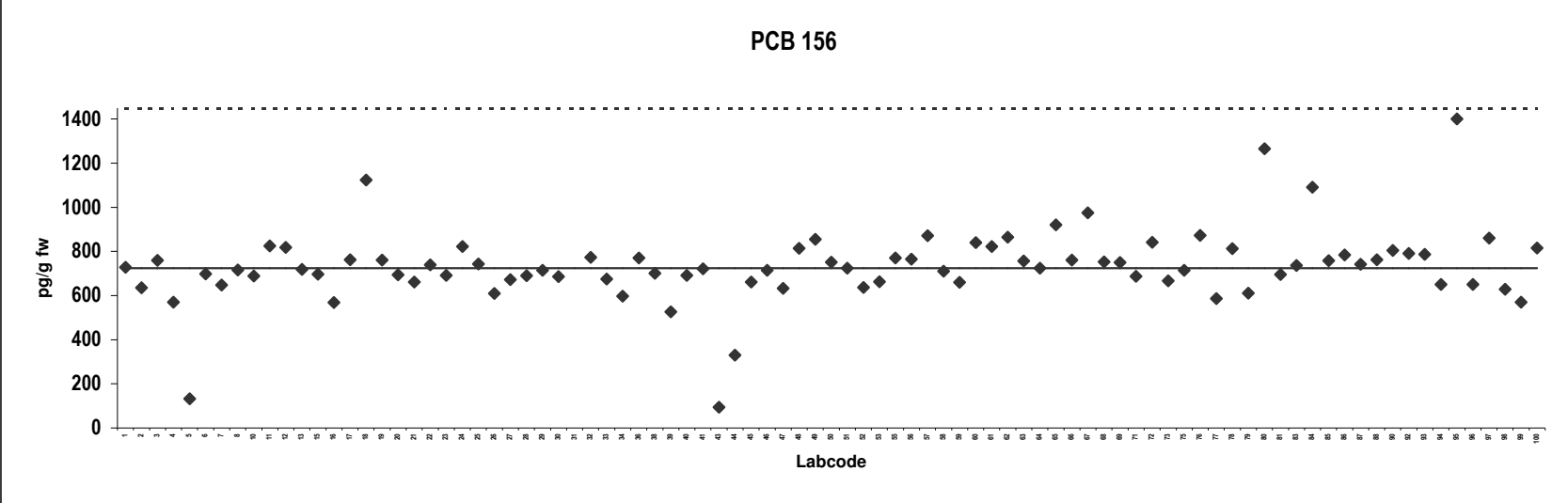
**Salmon**  
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	728		51	725	
2	636		52	637	
3	760		53	663	
4	570		55	770	
5	133		56	765	
6	698		57	872	
7	647		58	710	
8	716		59	660	
10	688		60	840	
11	824		61	822	
12	818		62	864	
13	718		63	757	
15	697		64	725	
16	568		65	920	
17	762		66	761	
18	1124		67	975	
19	762		68	753	
20	694		69	749	
21	661		71	688	
22	739		72	841	
23	691		73	667	
24	823		75	714	
25	743		76	873	
26	609		77	586	
27	672		78	813	
28	690		79	611	
29	715		80	1266	
30	686		81	695	
31	7900	Outlier	83	736	
32	773		84	1091	
33	675		85	759	
34	598		86	784	
36	771		87	742	
38	701		88	762	
39	526		90	804	
40	692		92	791	
41	721		93	786	
43	95		94	650	
44	330		95	1400	
45	661		96	651	
46	714		97	861	
47	633		98	628	
48	814		99	570	
49	855		100	816	
50	751				

**Consensus statistics**

Consensus median, pg/g	725
Median all values pg/g	725
Consensus mean, pg/g	732
Standard deviation, pg/g	170
Relative standard deviation, %	23
No. of values reported	89
No. of values removed	1
No. of reported non-detects	0





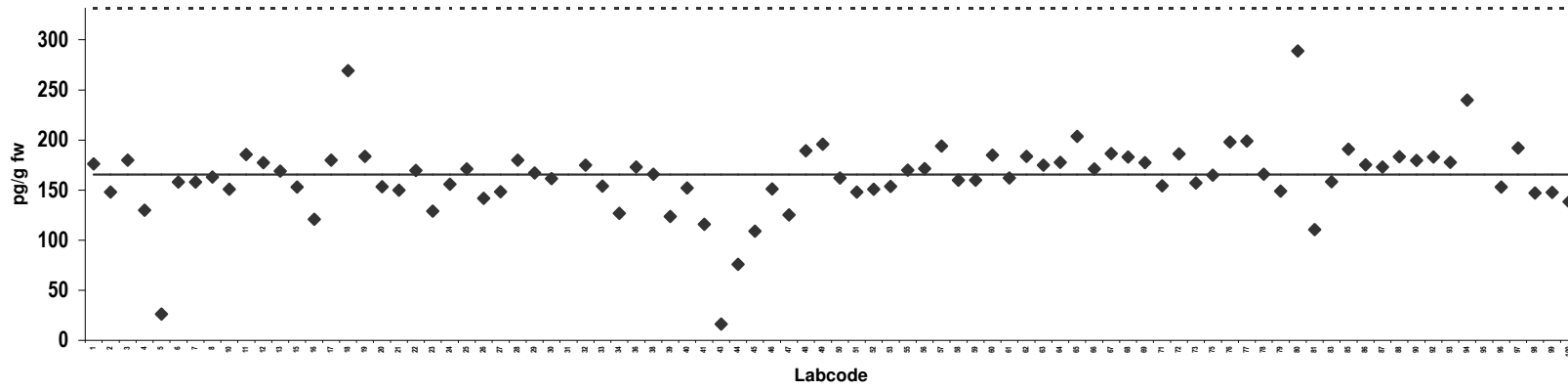
**Salmon**  
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	176		51	148	
2	148		52	151	
3	180		53	154	
4	130		55	170	
5	26		56	171	
6	158		57	194	
7	158		58	160	
8	163		59	160	
10	151		60	185	
11	186		61	162	
12	177		62	184	
13	169		63	175	
15	153		64	178	
16	121		65	204	
17	180		66	171	
18	269		67	186	
19	184		68	183	
20	153		69	178	
21	150		71	154	
22	170		72	186	
23	129		73	157	
24	156		75	165	
25	171		76	198	
26	142		77	199	
27	148		78	166	
28	180		79	149	
29	167		80	289	
30	162		81	110	
31	1910	Outlier	83	158	
32	175		85	191	
33	154		86	175	
34	127		87	173	
36	173		88	183	
38	166		90	180	
39	124		92	183	
40	152		93	178	
41	116		94	240	
43	16		95	1400	Outlier
44	76		96	153	
45	109		97	192	
46	151		98	147	
47	125		99	148	
48	189		100	138	
49	196				
50	162				

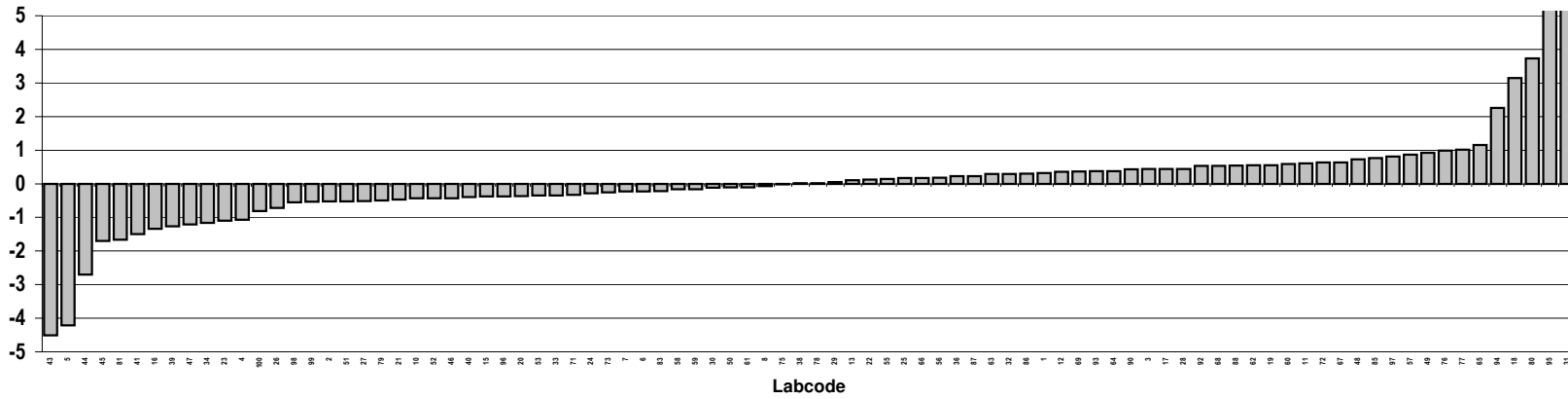
**Consensus statistics**

Consensus median, pg/g	165
Median all values pg/g	166
Consensus mean, pg/g	163
Standard deviation, pg/g	37
Relative standard deviation, %	23
No. of values reported	88
No. of values removed	2
No. of reported non-detects	0

### PCB 157



### Z-score: PCB 157



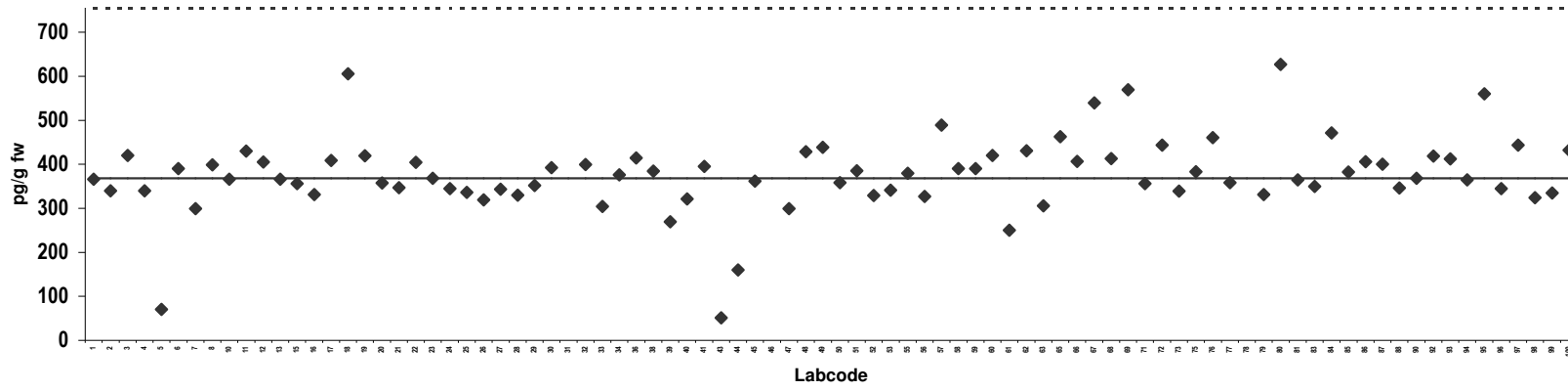
**Salmon**  
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	366		51	385	
2	340		52	329	
3	420		53	342	
4	340		55	380	
5	70		56	327	
6	391		57	489	
7	300		58	390	
8	399		59	390	
10	366		60	420	
11	430		61	250	
12	405		62	431	
13	366		63	306	
15	356		65	463	
16	331		66	407	
17	409		67	540	
18	606		68	413	
19	420		69	570	
20	357		71	356	
21	347		72	444	
22	405		73	339	
23	368		75	383	
24	345		76	461	
25	336		77	358	
26	319		78	1215	Outlier
27	343		79	331	
28	330		80	627	
29	352		81	365	
30	392		83	350	
31	4850	Outlier	84	471	
32	400		85	383	
33	305		86	406	
34	376		87	400	
36	414		88	346	
38	385		90	368	
39	269		92	419	
40	321		93	412	
41	395		94	365	
43	51		95	560	
44	160		96	345	
45	362		97	444	
46	1205	Outlier	98	324	
47	300		99	335	
48	429		100	432	
49	439				
50	358				

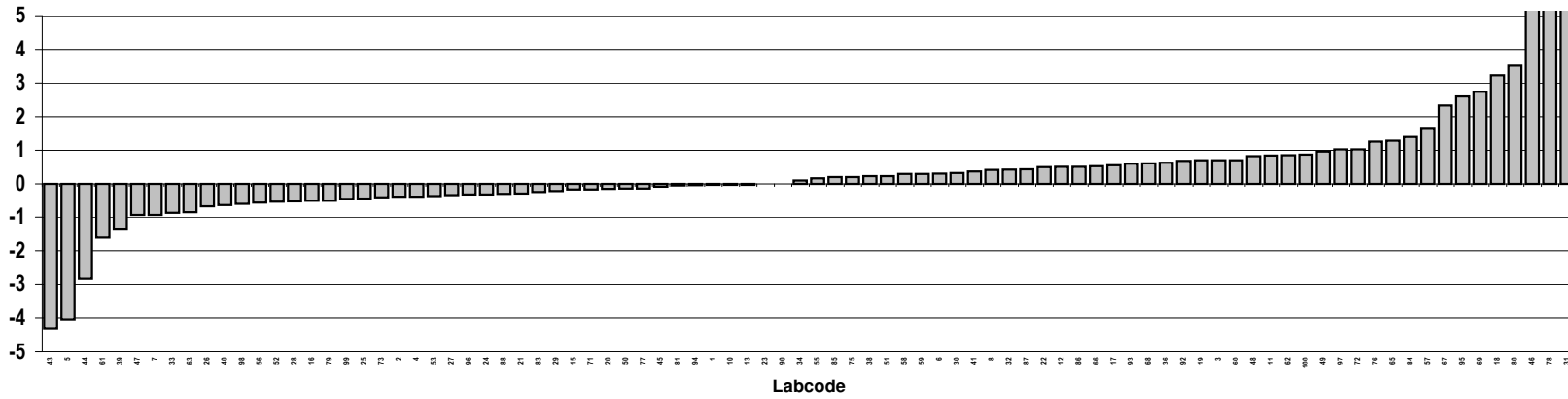
**Consensus statistics**

Consensus median, pg/g	368
Median all values pg/g	378
Consensus mean, pg/g	377
Standard deviation, pg/g	86
Relative standard deviation, %	23
No. of values reported	88
No. of values removed	3
No. of reported non-detects	0

### PCB 167



### Z-score: PCB 167

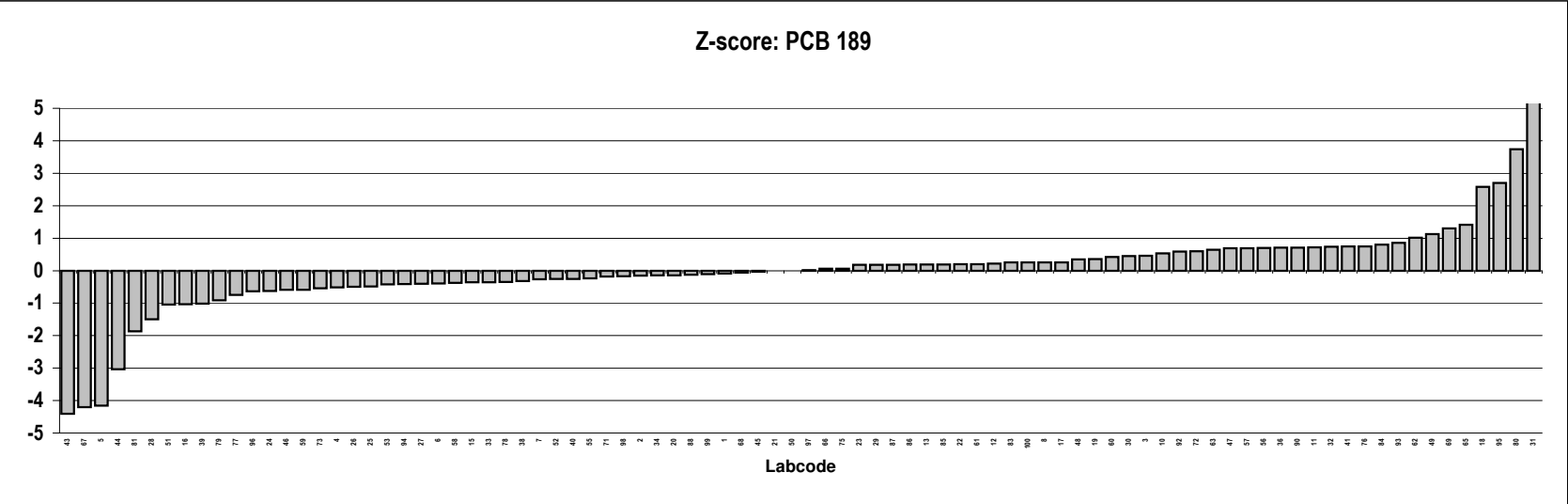
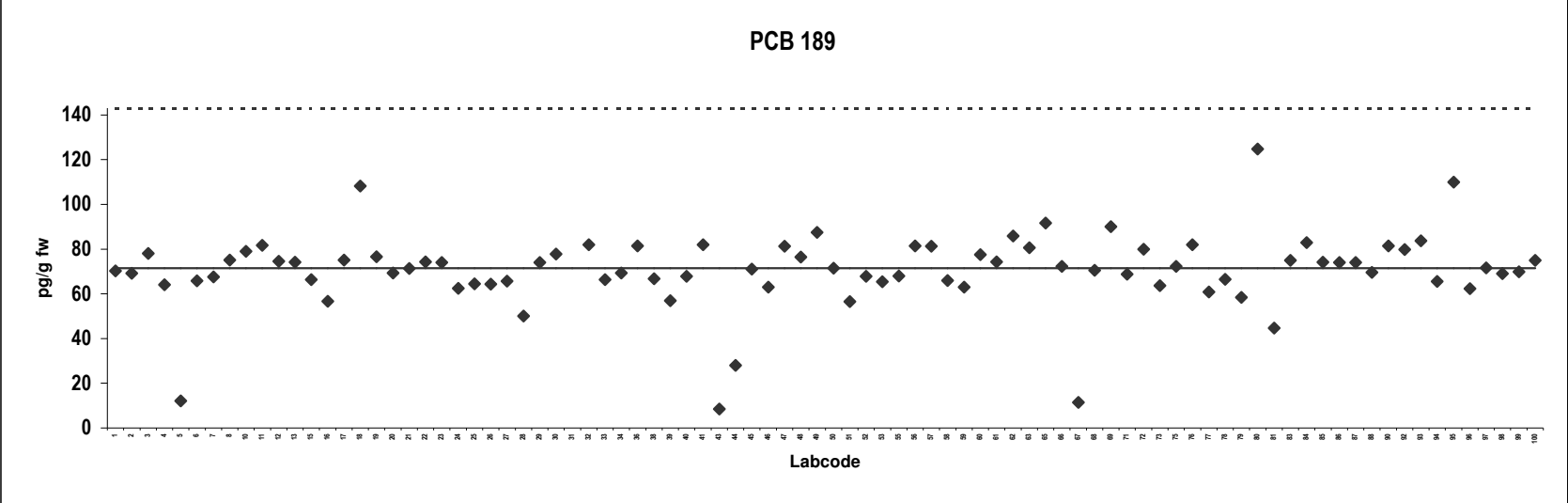


**Salmon**  
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	70		51	56	
2	69		52	68	
3	78		53	65	
4	64		55	68	
5	12		56	81	
6	66		57	81	
7	68		58	66	
8	75		59	63	
10	79		60	77	
11	82		61	74	
12	75		62	86	
13	74		63	81	
15	66		65	92	
16	57		66	72	
17	75		67	11	
18	108		68	71	
19	77		69	90	
20	69		71	69	
21	71		72	80	
22	74		73	64	
23	74		75	72	
24	62		76	82	
25	65		77	61	
26	64		78	67	
27	66		79	58	
28	50		80	125	
29	74		81	45	
30	78		83	75	
31	942	Outlier	84	83	
32	82		85	74	
33	66		86	74	
34	69		87	74	
36	81		88	70	
38	67		90	81	
39	57		92	80	
40	68		93	84	
41	82		94	66	
43	8.4		95	110	
44	28		96	62	
45	71		97	72	
46	63		98	69	
47	81		99	70	
48	76		100	75	
49	87				
50	71				

**Consensus statistics**

Consensus median, pg/g	71
Median all values pg/g	72
Consensus mean, pg/g	71
Standard deviation, pg/g	17
Relative standard deviation, %	24
No. of values reported	88
No. of values removed	1
No. of reported non-detects	0



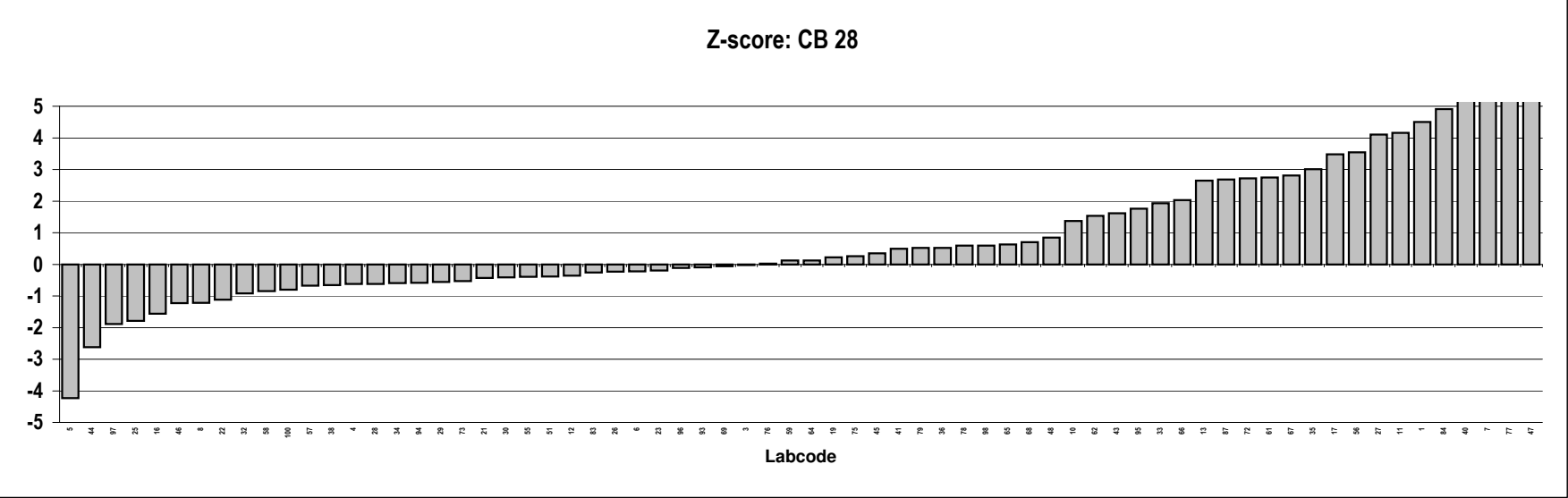
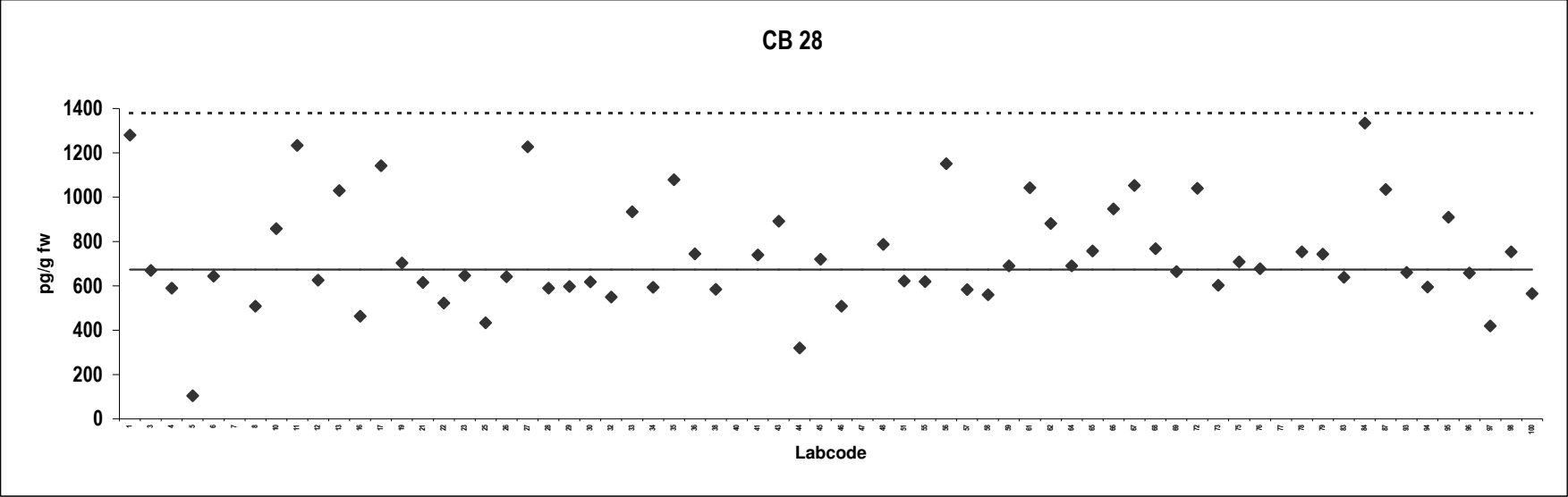
**Salmon**  
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1280		64	690	
3	670		65	758	
4	590		66	947	
5	104		67	1053	
6	644		68	768	
7	1410	Outlier	69	665	
8	509		72	1040	
10	858		73	602	
11	1233		75	709	
12	626		76	677	
13	1030		77	2050	Outlier
16	463		78	753	
17	1142		79	743	
19	703		83	639	
21	615		84	1335	
22	522		87	1035	
23	647		93	661	
25	433		94	595	
26	642		95	910	
27	1227		96	658	
28	590		97	419	
29	598		98	753	
30	618		100	565	
32	550				
33	934				
34	594				
35	1079				
36	744				
38	585				
40	1404	Outlier			
41	740				
43	891				
44	320				
45	720				
46	508				
47	2807	Outlier			
48	787				
51	622				
55	620				
56	1151				
57	583				
58	560				
59	690				
61	1043				
62	881				

**Consensus statistics**

Consensus median, pg/g	674
Median all values pg/g	690
Consensus mean, pg/g	739
Standard deviation, pg/g	240
Relative standard deviation, %	32
No. of values reported	68
No. of values removed	4
No. of reported non-detects	0





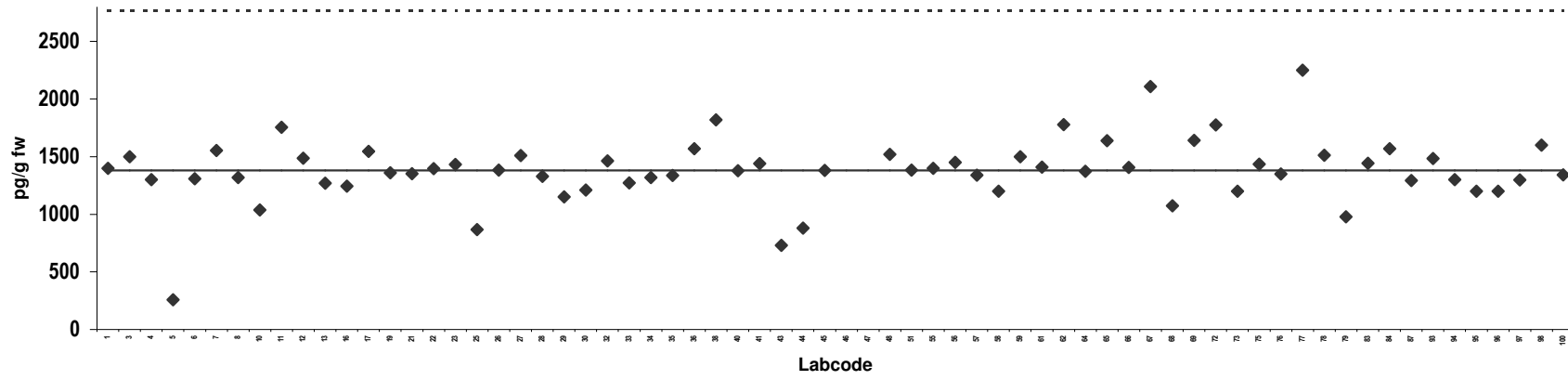
**Salmon**  
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1400		64	1373	
3	1500		65	1640	
4	1300		66	1406	
5	259		67	2108	
6	1309		68	1073	
7	1553		69	1641	
8	1320		72	1776	
10	1037		73	1200	
11	1754		75	1435	
12	1487		76	1350	
13	1270		77	2250	
16	1245		78	1513	
17	1545		79	977	
19	1359		83	1442	
21	1352		84	1568	
22	1396		87	1292	
23	1431		93	1483	
25	868		94	1300	
26	1384		95	1200	
27	1511		96	1200	
28	1330		97	1298	
29	1150		98	1600	
30	1209		100	1341	
32	1464				
33	1272				
34	1320				
35	1337				
36	1569				
38	1820				
40	1378				
41	1440				
43	730				
44	880				
45	1380				
46	98969	Outlier			
47	3220	Outlier			
48	1519				
51	1383				
55	1400				
56	1450				
57	1340				
58	1200				
59	1500				
61	1410				
62	1778				

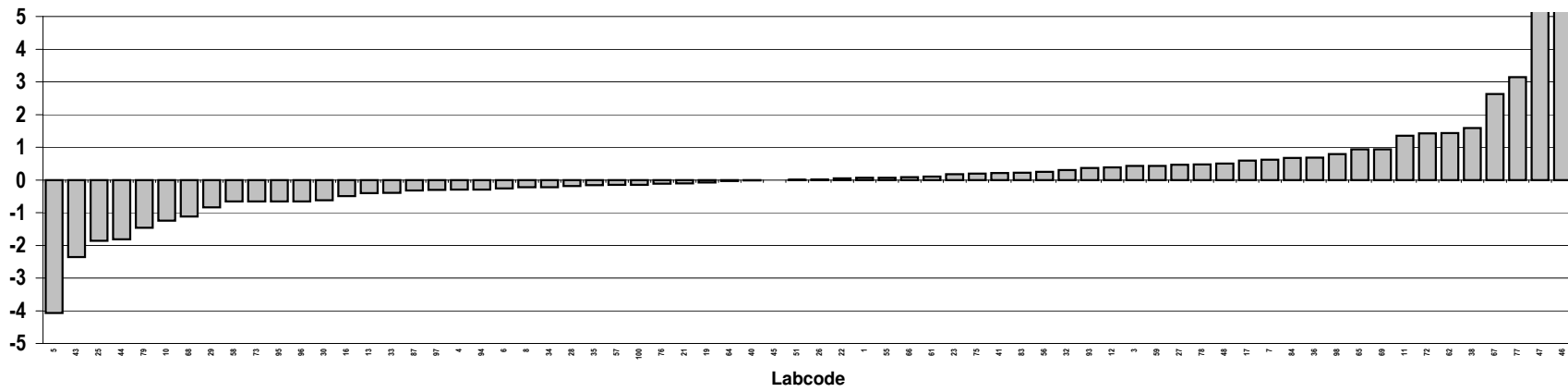
**Consensus statistics**

Consensus median, pg/g	1381
Median all values pg/g	1383
Consensus mean, pg/g	1379
Standard deviation, pg/g	284
Relative standard deviation, %	21
No. of values reported	68
No. of values removed	2
No. of reported non-detects	0

### CB 52



### Z-score: CB 52

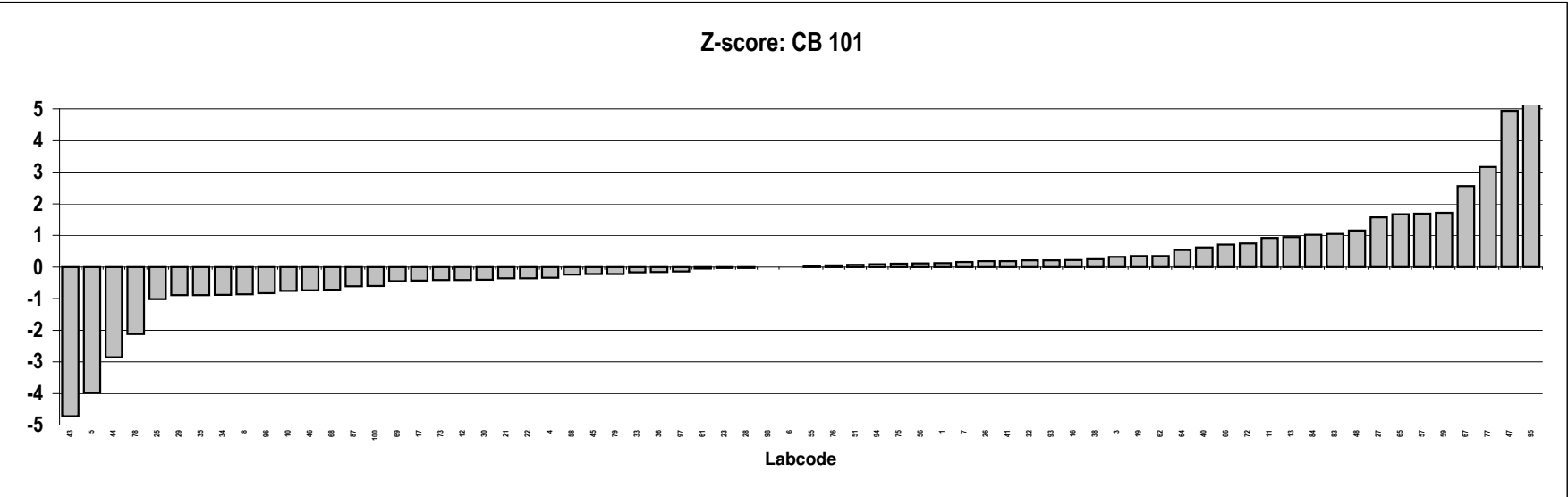
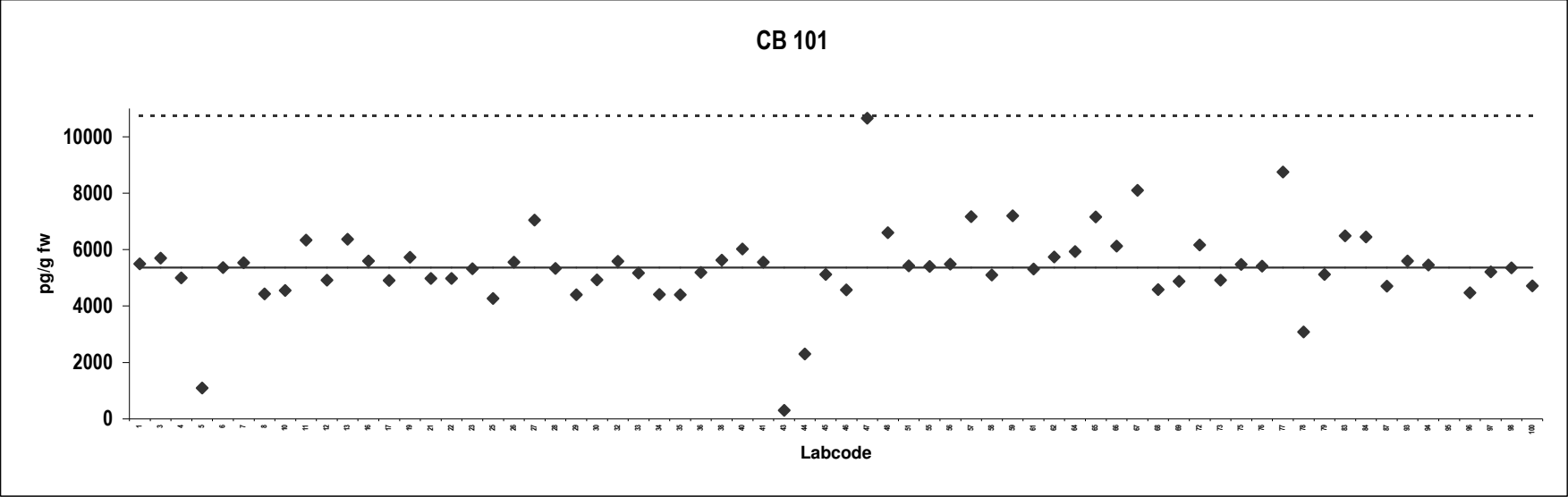


**Salmon**  
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5490		64	5932	
3	5700		65	7153	
4	5000		66	6125	
5	1094		67	8096	
6	5359		68	4585	
7	5533		69	4881	
8	4430		72	6163	
10	4549		73	4920	
11	6339		75	5471	
12	4922		76	5410	
13	6370		77	8750	
16	5600		78	3080	
17	4902		79	5123	
19	5730		83	6484	
21	4975		84	6451	
22	4975		87	4703	
23	5327		93	5591	
25	4270		94	5450	
26	5557		95	12000	Outlier
27	7042		96	4470	
28	5330		97	5212	
29	4400		98	5350	
30	4926		100	4714	
32	5588				
33	5175				
34	4410				
35	4404				
36	5187				
38	5630				
40	6023				
41	5560				
43	301				
44	2300				
45	5120				
46	4571				
47	10652				
48	6599				
51	5428				
55	5400				
56	5483				
57	7170				
58	5100				
59	7200				
61	5309				
62	5736				

**Consensus statistics**

Consensus median, pg/g	5359
Median all values pg/g	5380
Consensus mean, pg/g	5377
Standard deviation, pg/g	1440
Relative standard deviation, %	27
No. of values reported	68
No. of values removed	1
No. of reported non-detects	0



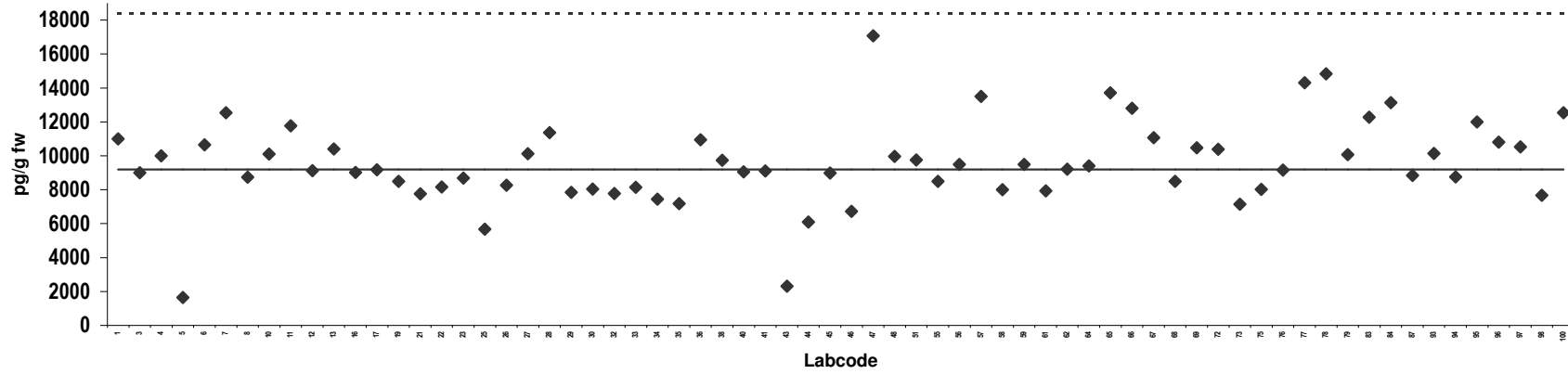
**Salmon**  
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11000		64	9396	
3	9000		65	13703	
4	10000		66	12800	
5	1643		67	11062	
6	10649		68	8497	
7	12537		69	10465	
8	8740		72	10385	
10	10098		73	7140	
11	11765		75	8016	
12	9117		76	9150	
13	10400		77	14300	
16	9026		78	14833	
17	9172		79	10072	
19	8494		83	12283	
21	7765		84	13136	
22	8163		87	8847	
23	8679		93	10138	
25	5670		94	8750	
26	8264		95	12000	
27	10117		96	10800	
28	11370		97	10518	
29	7850		98	7670	
30	8046		100	12532	
32	7779				
33	8135				
34	7440				
35	7187				
36	10943				
38	9740				
40	9060				
41	9110				
43	2303				
44	6100				
45	8980				
46	6723				
47	17077				
48	9962				
51	9749				
55	8500				
56	9496				
57	13500				
58	8000				
59	9500				
61	7937				
62	9219				

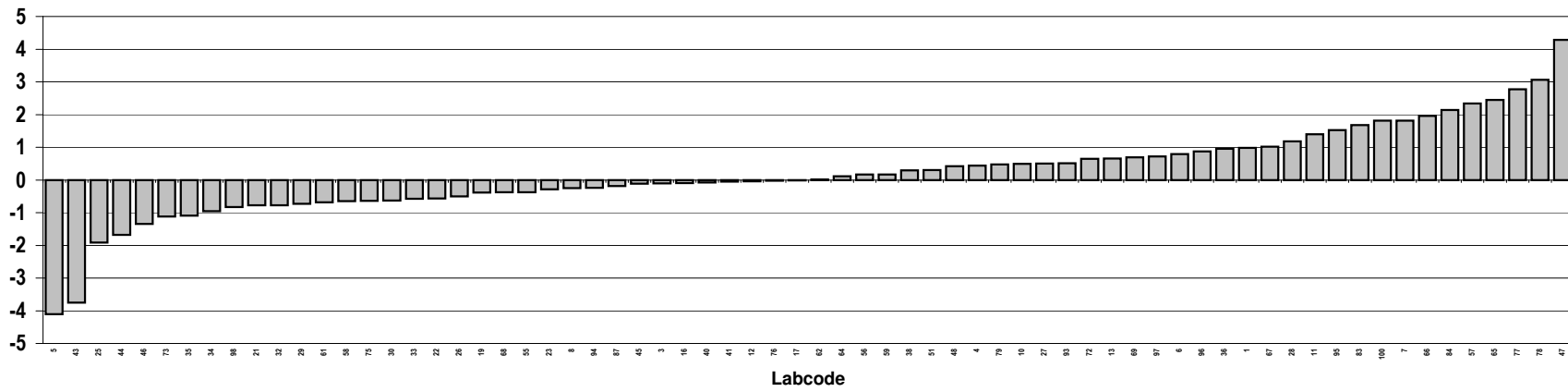
**Consensus statistics**

Consensus median, pg/g	9195
Median all values pg/g	9195
Consensus mean, pg/g	9566
Standard deviation, pg/g	2499
Relative standard deviation, %	26
No. of values reported	68
No. of values removed	0
No. of reported non-detects	0

### CB 138



### Z-score: CB 138



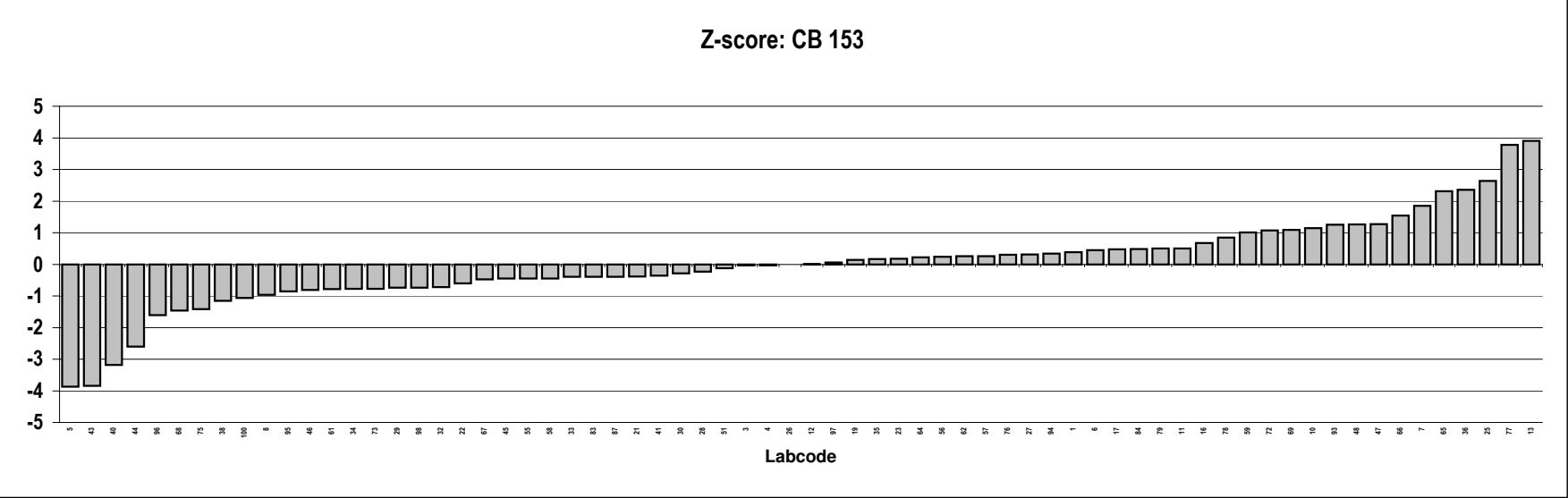
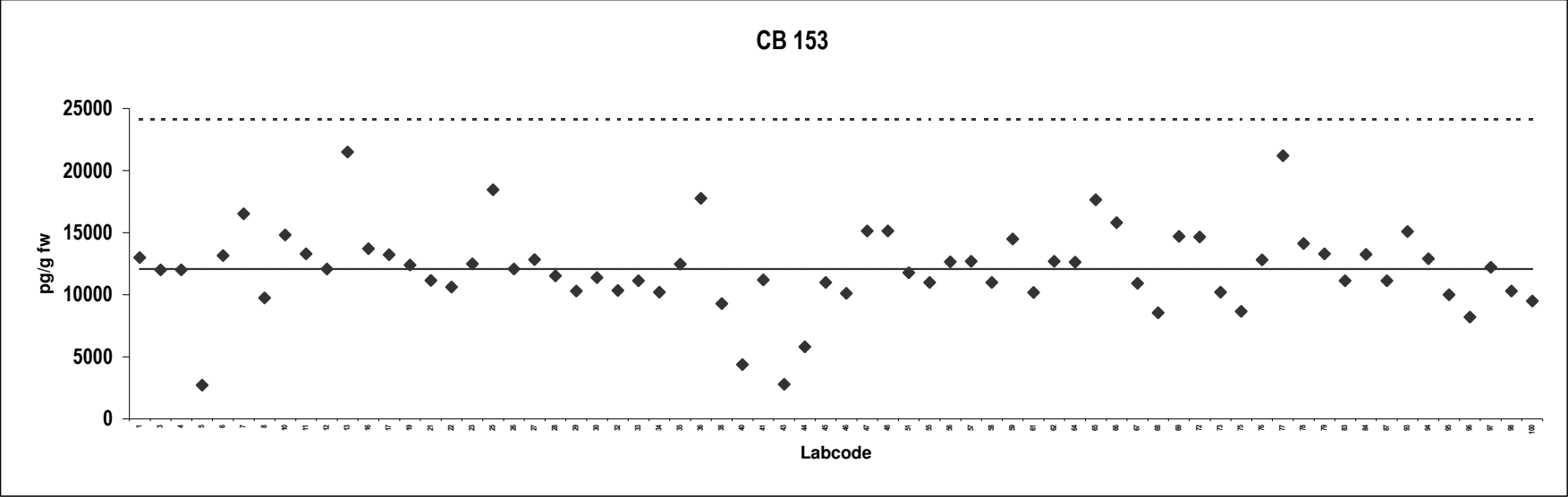
**Salmon**  
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	13000		64	12616	
3	12000		65	17651	
4	12000		66	15800	
5	2726		67	10926	
6	13149		68	8540	
7	16532		69	14712	
8	9740		72	14656	
10	14827		73	10200	
11	13285		75	8664	
12	12083		76	12800	
13	21500		77	21200	
16	13699		78	14118	
17	13230		79	13284	
19	12403		83	11122	
21	11149		84	13242	
22	10617		87	11130	
23	12495		93	15095	
25	18451		94	12900	
26	12062		95	10000	
27	12832		96	8200	
28	11510		97	12219	
29	10300		98	10300	
30	11381		100	9503	
32	10337				
33	11122				
34	10200				
35	12468				
36	17771				
38	9290				
40	4387				
41	11200				
43	2797				
44	5800				
45	11000				
46	10112				
47	15141				
48	15128				
51	11770				
55	11000				
56	12655				
57	12700				
58	11000				
59	14500				
61	10188				
62	12690				

**Consensus statistics**

Consensus median, pg/g	12073
Median all values pg/g	12073
Consensus mean, pg/g	12104
Standard deviation, pg/g	3355
Relative standard deviation, %	28
No. of values reported	68
No. of values removed	0
No. of reported non-detects	0





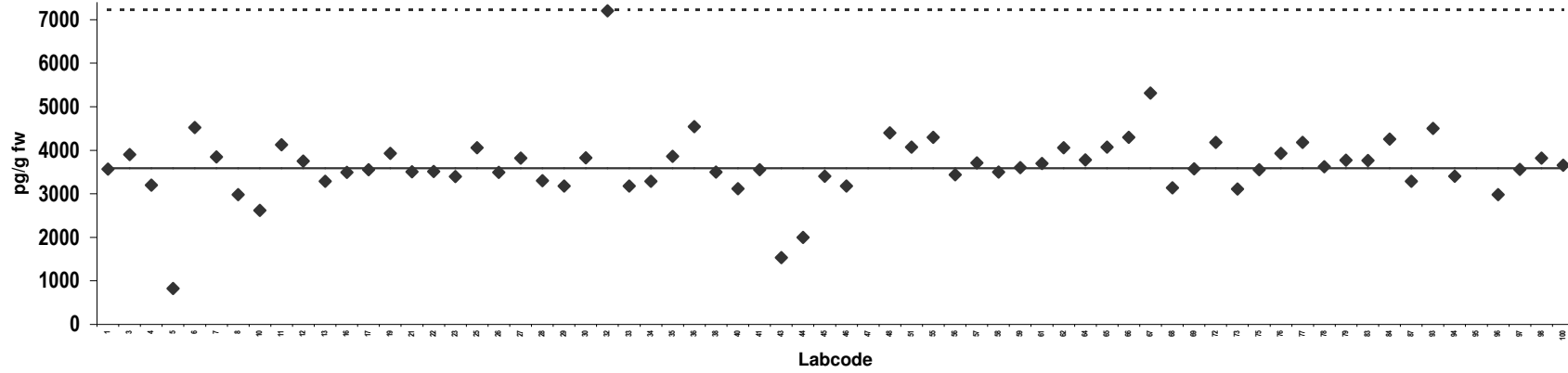
**Salmon**  
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	3570		64	3780	
3	3900		65	4071	
4	3200		66	4300	
5	825		67	5316	
6	4520		68	3140	
7	3845		69	3572	
8	2980		72	4182	
10	2616		73	3110	
11	4124		75	3556	
12	3749		76	3930	
13	3290		77	4180	
16	3491		78	3622	
17	3550		79	3774	
19	3931		83	3762	
21	3503		84	4258	
22	3512		87	3284	
23	3396		93	4503	
25	4060		94	3400	
26	3495		95	11000	Outlier
27	3819		96	2980	
28	3300		97	3560	
29	3180		98	3820	
30	3827		100	3653	
32	7204				
33	3179				
34	3290				
35	3861				
36	4545				
38	3500				
40	3116				
41	3550				
43	1537				
44	2000				
45	3400				
46	3175				
47	8893	Outlier			
48	4402				
51	4071				
55	4300				
56	3438				
57	3710				
58	3500				
59	3600				
61	3699				
62	4055				

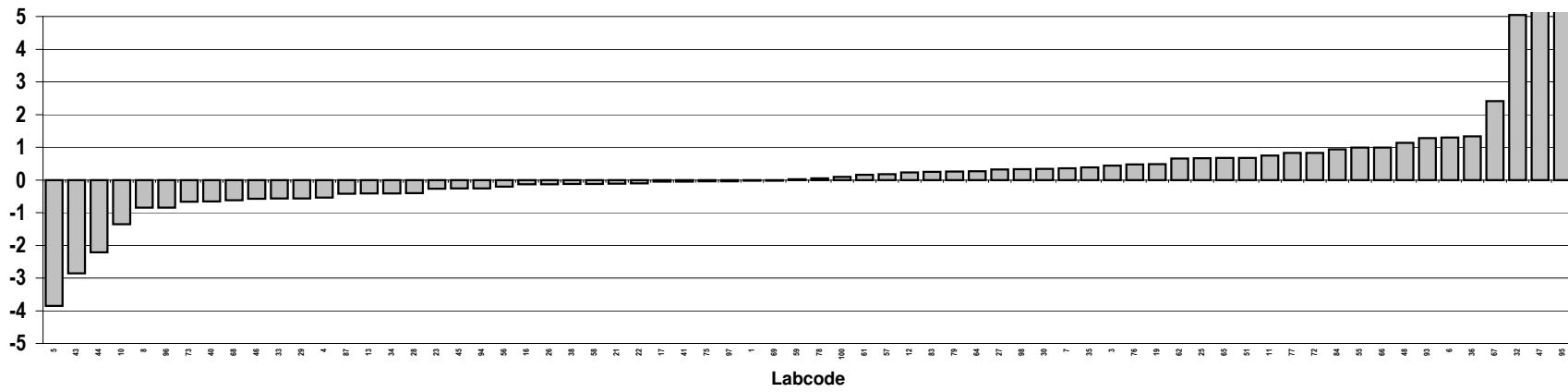
**Consensus statistics**

Consensus median, pg/g	3586
Median all values pg/g	3611
Consensus mean, pg/g	3645
Standard deviation, pg/g	796
Relative standard deviation, %	22
No. of values reported	68
No. of values removed	2
No. of reported non-detects	0

### CB 180



### Z-score: CB 180

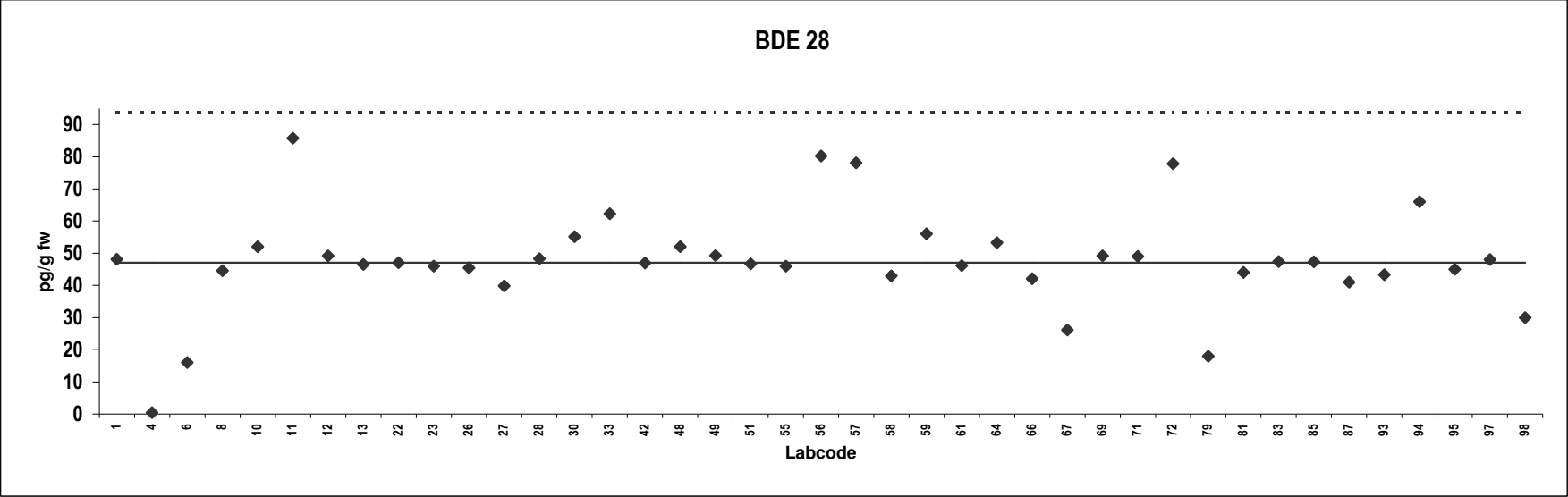


**Salmon**  
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	48				
4	0.44				
6	16				
8	45				
10	52				
11	86				
12	49				
13	47				
22	47				
23	46				
26	45				
27	40				
28	48				
30	55				
33	62				
42	47				
48	52				
49	49				
51	47				
55	46				
56	80				
57	78				
58	43				
59	56				
61	46				
64	53				
66	42				
67	26				
69	49				
71	49				
72	78				
79	18				
81	44				
83	47				
85	47				
87	41				
93	43				
94	66				
95	45				
97	48				
98	30				

**Consensus statistics**

Consensus median, pg/g	47
Median all values pg/g	47
Consensus mean, pg/g	48
Standard deviation, pg/g	16
Relative standard deviation, %	33
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0

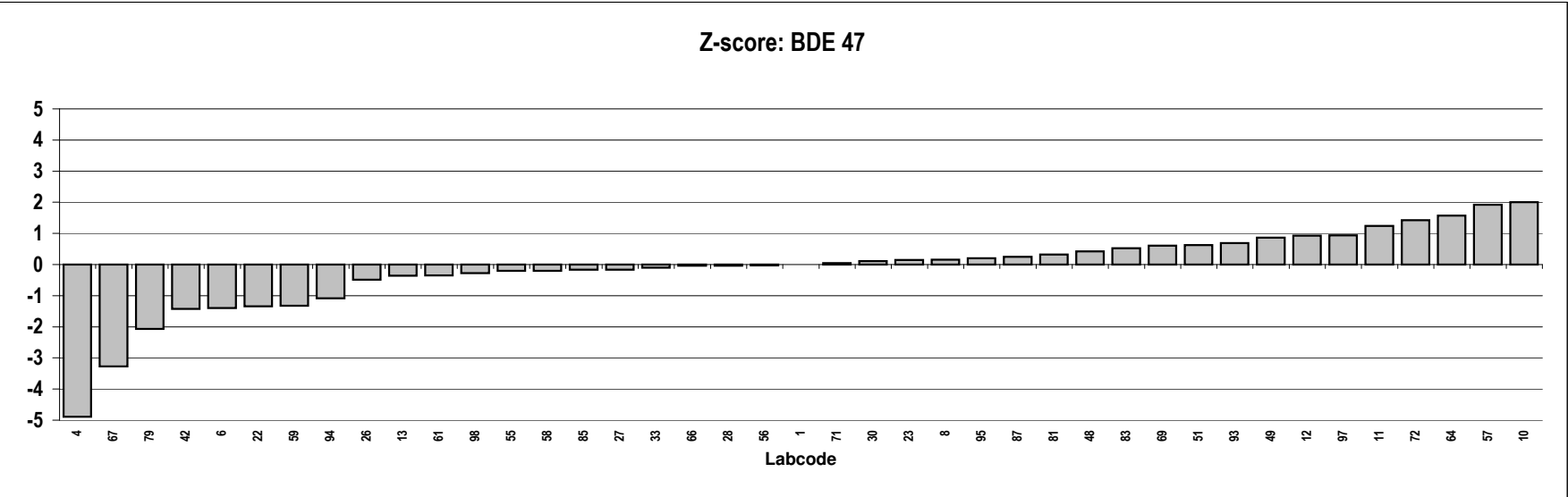
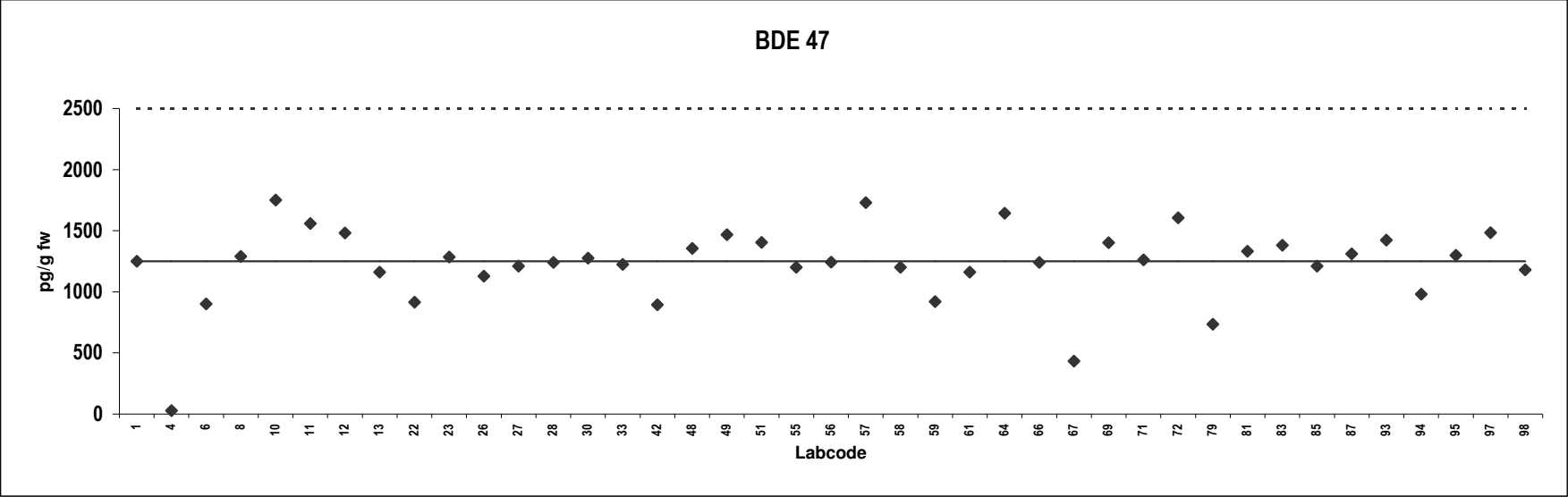


**Salmon**  
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1250				
4	28				
6	901				
8	1290				
10	1751				
11	1560				
12	1482				
13	1160				
22	915				
23	1286				
26	1128				
27	1210				
28	1241				
30	1277				
33	1225				
42	894				
48	1356				
49	1467				
51	1405				
55	1200				
56	1243				
57	1730				
58	1200				
59	920				
61	1162				
64	1644				
66	1240				
67	433				
69	1402				
71	1261				
72	1605				
79	734				
81	1331				
83	1381				
85	1210				
87	1311				
93	1422				
94	980				
95	1300				
97	1484				
98	1180				

**Consensus statistics**

Consensus median, pg/g	1250
Median all values pg/g	1250
Consensus mean, pg/g	1224
Standard deviation, pg/g	321
Relative standard deviation, %	26
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



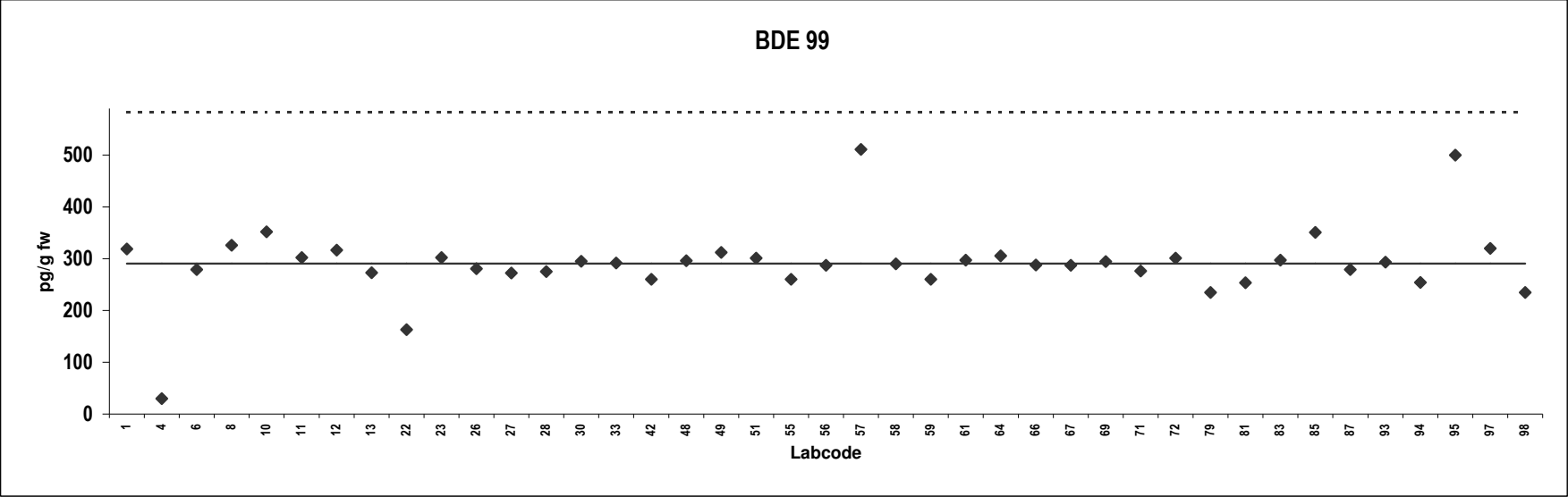
**Salmon**  
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	319				
4	30				
6	279				
8	326				
10	352				
11	302				
12	317				
13	273				
22	163				
23	302				
26	280				
27	272				
28	275				
30	295				
33	292				
42	260				
48	296				
49	312				
51	301				
55	260				
56	287				
57	511				
58	290				
59	260				
61	297				
64	306				
66	288				
67	287				
69	295				
71	276				
72	301				
79	235				
81	254				
83	297				
85	351				
87	279				
93	293				
94	254				
95	500	ND			
97	320				
98	235				

**Consensus statistics**

Consensus median, pg/g	291
Median all values pg/g	292
Consensus mean, pg/g	291
Standard deviation, pg/g	71
Relative standard deviation, %	24
No. of values reported	41
No. of values removed	0
No. of reported non-detects	1



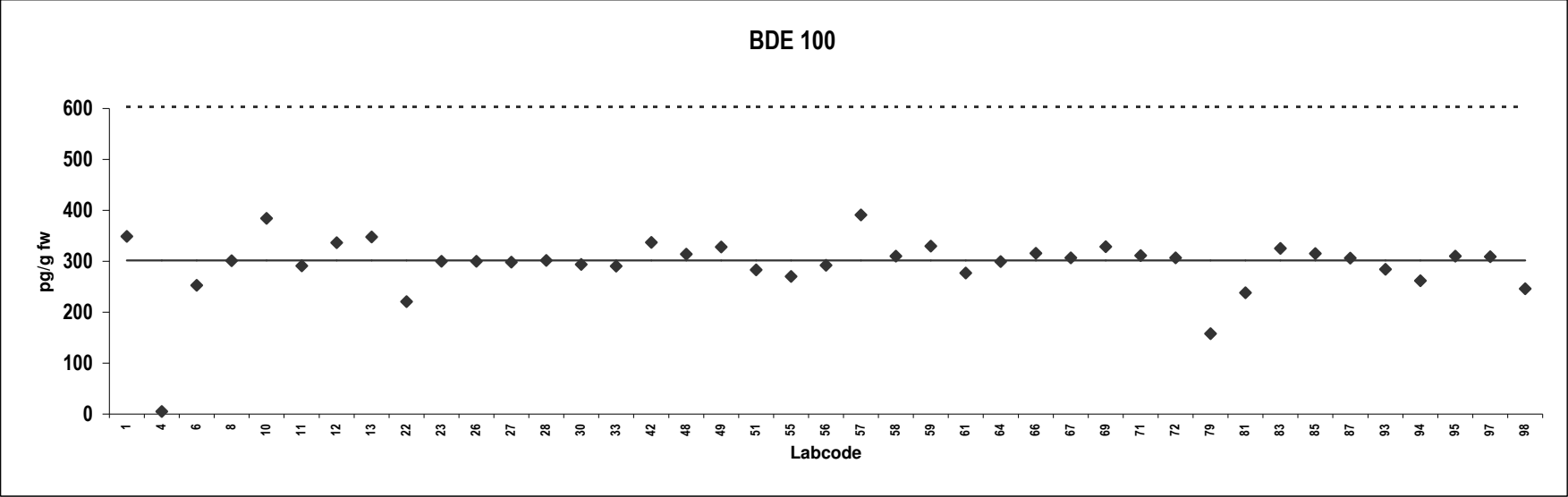


**Salmon**  
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	349				
4	5.0				
6	253				
8	301				
10	384				
11	291				
12	337				
13	348				
22	221				
23	300				
26	300				
27	298				
28	302				
30	294				
33	291				
42	337				
48	314				
49	328				
51	283				
55	270				
56	292				
57	391				
58	310				
59	330				
61	277				
64	300				
66	316				
67	307				
69	329				
71	311				
72	307				
79	158				
81	238				
83	325				
85	315				
87	306				
93	284				
94	262				
95	310				
97	309				
98	246				

**Consensus statistics**

Consensus median, pg/g	302
Median all values pg/g	302
Consensus mean, pg/g	293
Standard deviation, pg/g	62
Relative standard deviation, %	21
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0

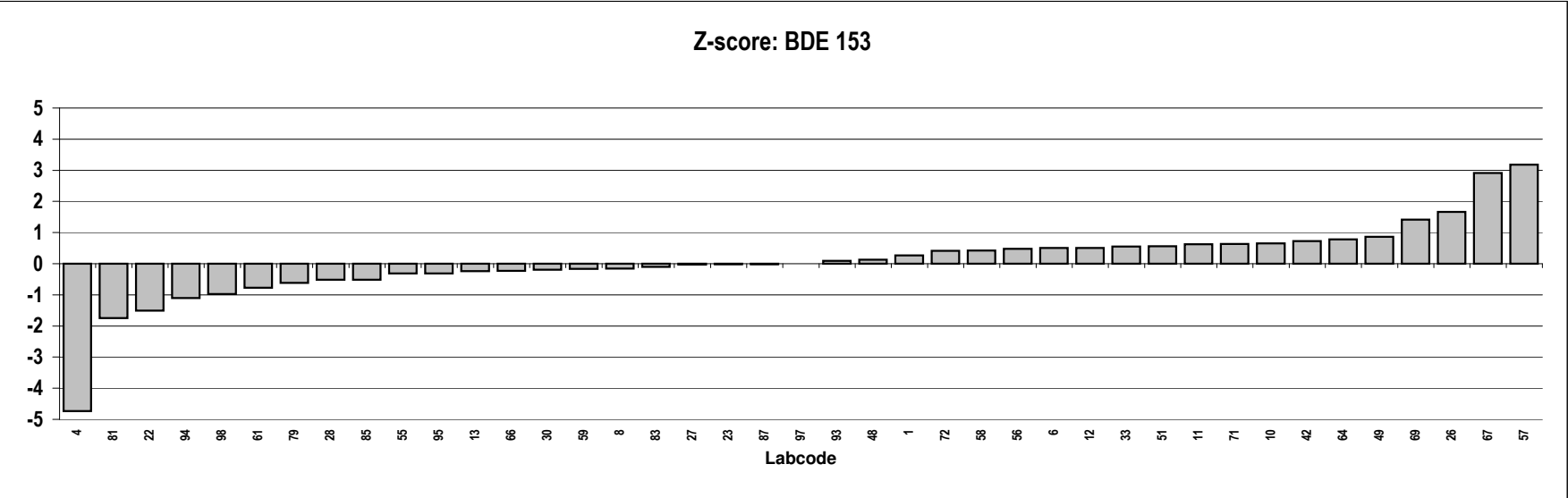
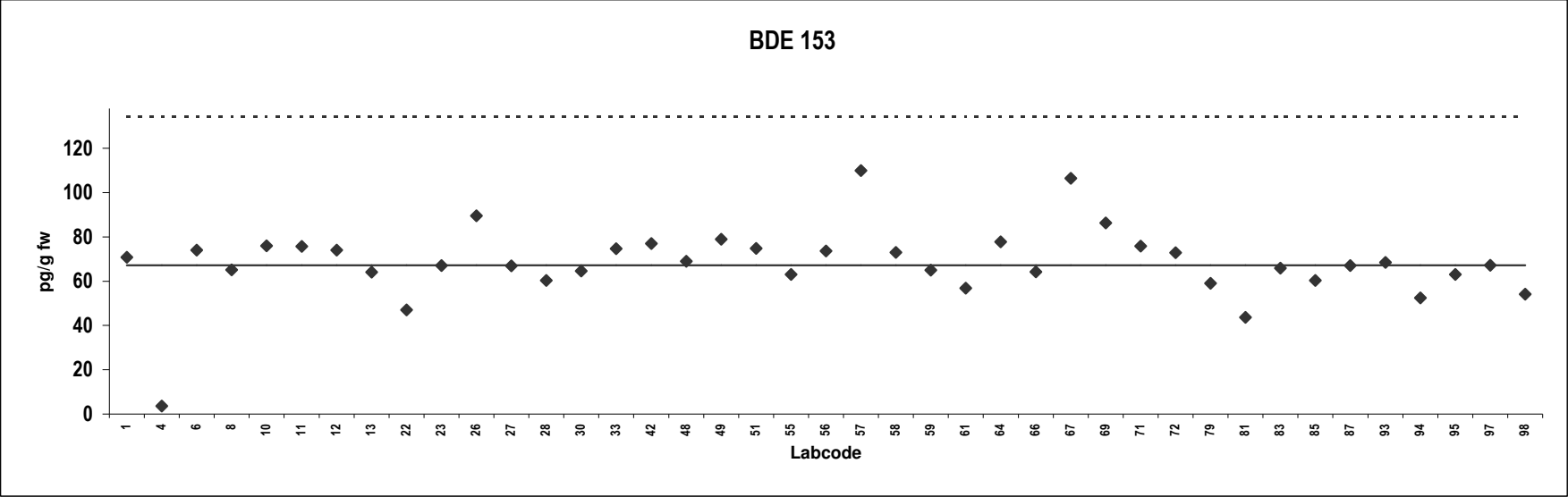


**Salmon**  
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	71				
4	3.6				
6	74				
8	65				
10	76				
11	76				
12	74				
13	64				
22	47				
23	67				
26	90				
27	67				
28	60				
30	65				
33	75				
42	77				
48	69				
49	79				
51	75				
55	63				
56	74				
57	110				
58	73				
59	65				
61	57				
64	78				
66	64				
67	106				
69	86				
71	76				
72	73				
79	59				
81	44				
83	66				
85	60				
87	67				
93	69				
94	52				
95	63				
97	67				
98	54				

**Consensus statistics**

Consensus median, pg/g	67
Median all values pg/g	67
Consensus mean, pg/g	68
Standard deviation, pg/g	16
Relative standard deviation, %	24
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0

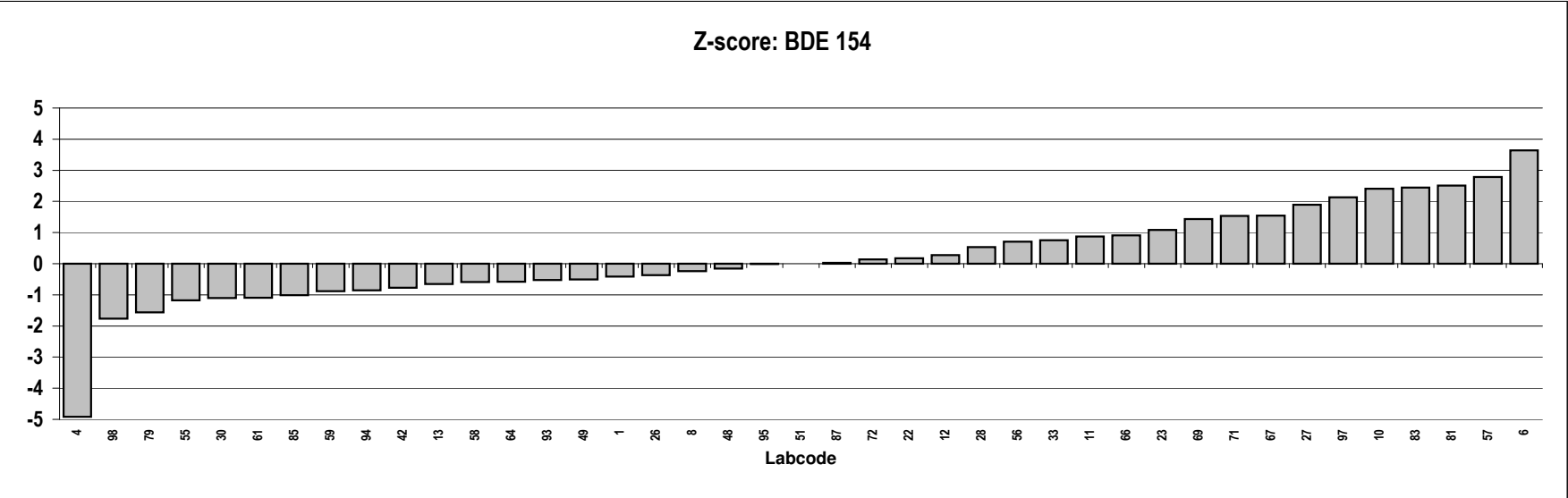
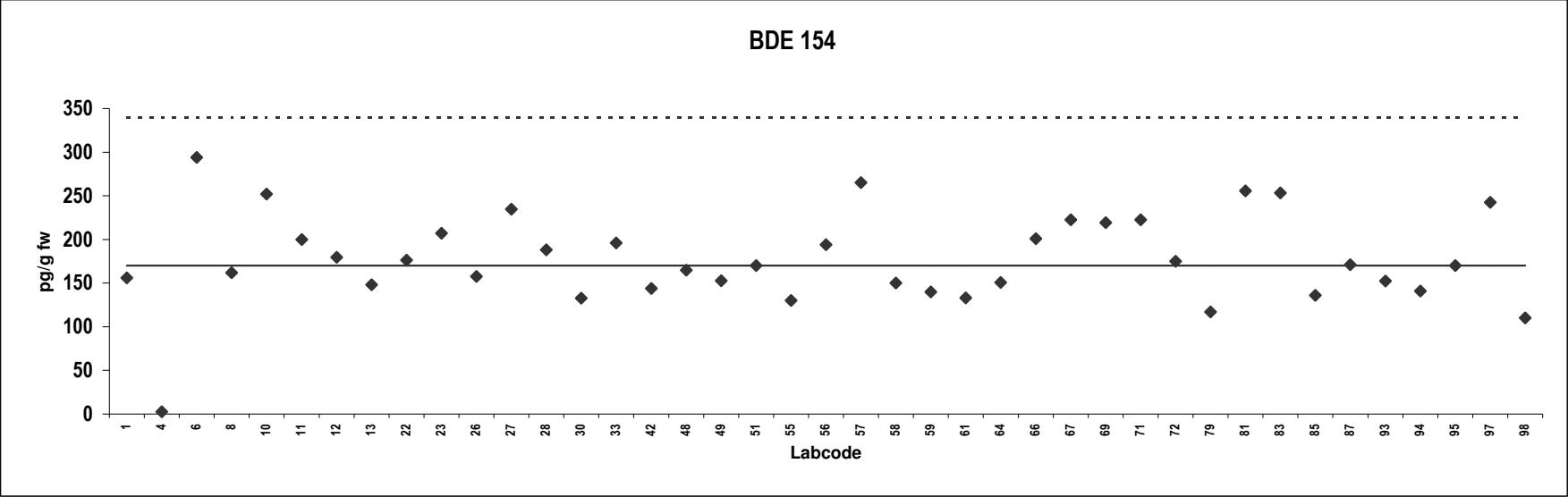


**Salmon**  
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	156				
4	2.7				
6	294				
8	162				
10	252				
11	200				
12	180				
13	148				
22	176				
23	207				
26	158				
27	235				
28	188				
30	133				
33	196				
42	144				
48	165				
49	153				
51	170				
55	130				
56	194				
57	265				
58	150				
59	140				
61	133				
64	151				
66	201				
67	223				
69	219				
71	222				
72	175				
79	117				
81	256				
83	253				
85	136				
87	171				
93	152				
94	141				
95	170				
97	243				
98	110				

**Consensus statistics**

Consensus median, pg/g	170
Median all values pg/g	170
Consensus mean, pg/g	177
Standard deviation, pg/g	52
Relative standard deviation, %	30
No. of values reported	41
No. of values removed	0
No. of reported non-detects	0



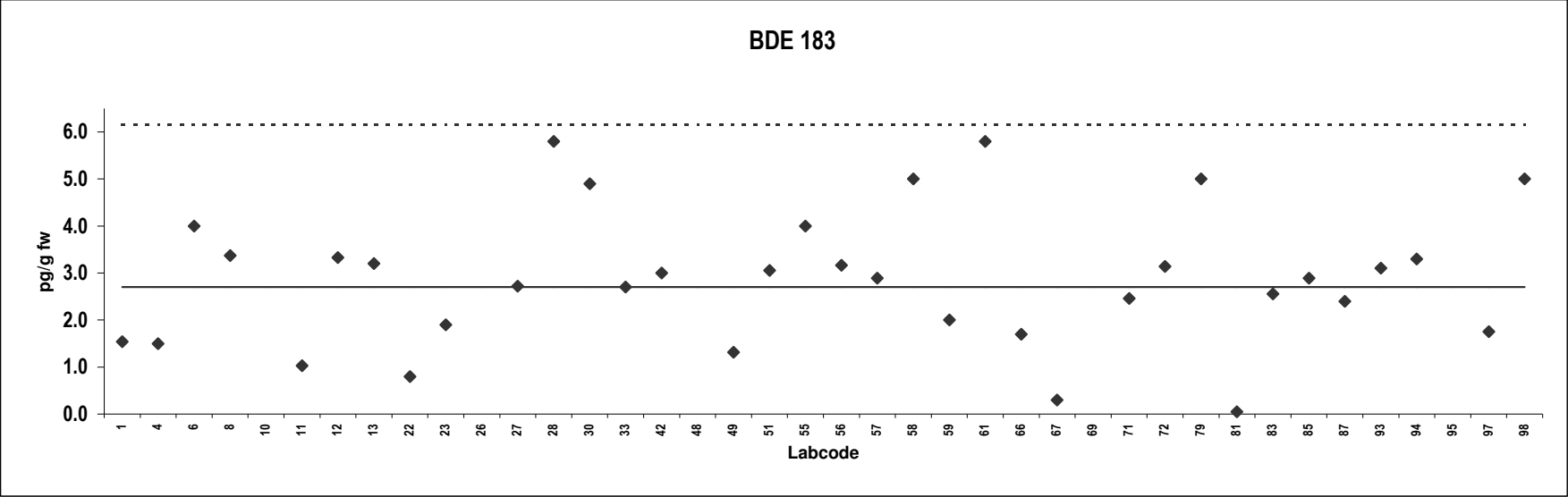
**Salmon**  
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.5				
4	1.5				
6	4.0				
8	3.4	ND			
10	10	Outlier,ND			
11	1.0				
12	3.3				
13	3.2	ND			
22	0.80	ND			
23	1.9				
26	47	Outlier			
27	2.7				
28	5.8				
30	4.9	ND			
33	2.7				
42	3.0	ND			
48	9.0	Outlier			
49	1.3				
51	3.1	ND			
55	4.0				
56	3.2				
57	2.9				
58	5.0	ND			
59	2.0				
61	5.8	ND			
66	1.7				
67	0.30	ND			
69	14	Outlier,ND			
71	2.5				
72	3.1				
79	5.0				
81	0.050	ND			
83	2.6				
85	2.9	ND			
87	2.4				
93	3.1				
94	3.3				
95	10	Outlier,ND			
97	1.8				
98	5.0	ND			

**Consensus statistics**

Consensus median, pg/g	2.7
Median all values pg/g	3.1
Consensus mean, pg/g	2.9
Standard deviation, pg/g	1.5
Relative standard deviation, %	50
No. of values reported	40
No. of values removed	5
No. of reported non-detects	15



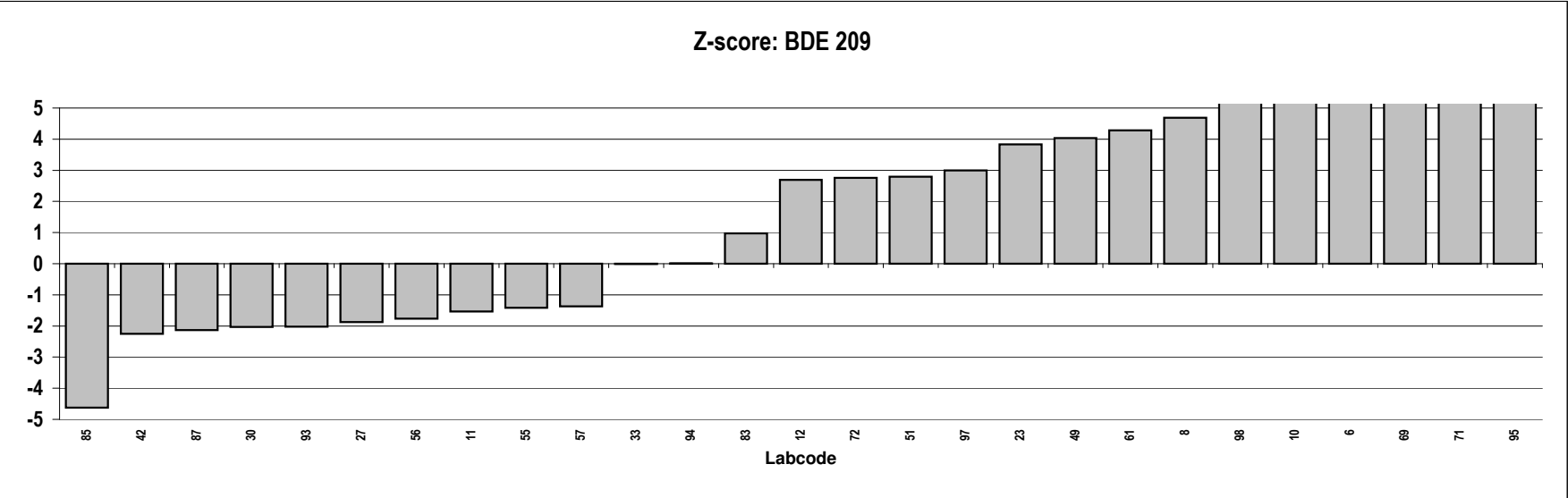
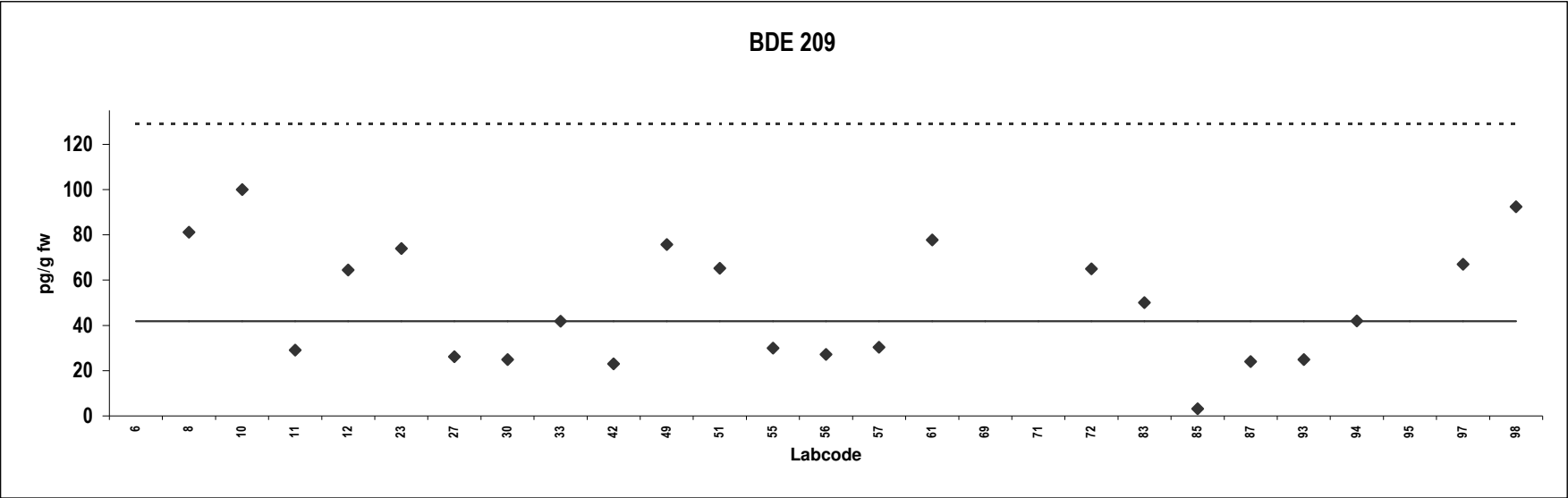


**Salmon**  
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	150	Outlier,ND			
8	81				
10	100	ND			
11	29				
12	64				
23	74	ND			
27	26				
30	25				
33	42				
42	23				
49	76				
51	65				
55	30				
56	27				
57	30				
61	78				
69	190	Outlier,ND			
71	249	Outlier			
72	65				
83	50				
85	3.2	ND			
87	24				
93	25				
94	42				
95	5000	Outlier,ND			
97	67				
98	92				

**Consensus statistics**

Consensus median, pg/g	42
Median all values pg/g	64
Consensus mean, pg/g	50
Standard deviation, pg/g	27
Relative standard deviation, %	54
No. of values reported	27
No. of values removed	4
No. of reported non-detects	6

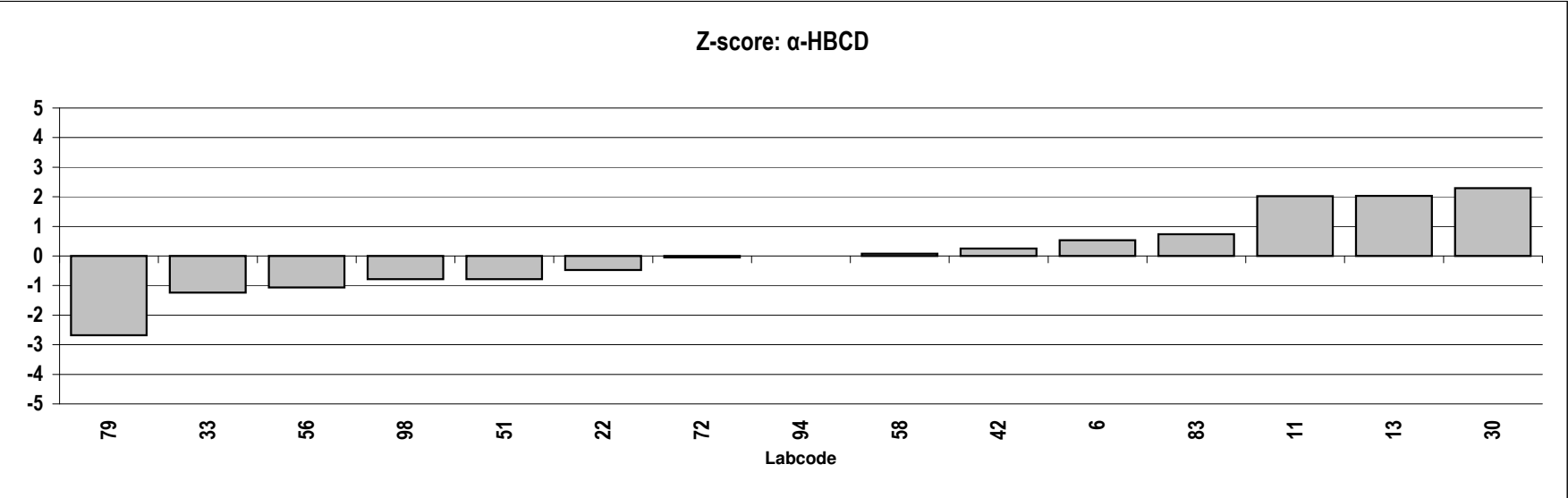
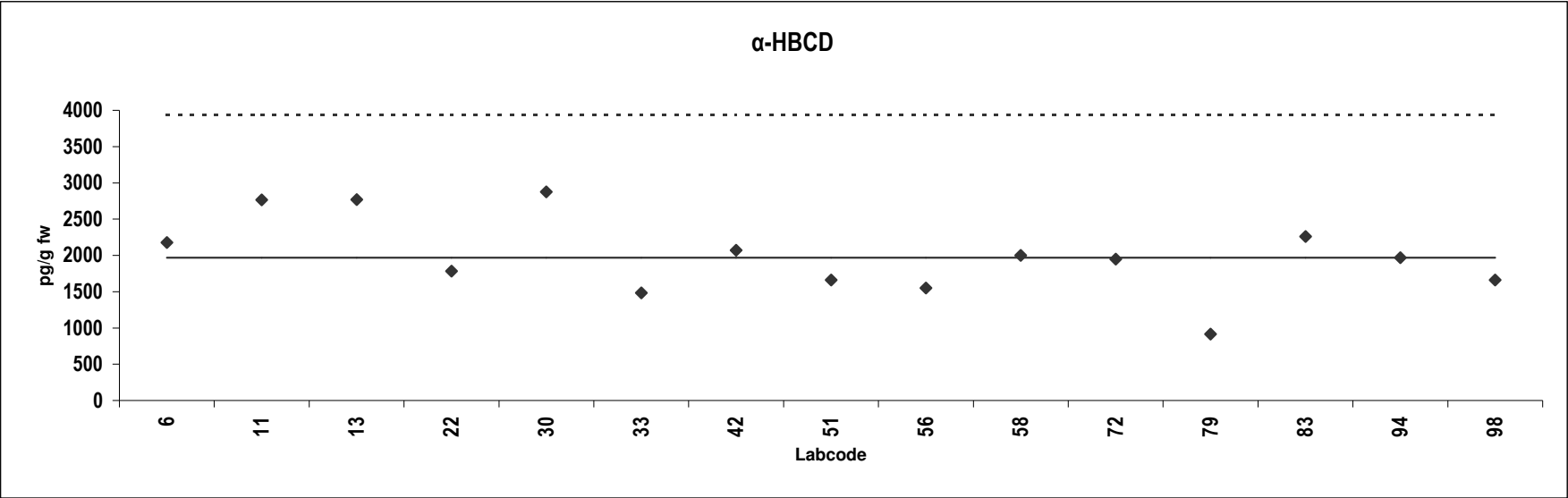


**Salmon**  
Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	2178				
11	2765				
13	2770				
22	1785				
30	2874				
33	1482				
42	2070				
51	1661				
56	1551				
58	2000				
72	1949				
79	915				
83	2259				
94	1970				
98	1660				

**Consensus statistics**

Consensus median, pg/g	1970
Median all values pg/g	1970
Consensus mean, pg/g	1993
Standard deviation, pg/g	533
Relative standard deviation, %	27
No. of values reported	15
No. of values removed	0
No. of reported non-detects	0

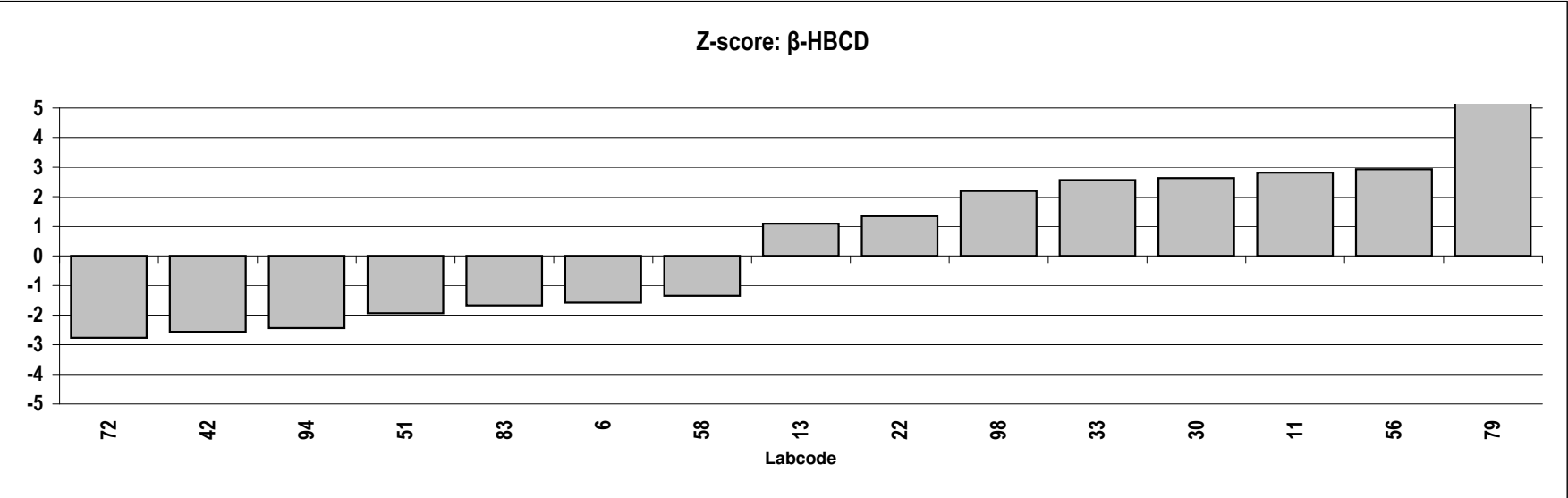
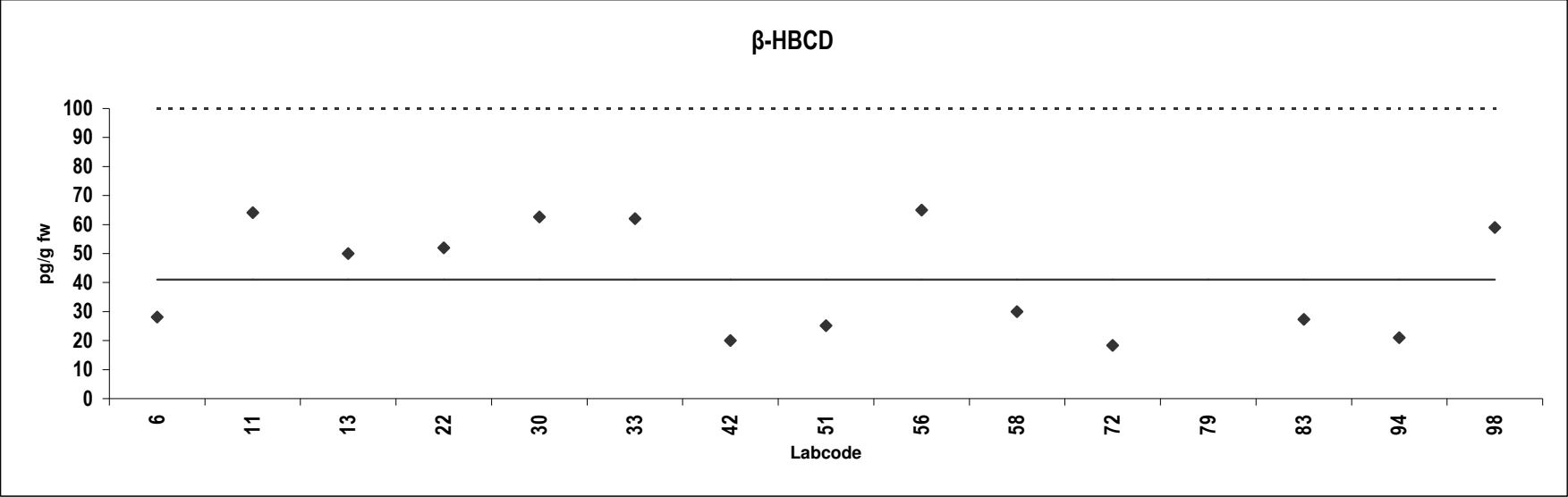


**Salmon**  
Congener:  $\beta$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	28				
11	64				
13	50	ND			
22	52				
30	63	ND			
33	62				
42	20				
51	25	ND			
56	65				
58	30				
72	18	ND			
79	400	Outlier,ND			
83	27				
94	21				
98	59				

**Consensus statistics**

Consensus median, pg/g	41
Median all values pg/g	50
Consensus mean, pg/g	42
Standard deviation, pg/g	19
Relative standard deviation, %	45
No. of values reported	15
No. of values removed	1
No. of reported non-detects	5



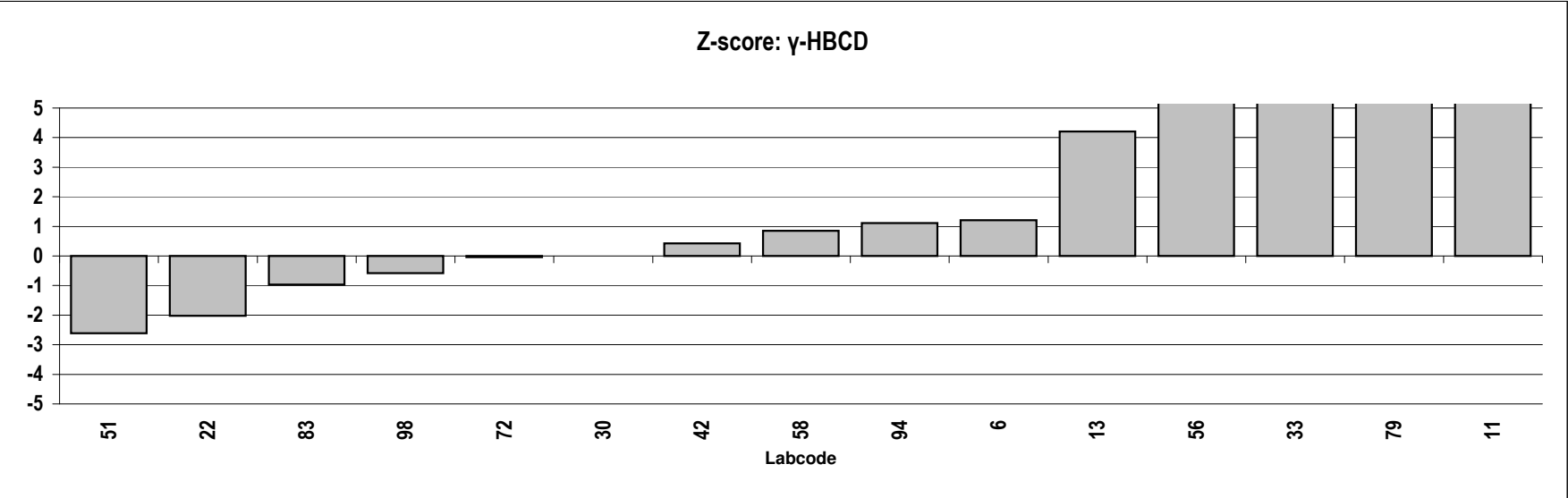
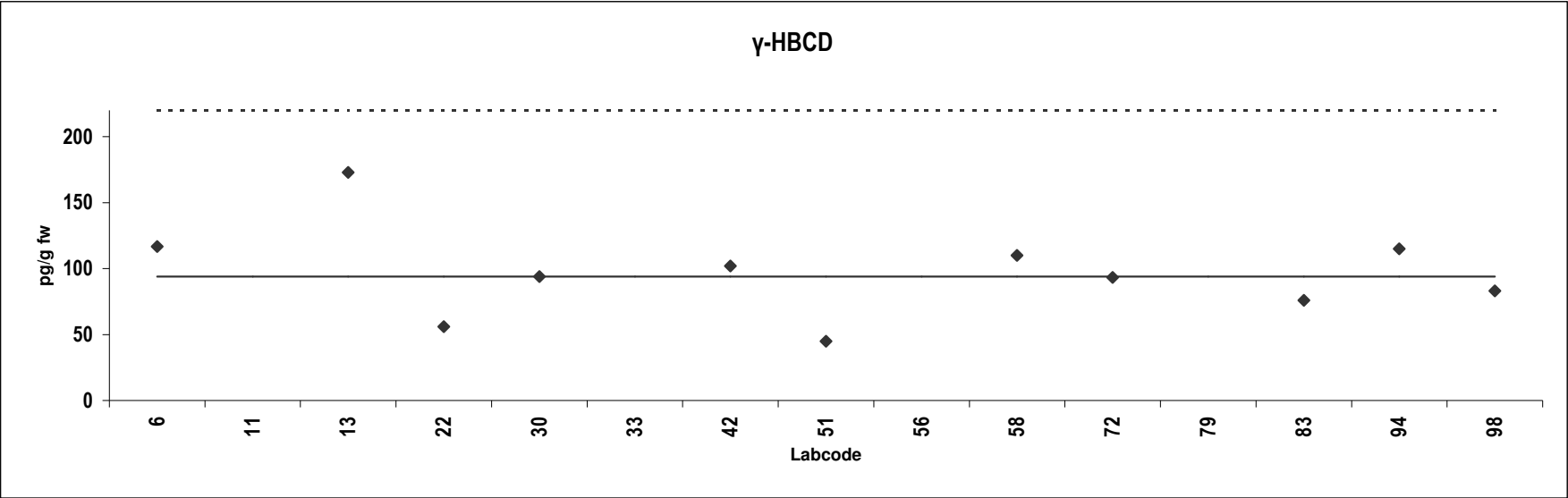
**Salmon**  
Congener:  $\gamma$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	117				
11	423	Outlier			
13	173				
22	56				
30	94				
33	275	Outlier			
42	102				
51	45				
56	267	Outlier			
58	110				
72	93				
79	400	Outlier,ND			
83	76				
94	115				
98	83				

**Consensus statistics**

Consensus median, pg/g	94
Median all values pg/g	110
Consensus mean, pg/g	97
Standard deviation, pg/g	34
Relative standard deviation, %	35
No. of values reported	15
No. of values removed	4
No. of reported non-detects	1



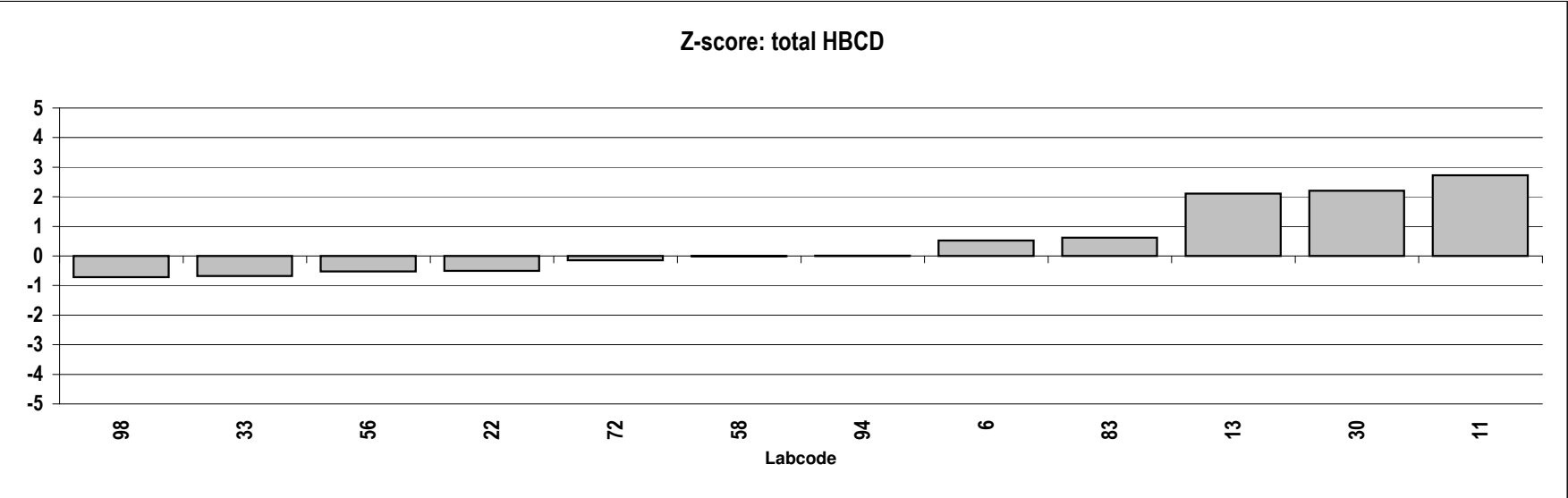
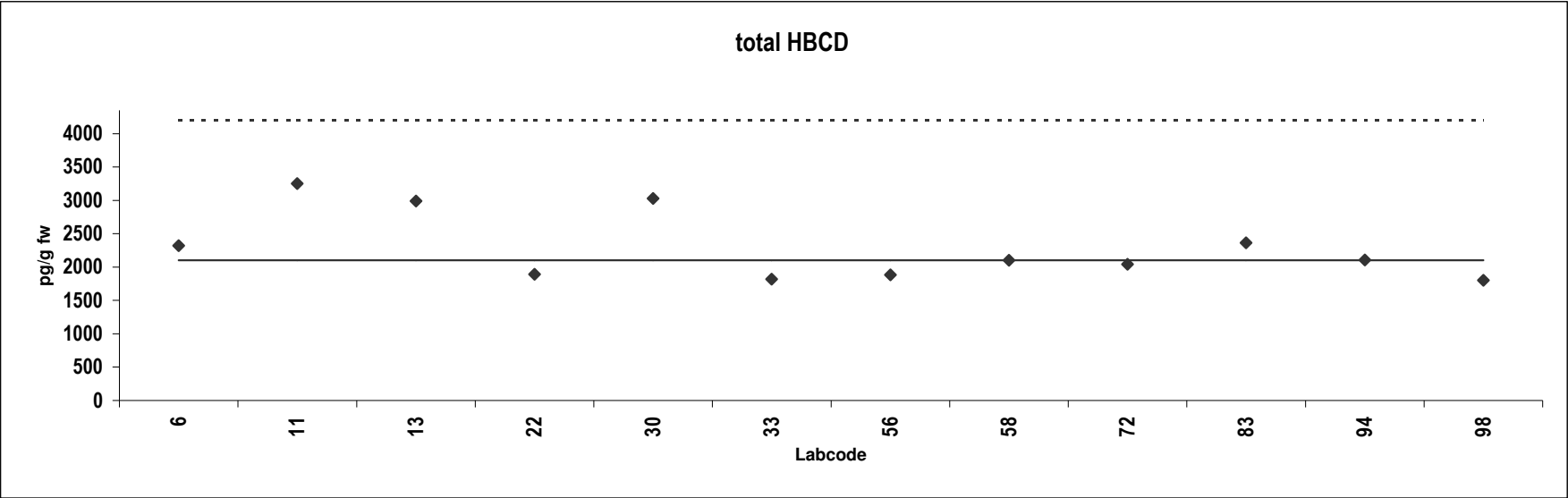


**Salmon**  
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	2323				
11	3251				
13	2990				
22	1893				
30	3031				
33	1819				
56	1883				
58	2100				
72	2042				
83	2362				
94	2106				
98	1802				

**Consensus statistics**

Consensus median, pg/g	2103
Median all values pg/g	2103
Consensus mean, pg/g	2300
Standard deviation, pg/g	512
Relative standard deviation, %	22
No. of values reported	12
No. of values removed	0
No. of reported non-detects	0





## **Appendix 3:**

Presentation of results  
for mozzarella cheese



## Appendix 3: Presentation of results: Mozzarella Cheese

### Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

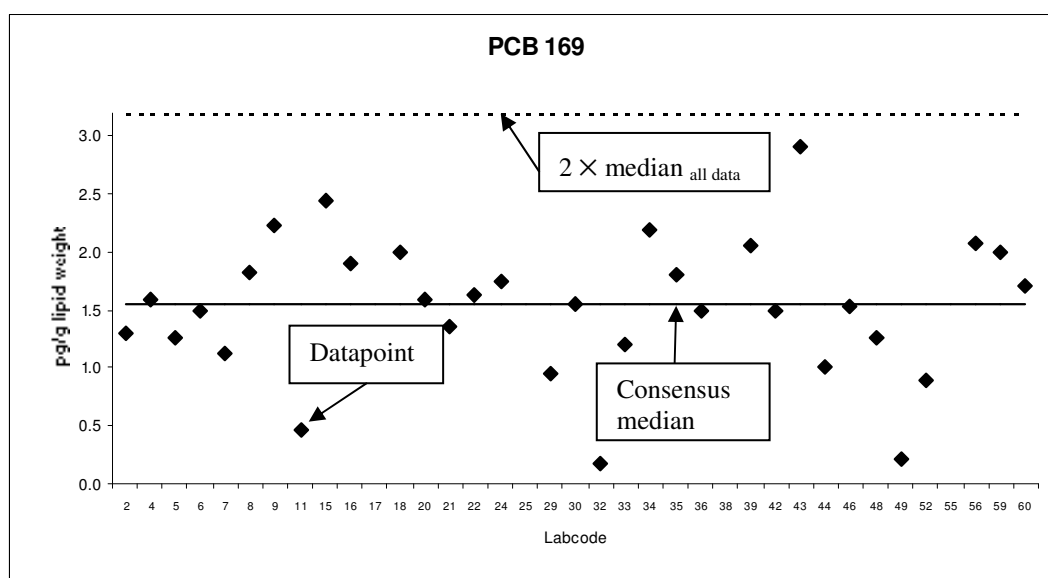
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

### Statistic calculations for indicator PCBs, PBDEs and HBCD

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).
2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set. The NDs were also removed.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

The diagram shows the reported data up to approximately the limit for outliers ( $2 \times$  the first median).



### Z-Scores of individual congeners

Z-scores of each congener were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

## Mozzarella Cheese

Congener: 2,3,7,8 TCDD

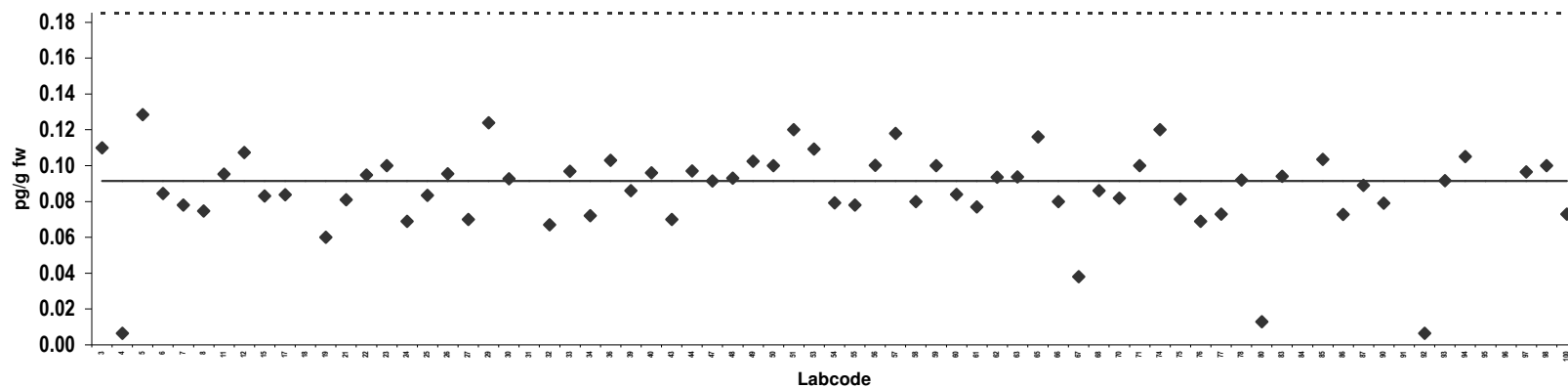
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.11		63	0.094	
4	0.0065	ND	65	0.12	
5	0.13		66	0.080	
6	0.085		67	0.038	
7	0.078		68	0.086	
8	0.075		70	0.082	
11	0.095		71	0.10	
12	0.11		74	0.12	
15	0.083		75	0.081	
17	0.084		76	0.069	
18	0.41	Outlier	77	0.073	
19	0.060		78	0.092	
21	0.081		80	0.013	
22	0.095		83	0.094	
23	0.10		84	0.19	Outlier,ND
24	0.069		85	0.10	
25	0.083		86	0.073	
26	0.095		87	0.089	
27	0.070		90	0.079	
29	0.12		91	0.29	Outlier
30	0.093		92	0.0064	ND
31	0.38	Outlier	93	0.092	
32	0.067		94	0.11	
33	0.097		95	0.36	Outlier,ND
34	0.072		96	0.59	Outlier
36	0.10		97	0.096	
39	0.086		98	0.10	
40	0.096		100	0.073	
43	0.070	ND			
44	0.097	ND			
47	0.091				
48	0.093				
49	0.10				
50	0.10				
51	0.12				
53	0.11				
54	0.079				
55	0.078				
56	0.10				
57	0.12				
58	0.080				
59	0.10				
60	0.084				
61	0.077				
62	0.094				

### Consensus statistics

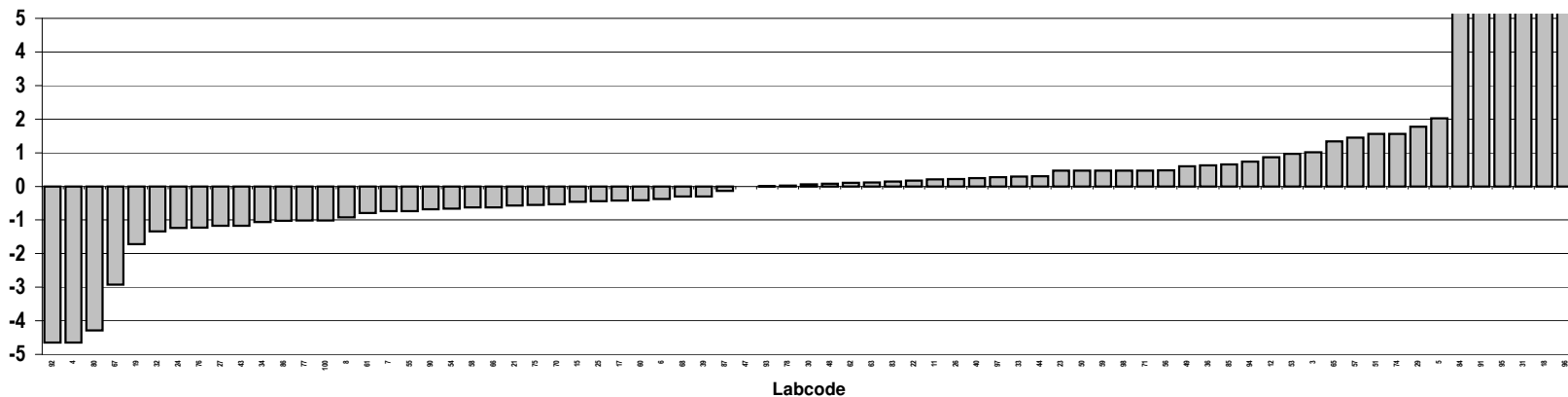
Consensus median, pg/g	0.091
Median all values pg/g	0.093
Consensus mean, pg/g	0.086
Standard deviation, pg/g	0.023
Relative standard deviation, %	27
No. of values reported	73
No. of values removed	6
No. of reported non-detects	6



### 2,3,7,8 TCDD



### Z-score: 2,3,7,8 TCDD

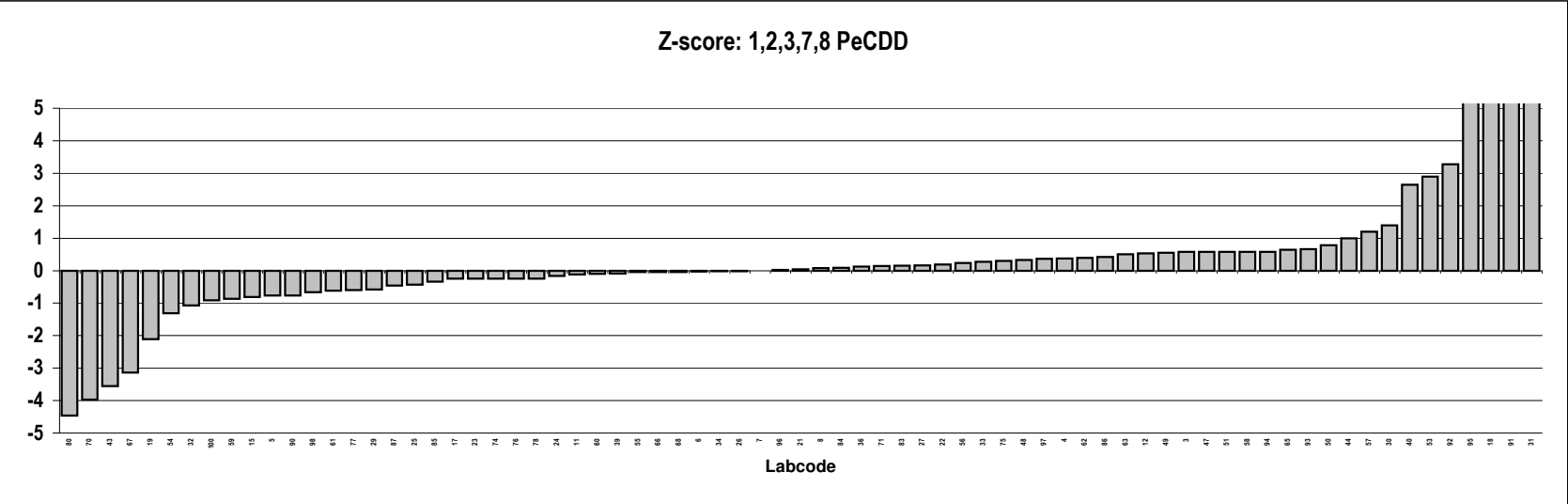
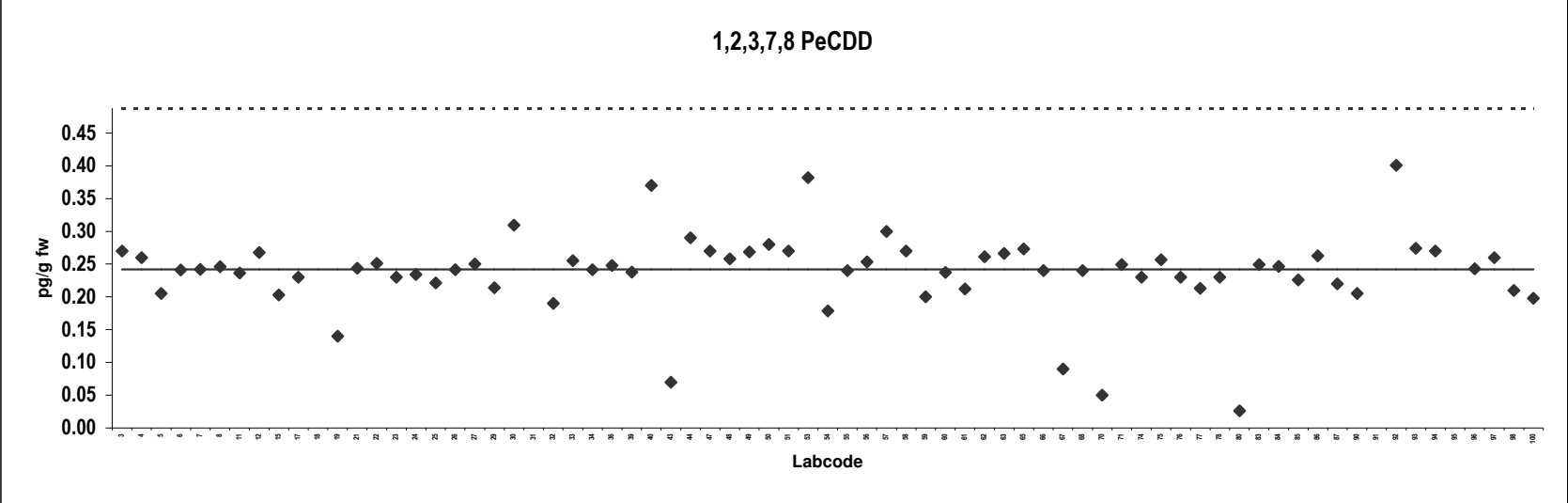


**Mozzarella Cheese**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.27		63	0.27	
4	0.26		65	0.27	
5	0.21		66	0.24	
6	0.24		67	0.090	
7	0.24		68	0.24	
8	0.25		70	0.050	ND
11	0.24		71	0.25	
12	0.27		74	0.23	
15	0.20		75	0.26	
17	0.23		76	0.23	
18	0.80	Outlier	77	0.21	
19	0.14		78	0.23	
21	0.24		80	0.026	
22	0.25		83	0.25	
23	0.23		84	0.25	ND
24	0.23		85	0.23	
25	0.22		86	0.26	
26	0.24		87	0.22	
27	0.25		90	0.21	
29	0.21		91	0.80	Outlier
30	0.31		92	0.40	
31	1.00	Outlier	93	0.27	
32	0.19		94	0.27	
33	0.26		95	0.50	Outlier,ND
34	0.24		96	0.24	
36	0.25		97	0.26	
39	0.24		98	0.21	
40	0.37		100	0.20	
43	0.070	ND			
44	0.29	ND			
47	0.27				
48	0.26				
49	0.27				
50	0.28				
51	0.27				
53	0.38				
54	0.18				
55	0.24				
56	0.25				
57	0.30				
58	0.27				
59	0.20				
60	0.24				
61	0.21				
62	0.26				

**Consensus statistics**

Consensus median, pg/g	0.24
Median all values pg/g	0.24
Consensus mean, pg/g	0.24
Standard deviation, pg/g	0.060
Relative standard deviation, %	25
No. of values reported	73
No. of values removed	4
No. of reported non-detects	5

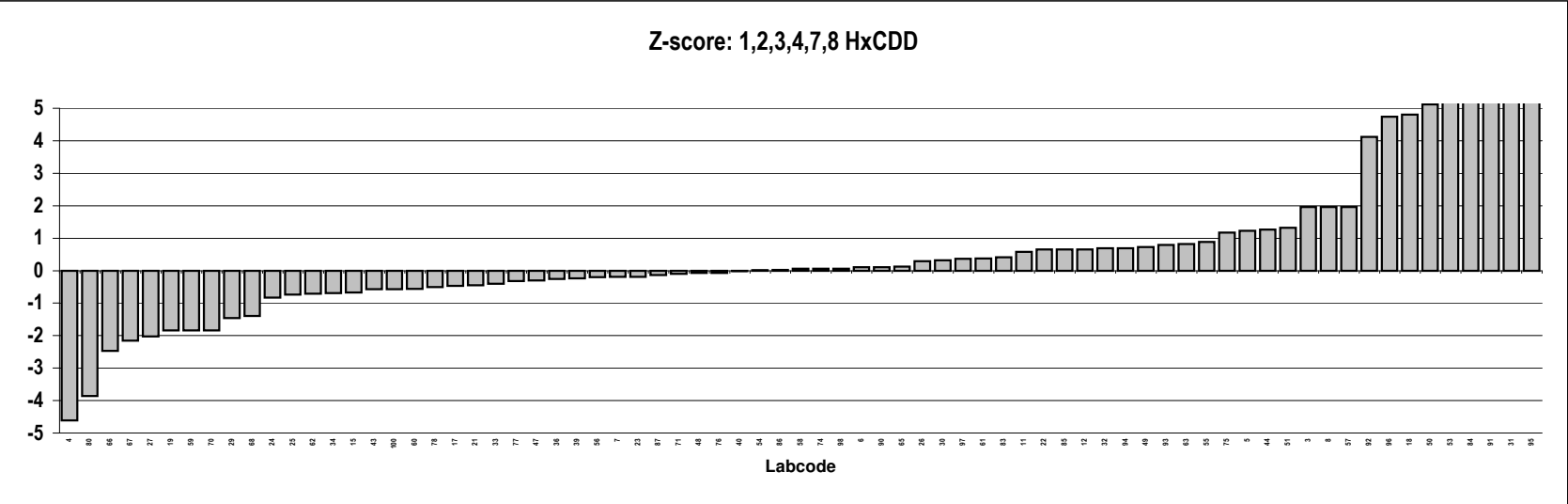
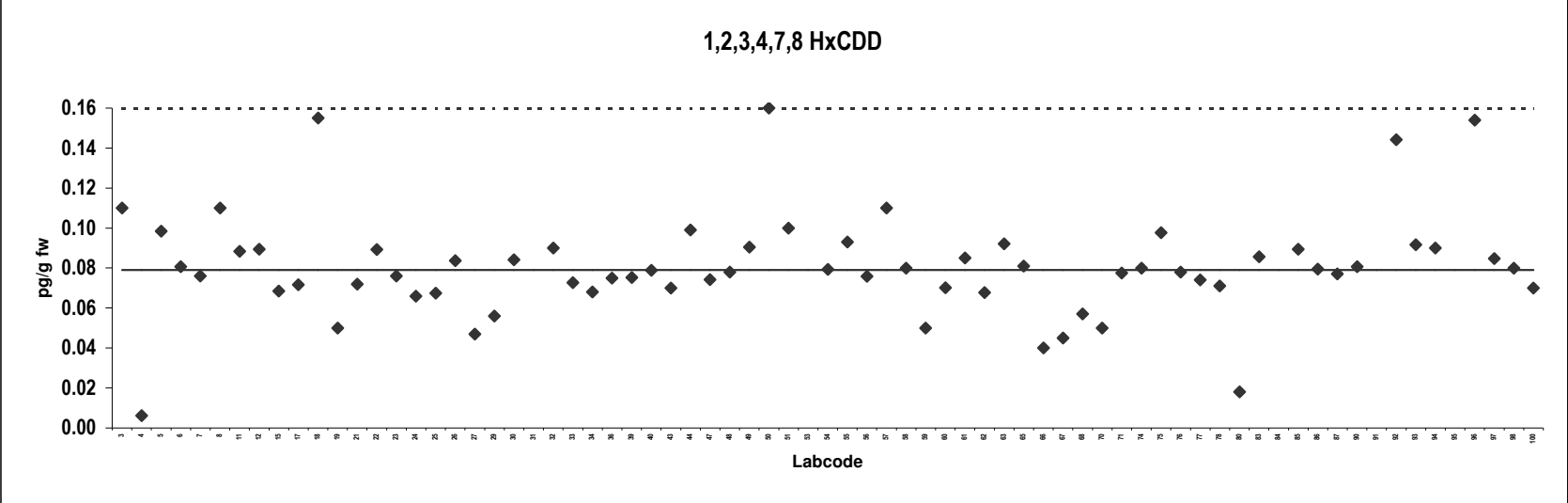


**Mozzarella Cheese**  
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.11		63	0.092	
4	0.0062	ND	65	0.081	
5	0.099		66	0.040	
6	0.081		67	0.045	
7	0.076		68	0.057	
8	0.11		70	0.050	ND
11	0.088		71	0.077	
12	0.089		74	0.080	
15	0.068		75	0.098	
17	0.072		76	0.078	
18	0.16	ND	77	0.074	
19	0.050	ND	78	0.071	
21	0.072		80	0.018	
22	0.089		83	0.086	
23	0.076		84	0.20	Outlier
24	0.066		85	0.089	
25	0.067		86	0.079	
26	0.084		87	0.077	
27	0.047		90	0.081	
29	0.056		91	0.25	Outlier
30	0.084		92	0.14	
31	0.28	Outlier	93	0.092	
32	0.090		94	0.090	
33	0.073		95	0.35	Outlier,ND
34	0.068		96	0.15	
36	0.075		97	0.085	
39	0.075		98	0.080	
40	0.079		100	0.070	
43	0.070	ND			
44	0.099	ND			
47	0.074				
48	0.078				
49	0.091				
50	0.16				
51	0.10				
53	0.18	Outlier			
54	0.079				
55	0.093				
56	0.076				
57	0.11				
58	0.080				
59	0.050				
60	0.070				
61	0.085				
62	0.068				

**Consensus statistics**

Consensus median, pg/g	0.079
Median all values pg/g	0.080
Consensus mean, pg/g	0.081
Standard deviation, pg/g	0.026
Relative standard deviation, %	32
No. of values reported	73
No. of values removed	5
No. of reported non-detects	7

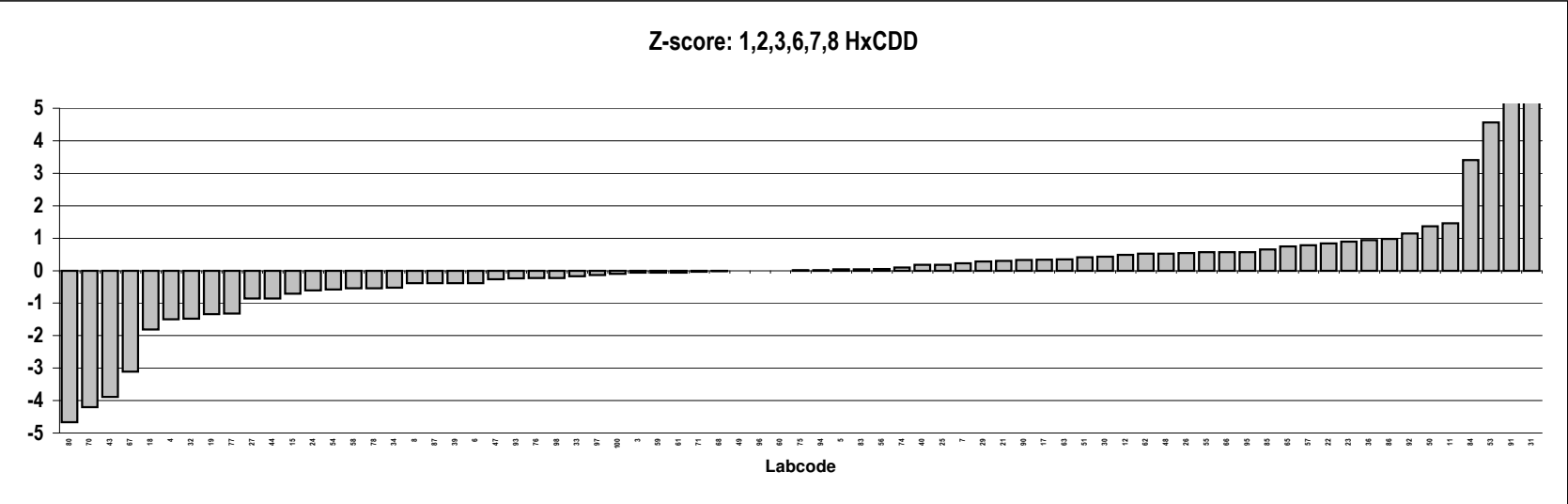
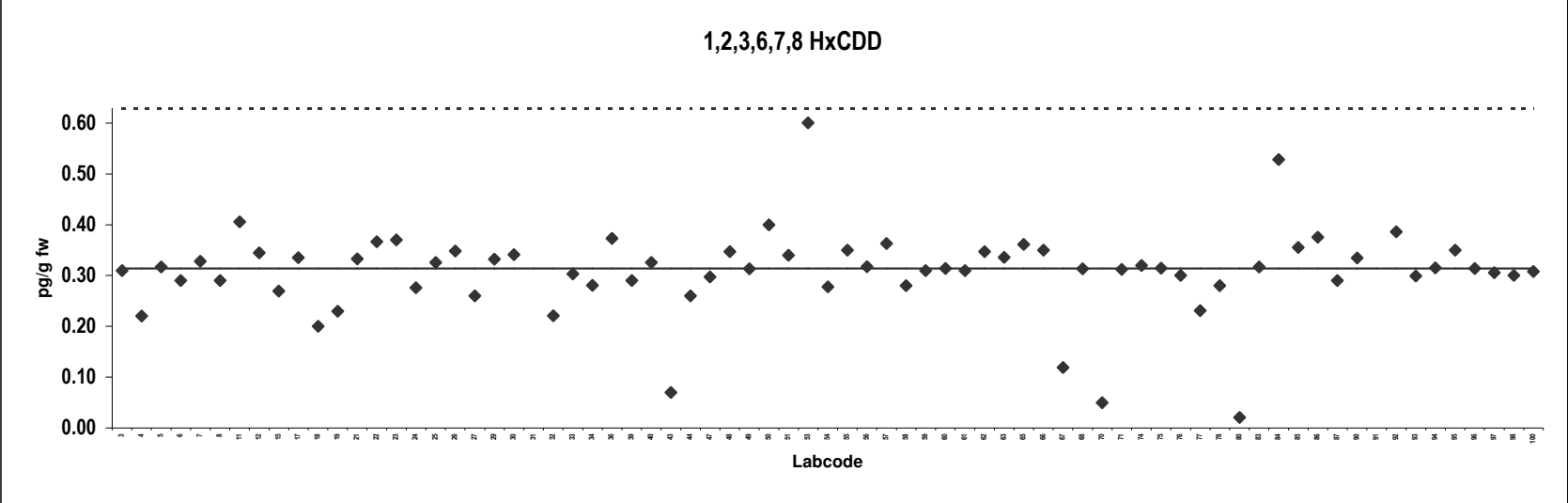


**Mozzarella Cheese**  
Congener: 1,2,3,6,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.31		63	0.34	
4	0.22		65	0.36	
5	0.32		66	0.35	
6	0.29		67	0.12	
7	0.33		68	0.31	
8	0.29		70	0.050	ND
11	0.41		71	0.31	
12	0.34		74	0.32	
15	0.27		75	0.31	
17	0.34		76	0.30	
18	0.20	ND	77	0.23	
19	0.23		78	0.28	
21	0.33		80	0.021	
22	0.37		83	0.32	
23	0.37		84	0.53	
24	0.28		85	0.36	
25	0.33		86	0.38	
26	0.35		87	0.29	
27	0.26		90	0.33	
29	0.33		91	1.0	Outlier
30	0.34		92	0.39	
31	1.5	Outlier	93	0.30	
32	0.22		94	0.32	
33	0.30		95	0.35	ND
34	0.28		96	0.31	
36	0.37		97	0.31	
39	0.29		98	0.30	
40	0.33		100	0.31	
43	0.070	ND			
44	0.26				
47	0.30				
48	0.35				
49	0.31				
50	0.40				
51	0.34				
53	0.60				
54	0.28				
55	0.35				
56	0.32				
57	0.36				
58	0.28				
59	0.31				
60	0.31				
61	0.31				
62	0.35				

**Consensus statistics**

Consensus median, pg/g	0.31
Median all values pg/g	0.31
Consensus mean, pg/g	0.31
Standard deviation, pg/g	0.084
Relative standard deviation, %	27
No. of values reported	73
No. of values removed	2
No. of reported non-detects	4



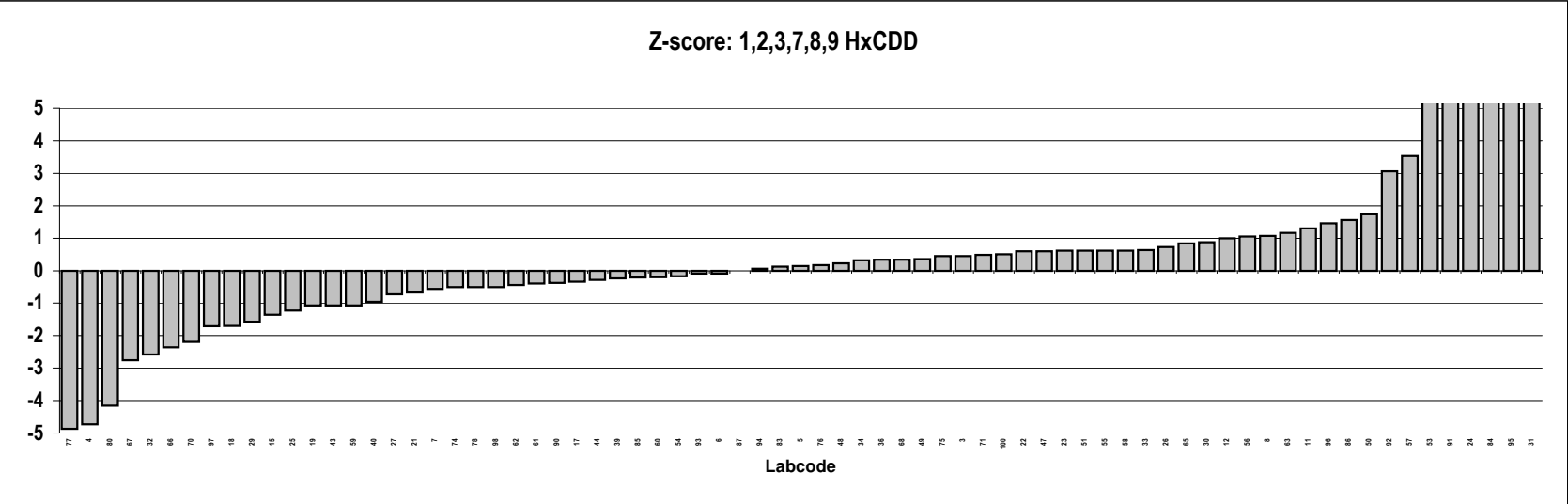
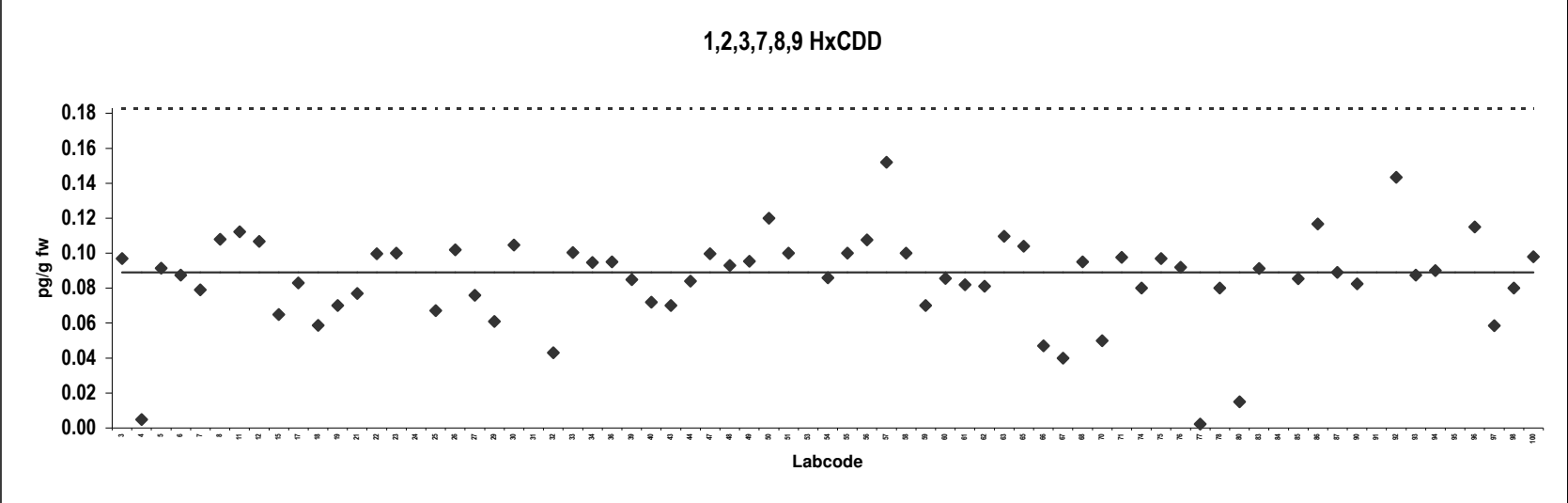
**Mozzarella Cheese**  
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.097		63	0.11	
4	0.0048	ND	65	0.10	
5	0.092		66	0.047	
6	0.088		67	0.040	
7	0.079		68	0.095	
8	0.11		70	0.050	ND
11	0.11		71	0.098	
12	0.11		74	0.080	
15	0.065		75	0.097	
17	0.083		76	0.092	
18	0.059	ND	77	0.0023	ND
19	0.070		78	0.080	
21	0.077		80	0.015	
22	0.100		83	0.091	
23	0.10		84	0.31	Outlier,ND
24	0.30	Outlier	85	0.085	
25	0.067		86	0.12	
26	0.10		87	0.089	
27	0.076		90	0.082	
29	0.061		91	0.28	Outlier
30	0.10		92	0.14	
31	0.45	Outlier	93	0.087	
32	0.043	ND	94	0.090	
33	0.10		95	0.32	Outlier,ND
34	0.095		96	0.12	
36	0.095		97	0.059	
39	0.085		98	0.080	
40	0.072		100	0.098	
43	0.070	ND			
44	0.084	ND			
47	0.100				
48	0.093				
49	0.095				
50	0.12				
51	0.10				
53	0.22	Outlier			
54	0.086				
55	0.10				
56	0.11				
57	0.15				
58	0.10				
59	0.070				
60	0.085				
61	0.082				
62	0.081				

**Consensus statistics**

Consensus median, pg/g	0.089
Median all values pg/g	0.092
Consensus mean, pg/g	0.085
Standard deviation, pg/g	0.026
Relative standard deviation, %	31
No. of values reported	73
No. of values removed	6
No. of reported non-detects	9





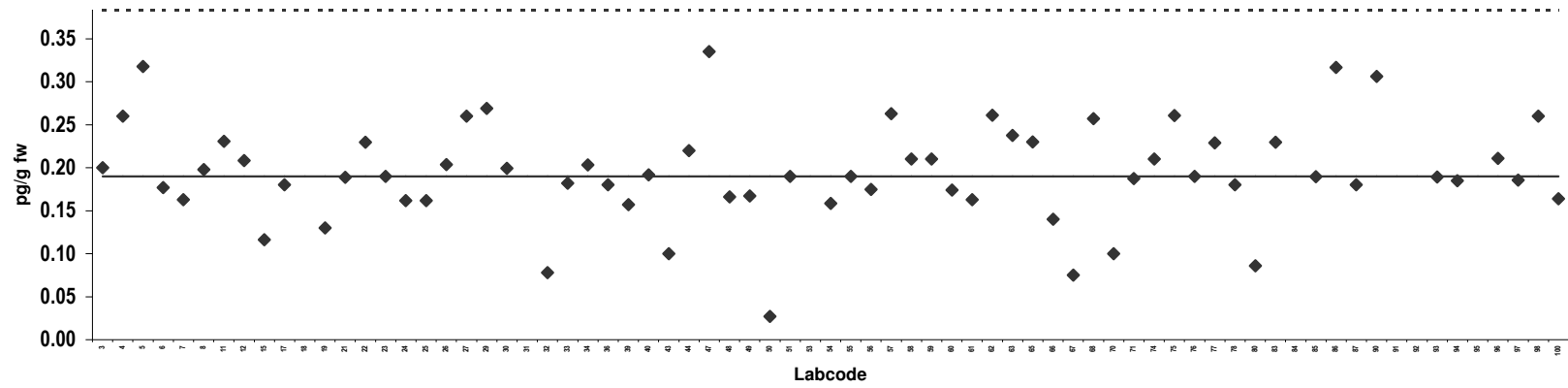
**Mozzarella Cheese**  
**Congener: 1,2,3,4,6,7,8 HpCDD**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.20		63	0.24	
4	0.26		65	0.23	
5	0.32		66	0.14	
6	0.18		67	0.075	
7	0.16		68	0.26	
8	0.20		70	0.10	ND
11	0.23		71	0.19	
12	0.21		74	0.21	
15	0.12		75	0.26	
17	0.18		76	0.19	
18	2.4	Outlier	77	0.23	
19	0.13		78	0.18	
21	0.19		80	0.086	
22	0.23		83	0.23	
23	0.19		84	0.52	Outlier,ND
24	0.16		85	0.19	
25	0.16		86	0.32	
26	0.20		87	0.18	
27	0.26		90	0.31	
29	0.27		91	0.73	Outlier
30	0.20		92	0.50	Outlier
31	0.80	Outlier	93	0.19	
32	0.078		94	0.19	
33	0.18		95	0.43	Outlier,ND
34	0.20		96	0.21	
36	0.18		97	0.19	
39	0.16		98	0.26	ND
40	0.19		100	0.16	
43	0.10	ND			
44	0.22	ND			
47	0.34				
48	0.17				
49	0.17				
50	0.027	ND			
51	0.19				
53	0.80	Outlier			
54	0.16				
55	0.19				
56	0.17				
57	0.26				
58	0.21				
59	0.21				
60	0.17				
61	0.16				
62	0.26				

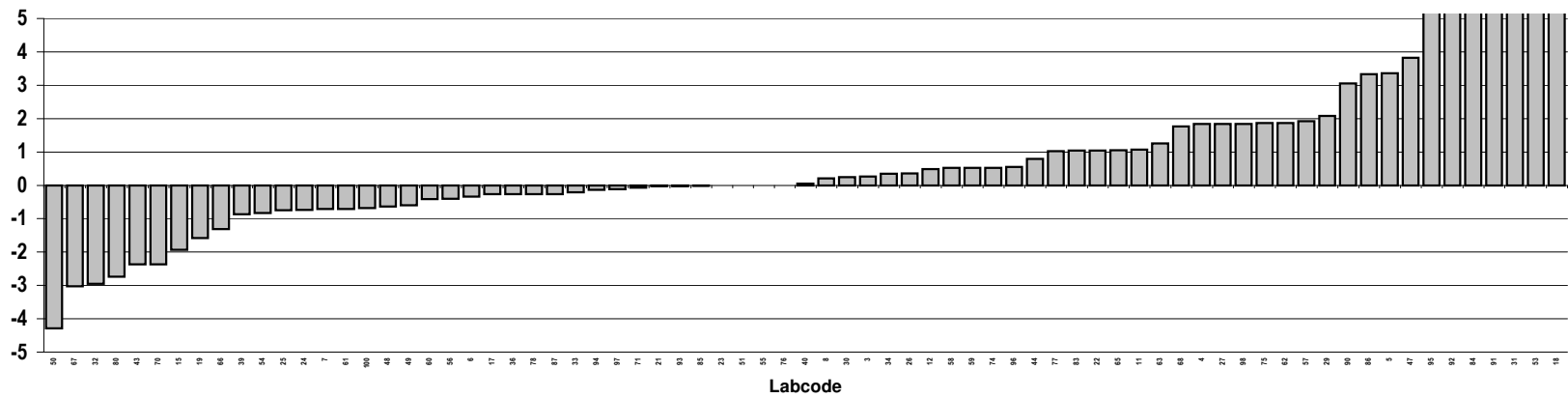
**Consensus statistics**

Consensus median, pg/g	0.19
Median all values pg/g	0.19
Consensus mean, pg/g	0.19
Standard deviation, pg/g	0.058
Relative standard deviation, %	30
No. of values reported	73
No. of values removed	7
No. of reported non-detects	7

### 1,2,3,4,6,7,8 HpCDD



### Z-score: 1,2,3,4,6,7,8 HpCDD



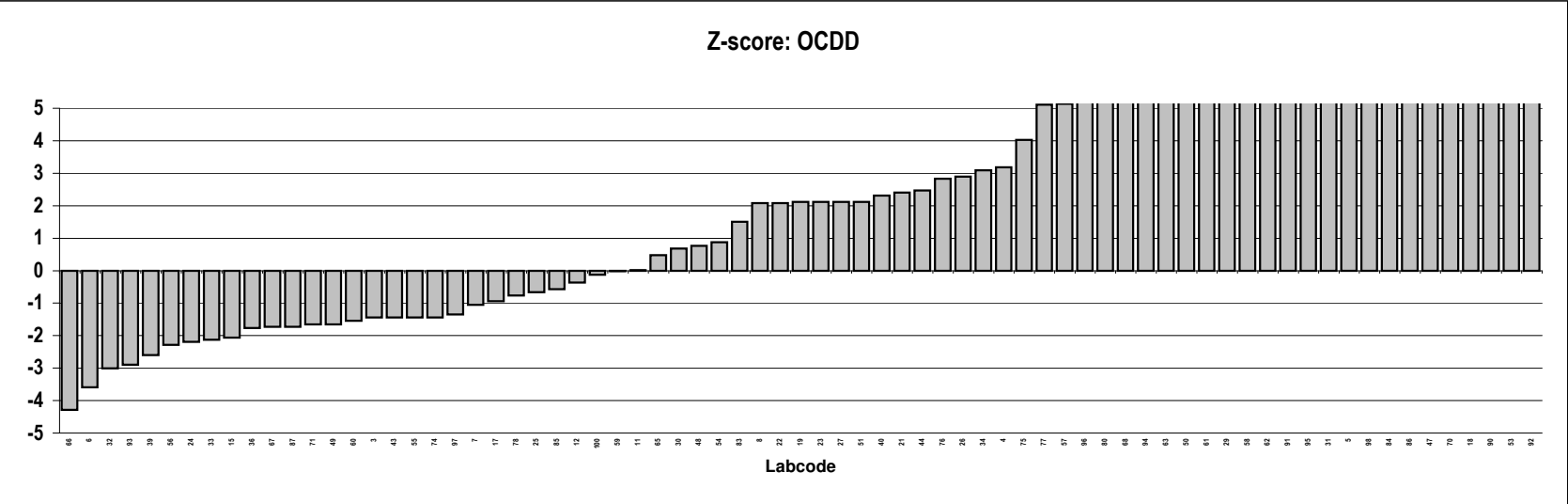
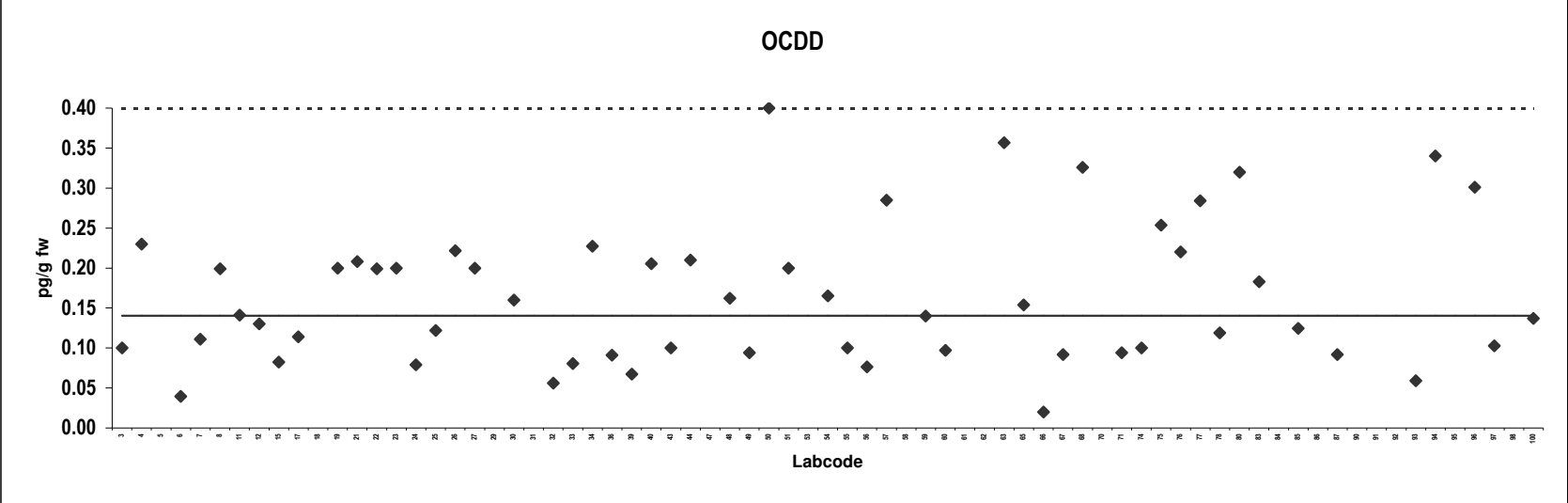
## Mozzarella Cheese

Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.10		63	0.36	
4	0.23		65	0.15	
5	0.74	Outlier	66	0.020	
6	0.040		67	0.092	
7	0.11		68	0.33	
8	0.20		70	1.0	Outlier,ND
11	0.14		71	0.094	
12	0.13		74	0.10	ND
15	0.083		75	0.25	
17	0.11		76	0.22	
18	1.3	Outlier	77	0.28	
19	0.20	ND	78	0.12	ND
21	0.21		80	0.32	
22	0.20		83	0.18	
23	0.20		84	0.86	Outlier,ND
24	0.079		85	0.12	
25	0.12		86	0.91	Outlier
26	0.22		87	0.092	
27	0.20		90	1.4	Outlier
29	0.47	Outlier	91	0.58	Outlier
30	0.16		92	3.7	Outlier
31	0.70	Outlier	93	0.059	ND
32	0.056	ND	94	0.34	
33	0.081		95	0.61	Outlier
34	0.23		96	0.30	
36	0.091		97	0.10	
39	0.068		98	0.85	Outlier,ND
40	0.21		100	0.14	
43	0.10	ND			
44	0.21	ND			
47	0.91	Outlier			
48	0.16				
49	0.094				
50	0.40				
51	0.20				
53	1.9	Outlier			
54	0.17				
55	0.10				
56	0.076				
57	0.29				
58	0.50	Outlier,ND			
59	0.14				
60	0.097				
61	0.40	Outlier			
62	0.50	Outlier,ND			

### Consensus statistics

Consensus median, pg/g	0.14
Median all values pg/g	0.20
Consensus mean, pg/g	0.16
Standard deviation, pg/g	0.087
Relative standard deviation, %	53
No. of values reported	73
No. of values removed	17
No. of reported non-detects	12



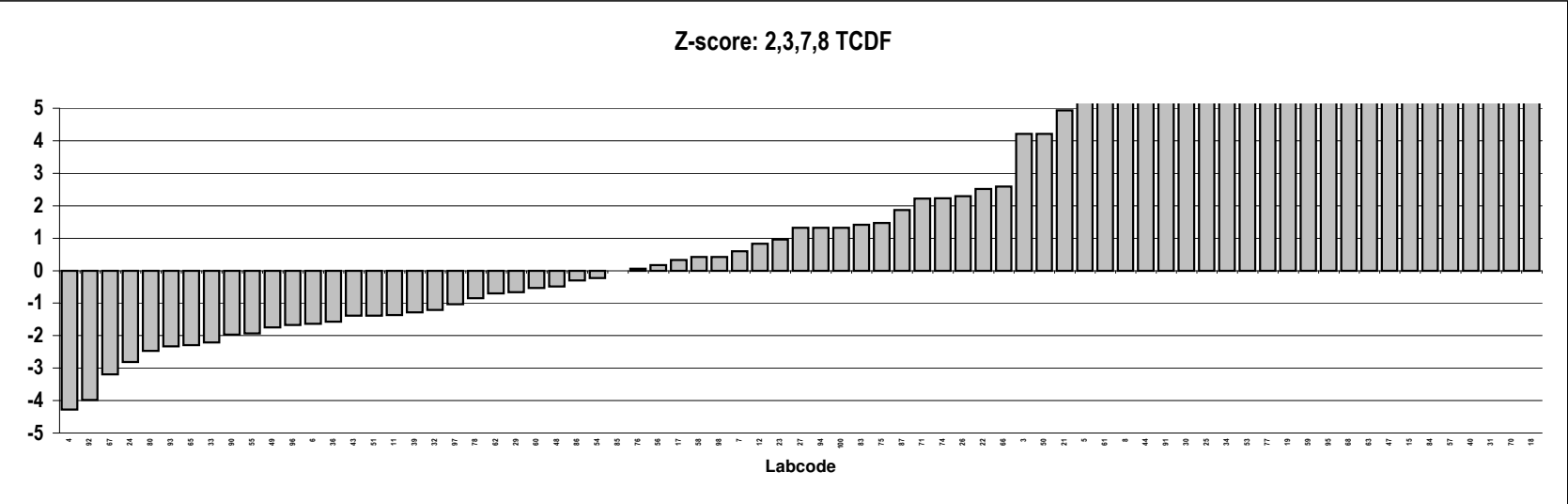
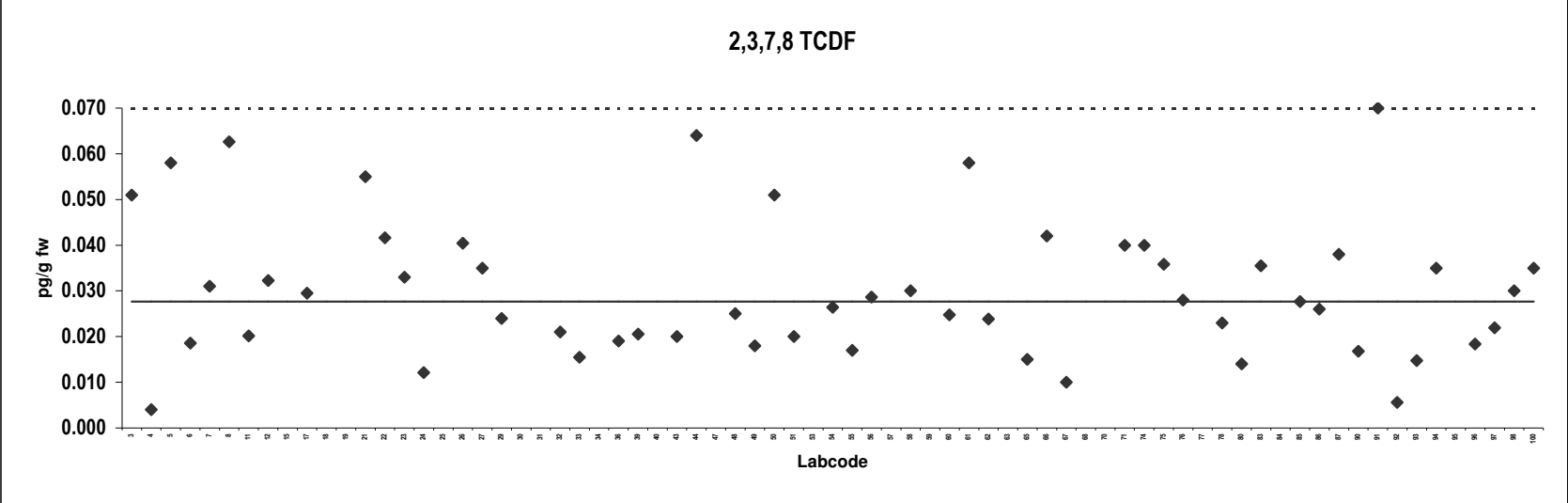
## Mozzarella Cheese

Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.051		63	0.16	Outlier
4	0.0040	ND	65	0.015	
5	0.058		66	0.042	
6	0.019		67	0.010	
7	0.031		68	0.11	Outlier
8	0.063		70	0.46	Outlier
11	0.020		71	0.040	
12	0.032		74	0.040	ND
15	0.23	Outlier	75	0.036	
17	0.030		76	0.028	
18	0.99	Outlier	77	0.095	Outlier
19	0.10	Outlier	78	0.023	
21	0.055		80	0.014	
22	0.042		83	0.036	
23	0.033		84	0.25	Outlier
24	0.012		85	0.028	ND
25	0.084	Outlier	86	0.026	
26	0.040		87	0.038	
27	0.035		90	0.017	
29	0.024		91	0.070	
30	0.072	Outlier	92	0.0056	ND
31	0.46	Outlier	93	0.015	
32	0.021	ND	94	0.035	
33	0.015		95	0.11	Outlier,ND
34	0.088	Outlier	96	0.018	ND
36	0.019		97	0.022	
39	0.021		98	0.030	ND
40	0.31	Outlier	100	0.035	
43	0.020	ND			
44	0.064	ND			
47	0.22	Outlier			
48	0.025				
49	0.018				
50	0.051				
51	0.020				
53	0.091	Outlier			
54	0.026				
55	0.017				
56	0.029				
57	0.28	Outlier			
58	0.030				
59	0.10	Outlier			
60	0.025				
61	0.058				
62	0.024				

### Consensus statistics

Consensus median, pg/g	0.028
Median all values pg/g	0.035
Consensus mean, pg/g	0.030
Standard deviation, pg/g	0.015
Relative standard deviation, %	50
No. of values reported	73
No. of values removed	18
No. of reported non-detects	10



## Mozzarella Cheese

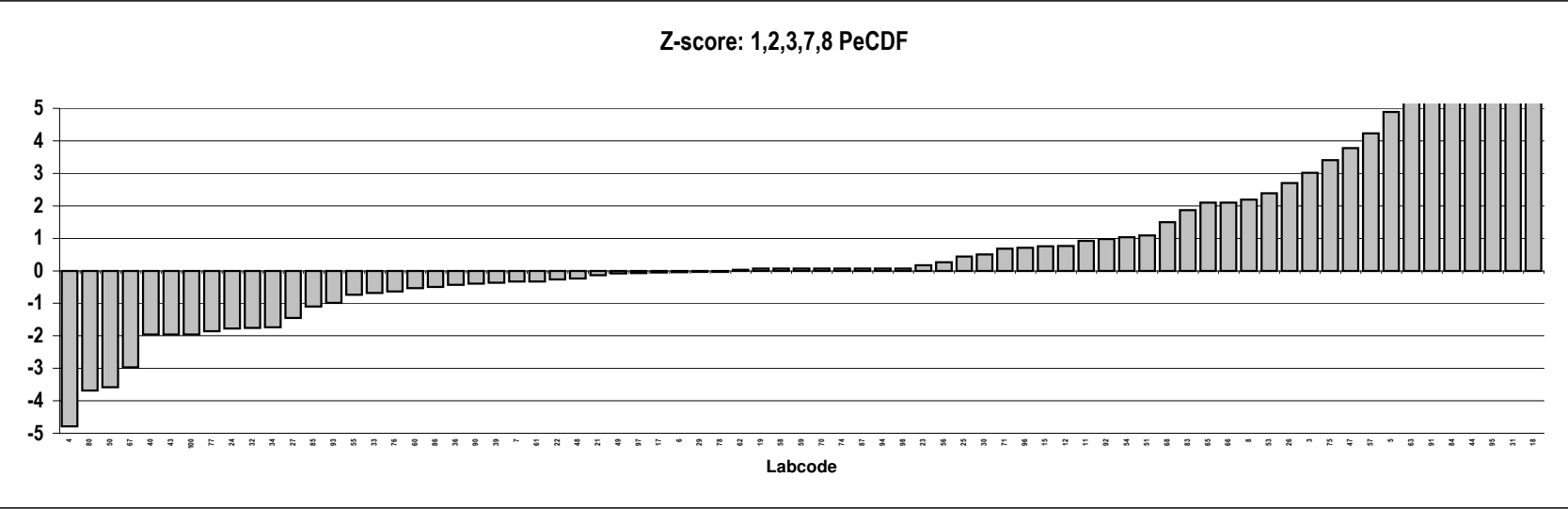
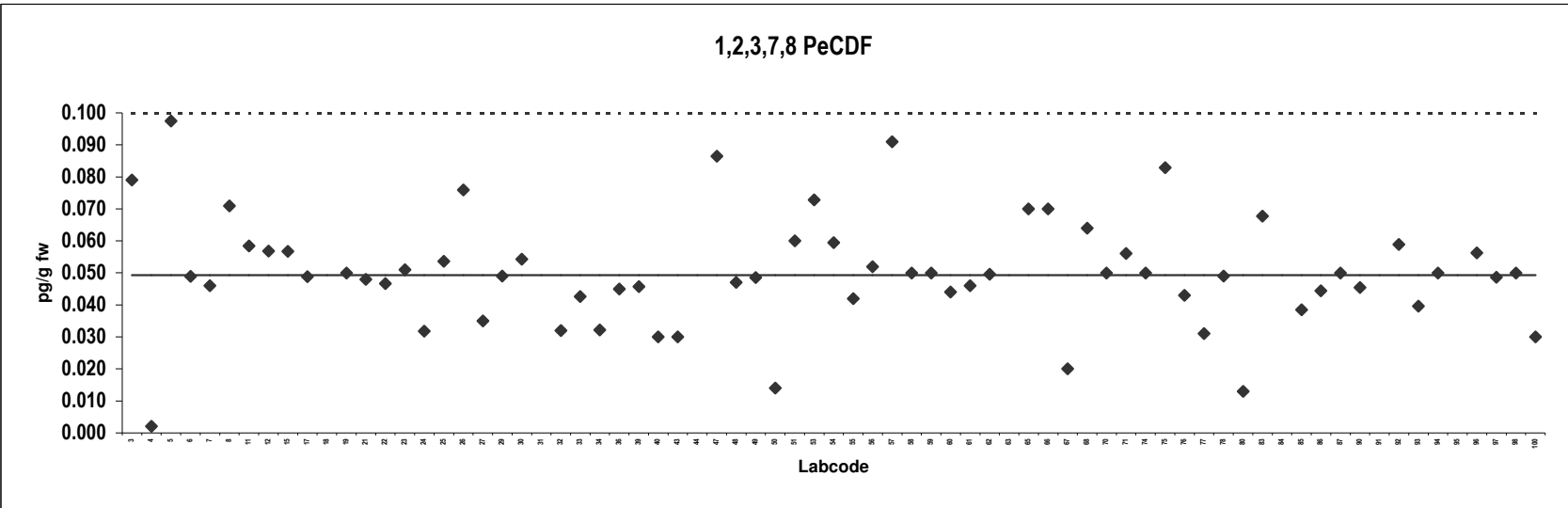
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.079		63	0.12	Outlier
4	0.0021	ND	65	0.070	
5	0.098		66	0.070	
6	0.049		67	0.020	
7	0.046		68	0.064	
8	0.071		70	0.050	ND
11	0.058		71	0.056	
12	0.057		74	0.050	
15	0.057		75	0.083	
17	0.049		76	0.043	
18	0.60	Outlier	77	0.031	
19	0.050	ND	78	0.049	
21	0.048		80	0.013	
22	0.047		83	0.068	
23	0.051		84	0.17	Outlier,ND
24	0.032		85	0.038	
25	0.054		86	0.044	
26	0.076		87	0.050	
27	0.035		90	0.045	
29	0.049		91	0.15	Outlier
30	0.054		92	0.059	
31	0.30	Outlier	93	0.040	
32	0.032	ND	94	0.050	
33	0.043		95	0.28	Outlier,ND
34	0.032		96	0.056	
36	0.045		97	0.049	
39	0.046		98	0.050	
40	0.030	ND	100	0.030	
43	0.030	ND			
44	0.21	Outlier,ND			
47	0.086				
48	0.047				
49	0.049				
50	0.014	ND			
51	0.060				
53	0.073				
54	0.059				
55	0.042				
56	0.052				
57	0.091				
58	0.050				
59	0.050				
60	0.044				
61	0.046				
62	0.050				

### Consensus statistics

Consensus median, pg/g	0.049
Median all values pg/g	0.050
Consensus mean, pg/g	0.050
Standard deviation, pg/g	0.017
Relative standard deviation, %	35
No. of values reported	73
No. of values removed	7
No. of reported non-detects	10





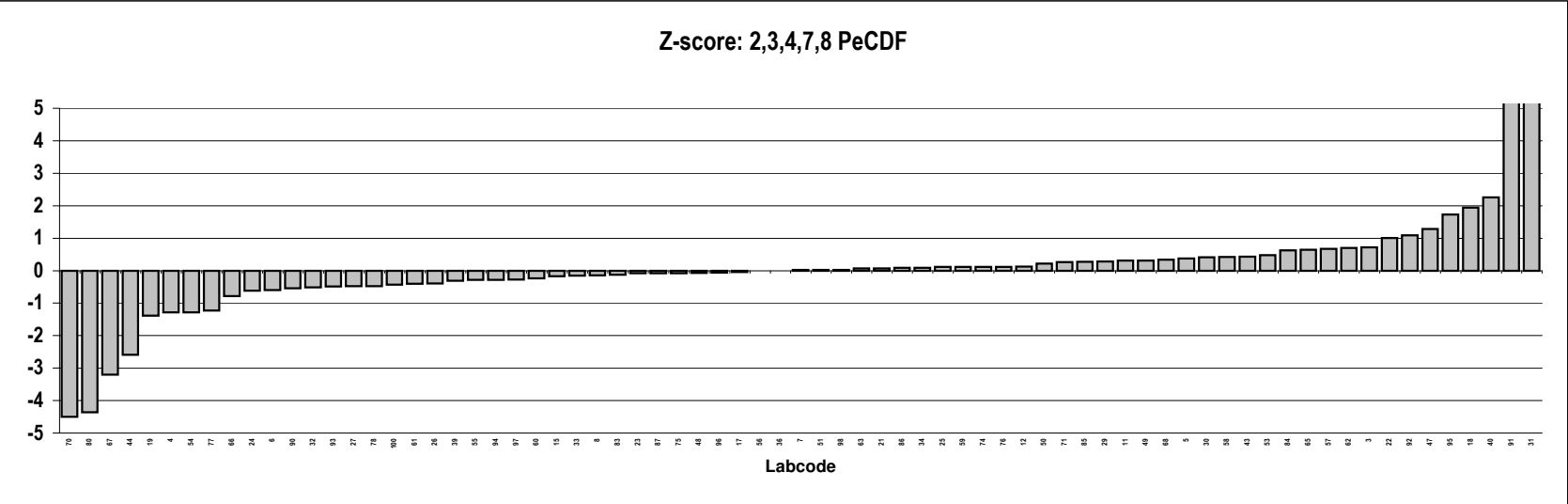
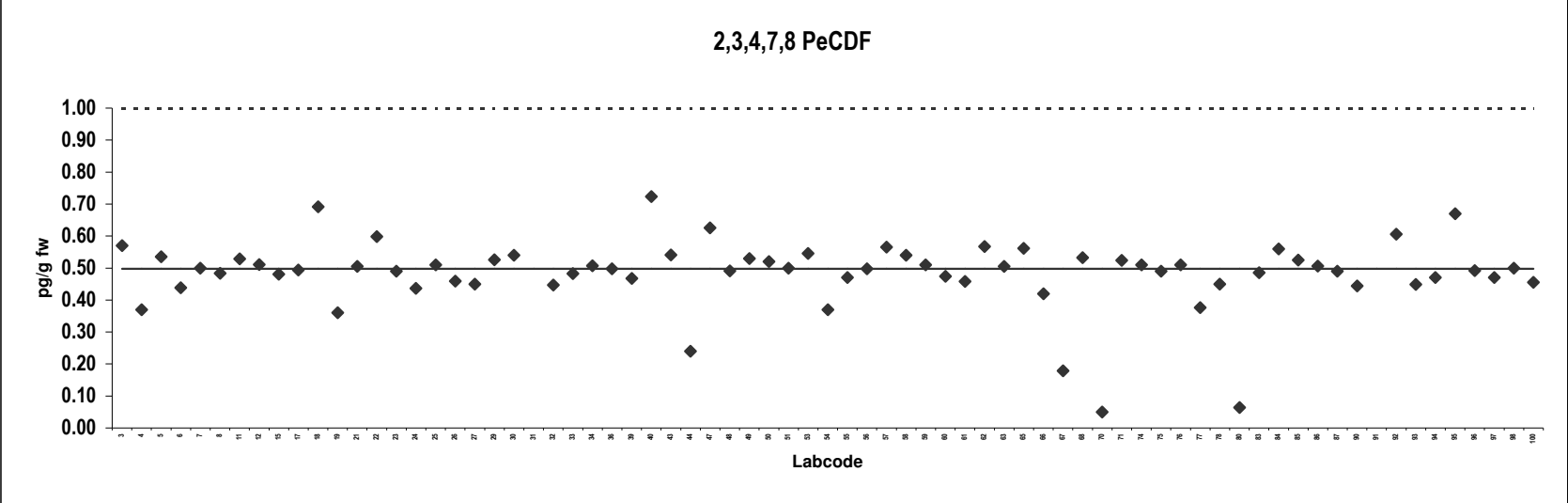
## Mozzarella Cheese

Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.57		63	0.50	
4	0.37		65	0.56	
5	0.54		66	0.42	
6	0.44		67	0.18	
7	0.50		68	0.53	
8	0.48		70	0.050	ND
11	0.53		71	0.52	
12	0.51		74	0.51	
15	0.48		75	0.49	
17	0.49		76	0.51	
18	0.69		77	0.38	
19	0.36		78	0.45	
21	0.51		80	0.064	
22	0.60		83	0.49	
23	0.49		84	0.56	
24	0.44		85	0.53	
25	0.51		86	0.51	
26	0.46		87	0.49	
27	0.45		90	0.44	
29	0.53		91	1.6	Outlier
30	0.54		92	0.61	
31	2.4	Outlier	93	0.45	
32	0.45		94	0.47	
33	0.48		95	0.67	ND
34	0.51		96	0.49	
36	0.50		97	0.47	
39	0.47		98	0.50	
40	0.72		100	0.46	
43	0.54				
44	0.24				
47	0.63				
48	0.49				
49	0.53				
50	0.52				
51	0.50				
53	0.55				
54	0.37				
55	0.47				
56	0.50				
57	0.57				
58	0.54				
59	0.51				
60	0.47				
61	0.46				
62	0.57				

### Consensus statistics

Consensus median, pg/g	0.50
Median all values pg/g	0.50
Consensus mean, pg/g	0.48
Standard deviation, pg/g	0.11
Relative standard deviation, %	23
No. of values reported	73
No. of values removed	2
No. of reported non-detects	2

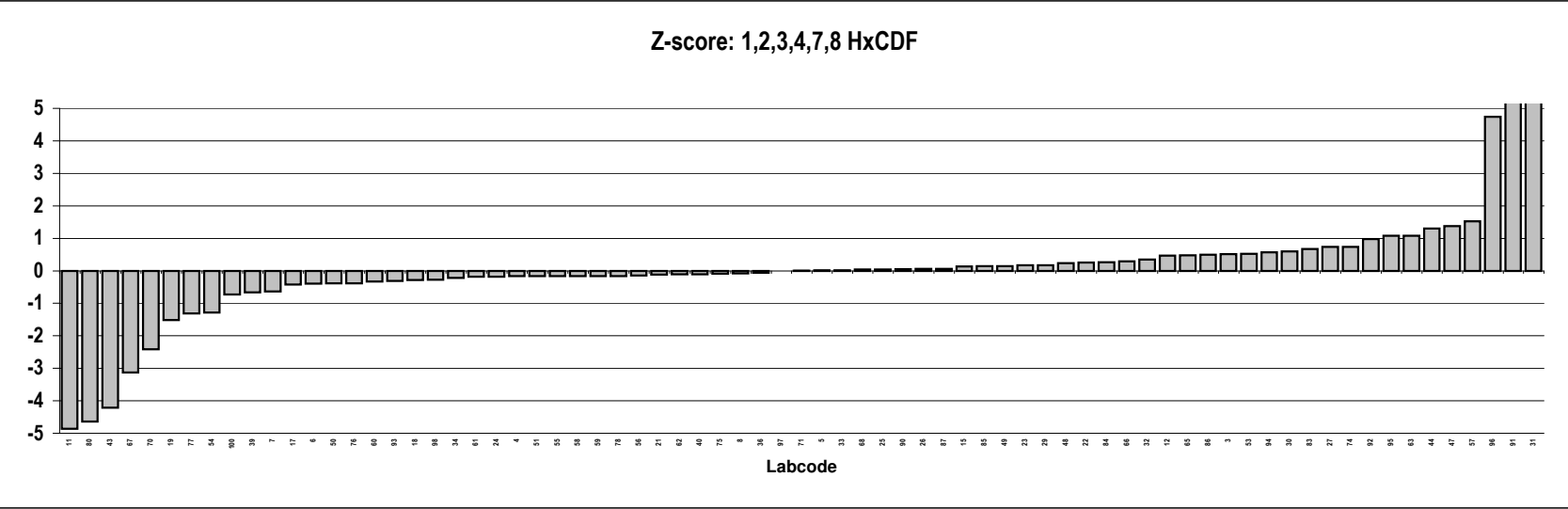
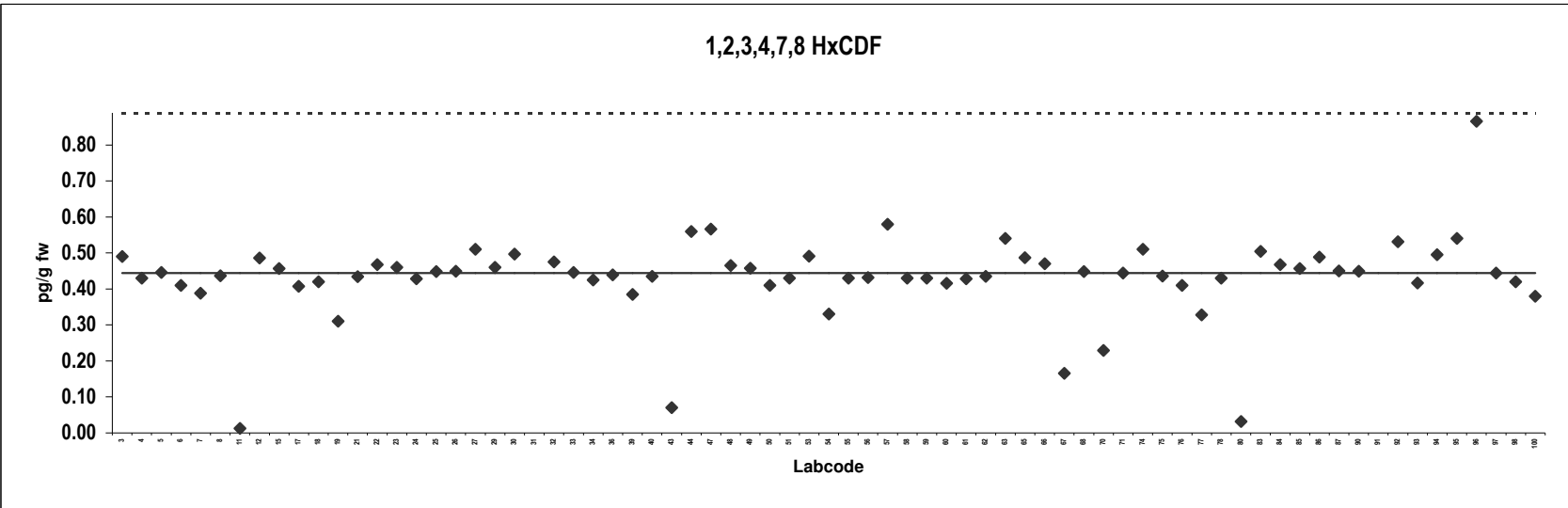


**Mozzarella Cheese**  
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.49		63	0.54	
4	0.43		65	0.49	
5	0.45		66	0.47	
6	0.41		67	0.17	
7	0.39		68	0.45	
8	0.44		70	0.23	
11	0.012	ND	71	0.44	
12	0.49		74	0.51	
15	0.46		75	0.44	
17	0.41		76	0.41	
18	0.42		77	0.33	
19	0.31		78	0.43	
21	0.43		80	0.032	
22	0.47		83	0.50	
23	0.46		84	0.47	
24	0.43		85	0.46	
25	0.45		86	0.49	
26	0.45		87	0.45	
27	0.51		90	0.45	
29	0.46		91	1.4	Outlier
30	0.50		92	0.53	
31	1.8	Outlier	93	0.42	
32	0.48		94	0.50	
33	0.45		95	0.54	
34	0.43		96	0.87	
36	0.44		97	0.44	
39	0.39		98	0.42	
40	0.44		100	0.38	
43	0.070	ND			
44	0.56				
47	0.57				
48	0.47				
49	0.46				
50	0.41				
51	0.43				
53	0.49				
54	0.33				
55	0.43				
56	0.43				
57	0.58				
58	0.43				
59	0.43				
60	0.42				
61	0.43				
62	0.43				

**Consensus statistics**

Consensus median, pg/g	0.44
Median all values pg/g	0.44
Consensus mean, pg/g	0.43
Standard deviation, pg/g	0.12
Relative standard deviation, %	27
No. of values reported	73
No. of values removed	2
No. of reported non-detects	2

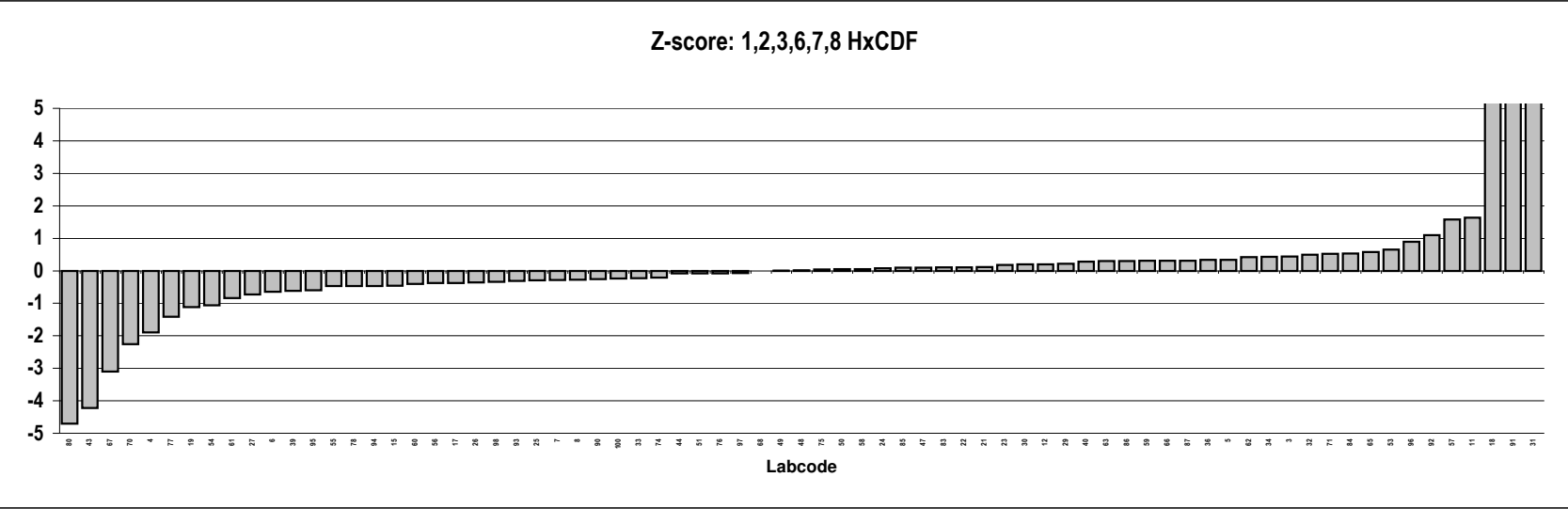
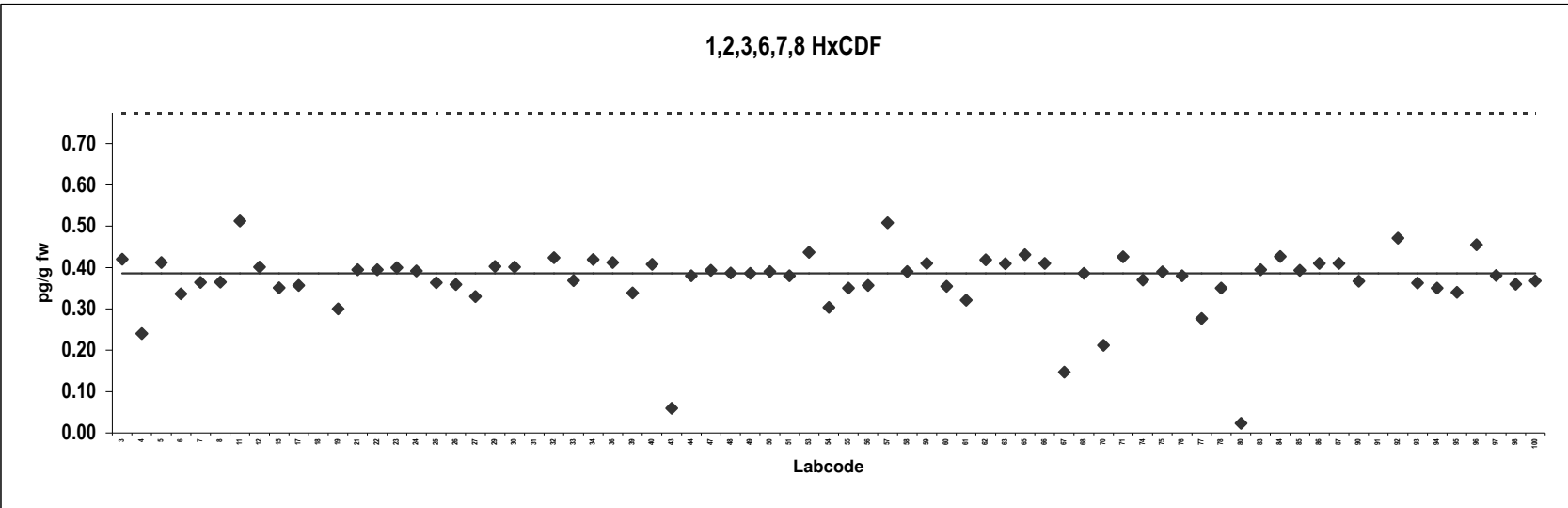


**Mozzarella Cheese**  
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.42		63	0.41	
4	0.24		65	0.43	
5	0.41		66	0.41	
6	0.34		67	0.15	
7	0.36		68	0.39	
8	0.37		70	0.21	
11	0.51		71	0.43	
12	0.40		74	0.37	
15	0.35		75	0.39	
17	0.36		76	0.38	
18	1.2	Outlier	77	0.28	
19	0.30		78	0.35	
21	0.40		80	0.023	
22	0.39		83	0.39	
23	0.40		84	0.43	
24	0.39		85	0.39	
25	0.36		86	0.41	
26	0.36		87	0.41	
27	0.33		90	0.37	
29	0.40		91	1.3	Outlier
30	0.40		92	0.47	
31	1.6	Outlier	93	0.36	
32	0.42		94	0.35	
33	0.37		95	0.34	
34	0.42		96	0.46	
36	0.41		97	0.38	
39	0.34		98	0.36	
40	0.41		100	0.37	
43	0.060	ND			
44	0.38				
47	0.39				
48	0.39				
49	0.39				
50	0.39				
51	0.38				
53	0.44				
54	0.30				
55	0.35				
56	0.36				
57	0.51				
58	0.39				
59	0.41				
60	0.35				
61	0.32				
62	0.42				

**Consensus statistics**

Consensus median, pg/g	0.39
Median all values pg/g	0.39
Consensus mean, pg/g	0.37
Standard deviation, pg/g	0.080
Relative standard deviation, %	22
No. of values reported	73
No. of values removed	3
No. of reported non-detects	1



## Mozzarella Cheese

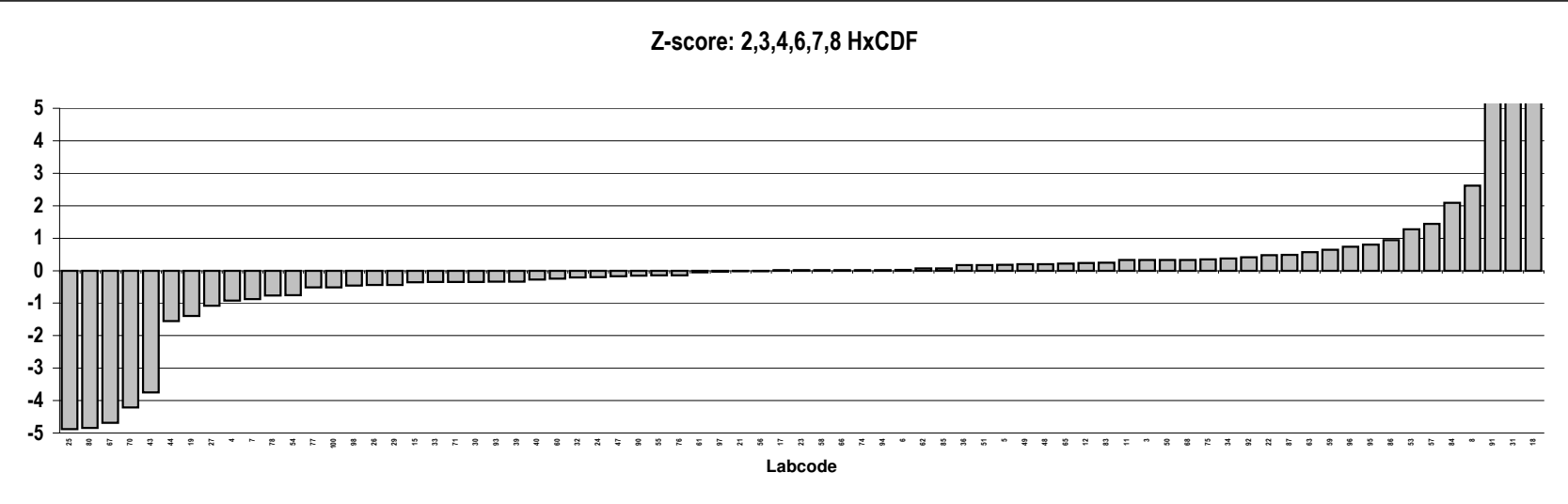
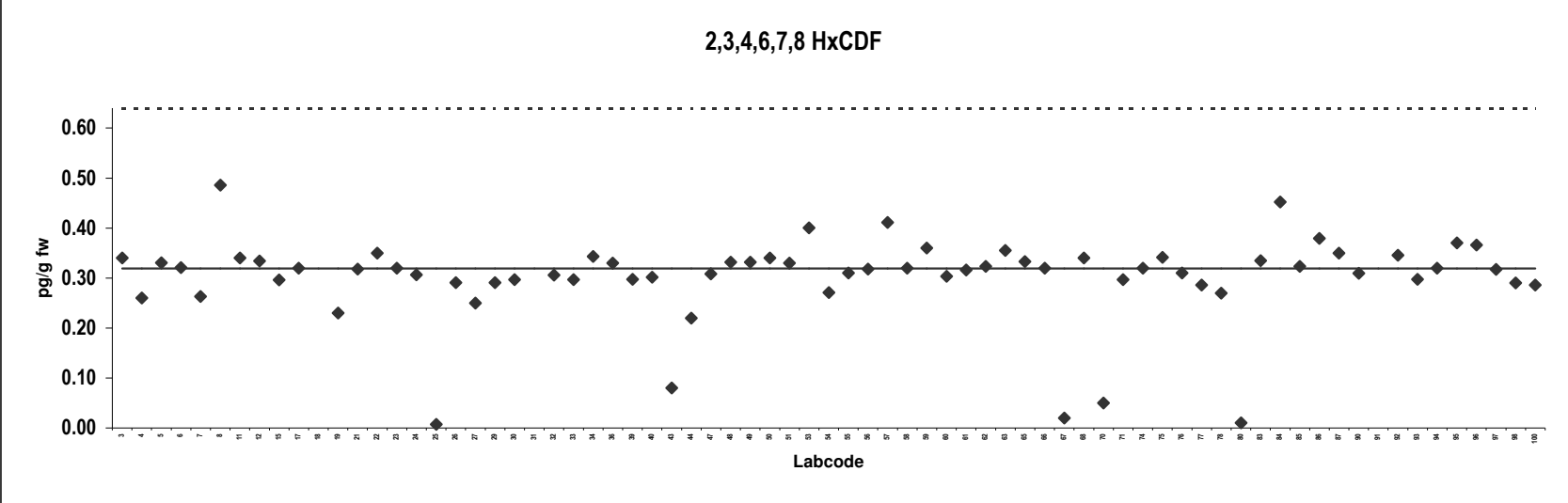
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.34		63	0.36	
4	0.26		65	0.33	
5	0.33		66	0.32	
6	0.32		67	0.020	ND
7	0.26		68	0.34	
8	0.49		70	0.050	ND
11	0.34		71	0.30	
12	0.33		74	0.32	
15	0.30		75	0.34	
17	0.32		76	0.31	
18	2.8	Outlier	77	0.29	
19	0.23		78	0.27	
21	0.32		80	0.010	ND
22	0.35		83	0.33	
23	0.32		84	0.45	
24	0.31		85	0.32	
25	0.0074	ND	86	0.38	
26	0.29		87	0.35	
27	0.25		90	0.31	
29	0.29		91	1.1	Outlier
30	0.30		92	0.35	
31	1.3	Outlier	93	0.30	
32	0.31		94	0.32	
33	0.30		95	0.37	
34	0.34		96	0.37	
36	0.33		97	0.32	
39	0.30		98	0.29	
40	0.30		100	0.29	
43	0.080	ND			
44	0.22				
47	0.31				
48	0.33				
49	0.33				
50	0.34				
51	0.33				
53	0.40				
54	0.27				
55	0.31				
56	0.32				
57	0.41				
58	0.32				
59	0.36				
60	0.30				
61	0.32				
62	0.32				

### Consensus statistics

Consensus median, pg/g	0.32
Median all values pg/g	0.32
Consensus mean, pg/g	0.30
Standard deviation, pg/g	0.086
Relative standard deviation, %	29
No. of values reported	73
No. of values removed	3
No. of reported non-detects	5





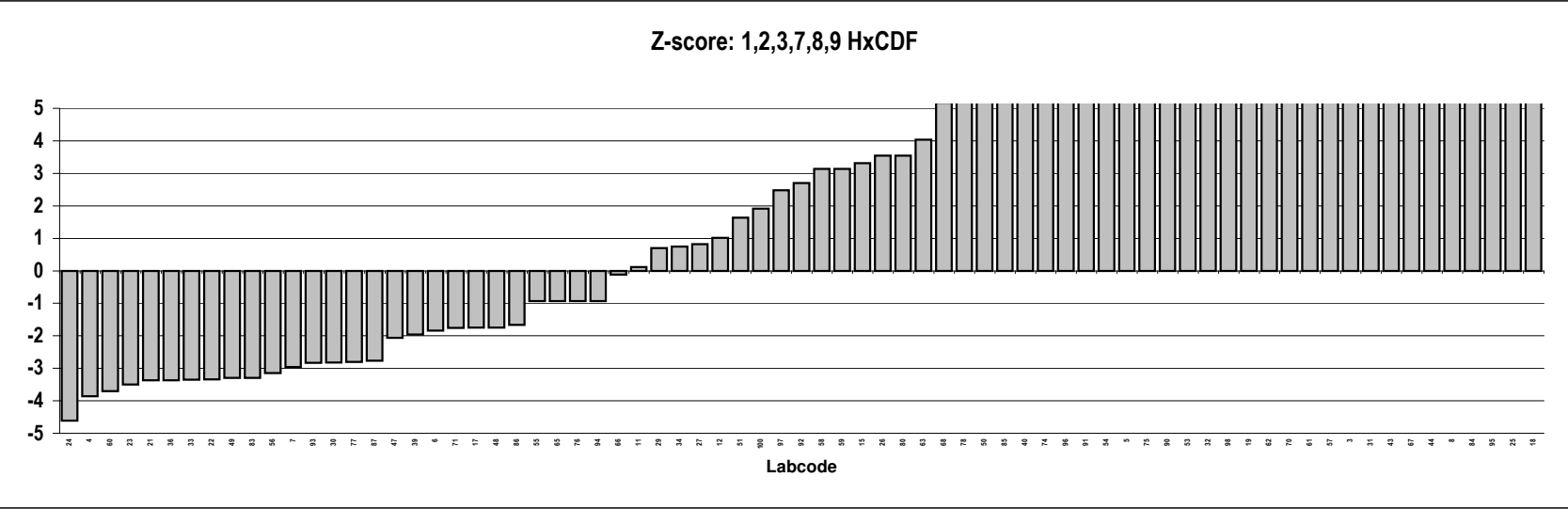
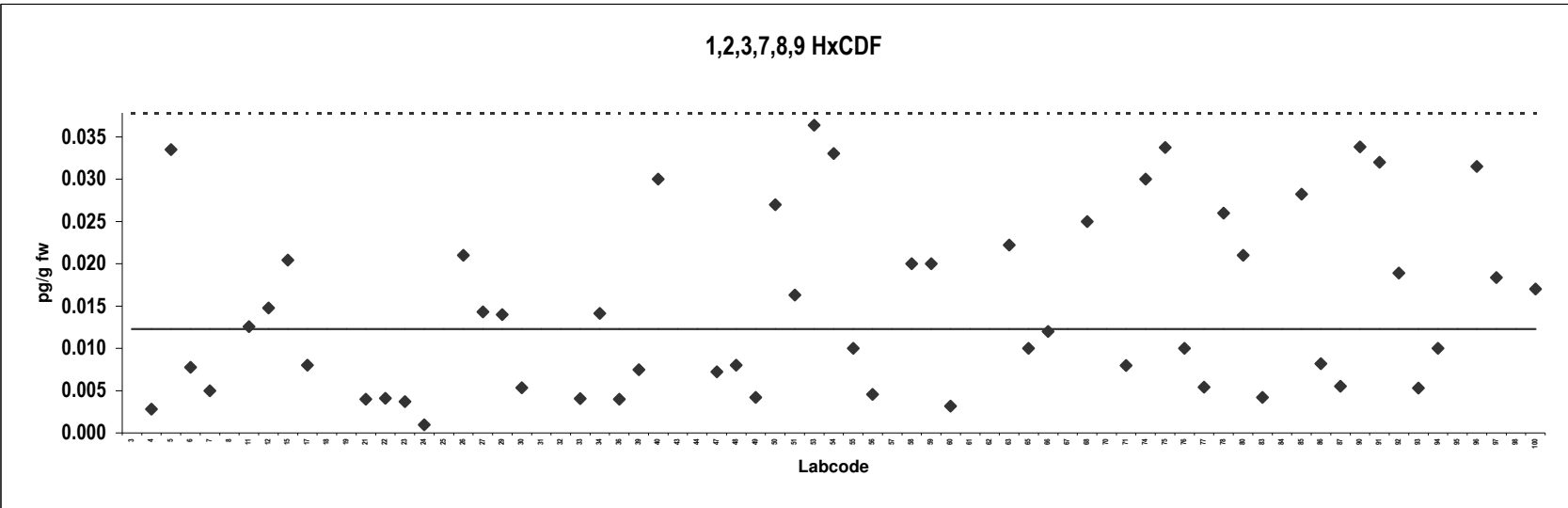
## Mozzarella Cheese

Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.056	Outlier	63	0.022	ND
4	0.0028	ND	65	0.010	ND
5	0.034	ND	66	0.012	
6	0.0078		67	0.10	Outlier
7	0.0050	ND	68	0.025	ND
8	0.20	Outlier	70	0.050	Outlier,ND
11	0.013	ND	71	0.0080	
12	0.015		74	0.030	ND
15	0.020		75	0.034	
17	0.0080	ND	76	0.010	ND
18	1.8	Outlier	77	0.0054	ND
19	0.050	Outlier,ND	78	0.026	ND
21	0.0040		80	0.021	
22	0.0041		83	0.0042	ND
23	0.0037		84	0.25	Outlier,ND
24	0.00097		85	0.028	ND
25	0.36	Outlier	86	0.0082	
26	0.021	ND	87	0.0055	
27	0.014	ND	90	0.034	ND
29	0.014		91	0.032	ND
30	0.0053	ND	92	0.019	ND
31	0.078	Outlier	93	0.0053	
32	0.040	Outlier,ND	94	0.010	ND
33	0.0041		95	0.25	Outlier,ND
34	0.014	ND	96	0.032	ND
36	0.0040	ND	97	0.018	ND
39	0.0075	ND	98	0.040	Outlier,ND
40	0.030	ND	100	0.017	
43	0.080	Outlier,ND			
44	0.14	Outlier,ND			
47	0.0072				
48	0.0080	ND			
49	0.0042				
50	0.027	ND			
51	0.016	ND			
53	0.036				
54	0.033				
55	0.010	ND			
56	0.0046				
57	0.053	Outlier,ND			
58	0.020	ND			
59	0.020	ND			
60	0.0032				
61	0.052	Outlier,ND			
62	0.050	Outlier,ND			

### Consensus statistics

Consensus median, pg/g	0.012
Median all values pg/g	0.019
Consensus mean, pg/g	0.015
Standard deviation, pg/g	0.010
Relative standard deviation, %	70
No. of values reported	73
No. of values removed	17
No. of reported non-detects	44



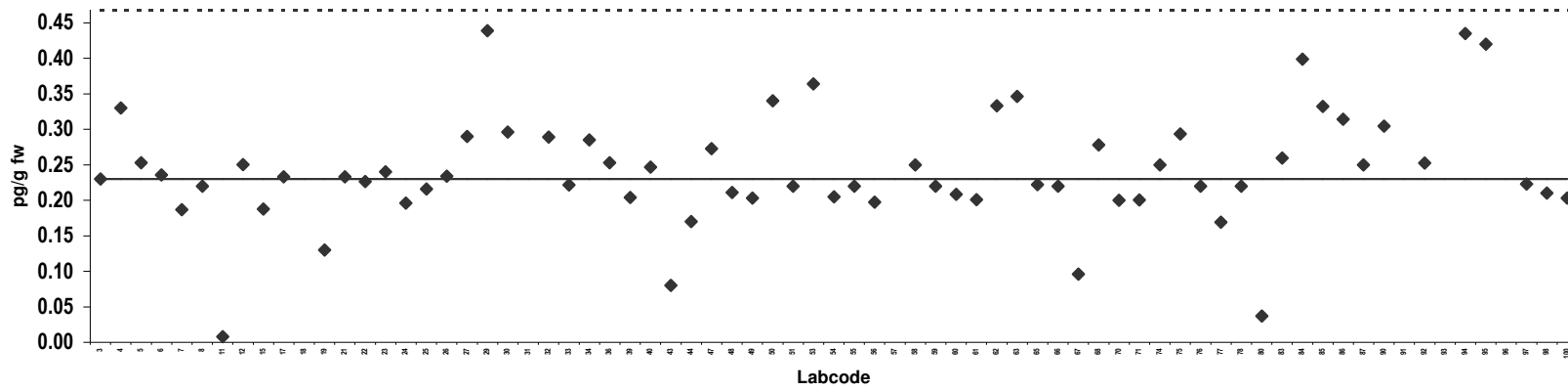
**Mozzarella Cheese**  
Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.23		63	0.35	
4	0.33		65	0.22	
5	0.25		66	0.22	
6	0.24		67	0.096	
7	0.19		68	0.28	
8	0.22		70	0.20	ND
11	0.0080	ND	71	0.20	
12	0.25		74	0.25	
15	0.19		75	0.29	
17	0.23		76	0.22	
18	2.0	Outlier	77	0.17	
19	0.13		78	0.22	
21	0.23		80	0.037	
22	0.23		83	0.26	
23	0.24		84	0.40	
24	0.20		85	0.33	
25	0.22		86	0.31	
26	0.23		87	0.25	
27	0.29		90	0.30	
29	0.44		91	0.68	Outlier
30	0.30		92	0.25	
31	1.1	Outlier	93	0.49	Outlier
32	0.29		94	0.44	
33	0.22		95	0.42	ND
34	0.29		96	1.8	Outlier
36	0.25		97	0.22	
39	0.20		98	0.21	
40	0.25		100	0.20	
43	0.080	ND			
44	0.17	ND			
47	0.27				
48	0.21				
49	0.20				
50	0.34				
51	0.22				
53	0.36				
54	0.20				
55	0.22				
56	0.20				
57	0.47	Outlier			
58	0.25				
59	0.22				
60	0.21				
61	0.20				
62	0.33				

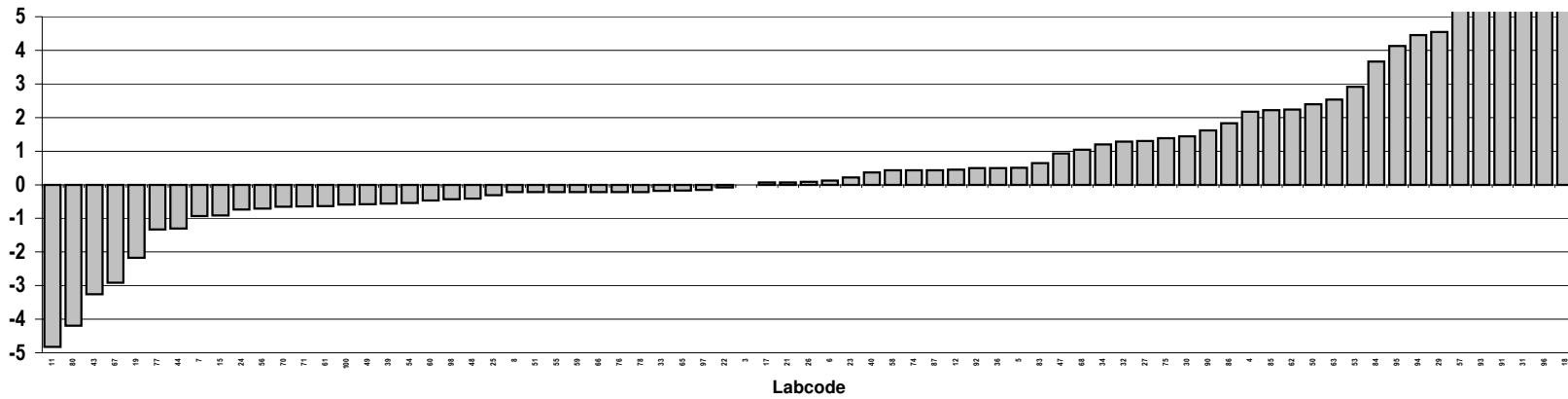
**Consensus statistics**

Consensus median, pg/g	0.23
Median all values pg/g	0.23
Consensus mean, pg/g	0.24
Standard deviation, pg/g	0.079
Relative standard deviation, %	33
No. of values reported	73
No. of values removed	6
No. of reported non-detects	5

1,2,3,4,6,7,8 HpCDF



Z-score: 1,2,3,4,6,7,8 HpCDF



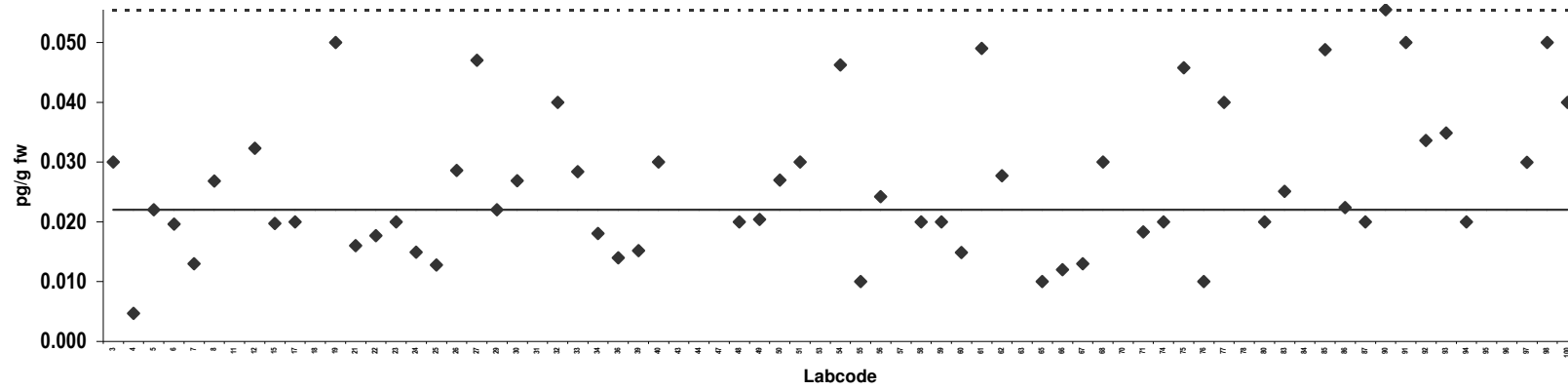
**Mozzarella Cheese**  
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.030	ND	63	0.080	Outlier
4	0.0047	ND	65	0.010	ND
5	0.022		66	0.012	
6	0.020		67	0.013	
7	0.013		68	0.030	ND
8	0.027		70	0.20	Outlier,ND
11	0.094	Outlier	71	0.018	
12	0.032		74	0.020	
15	0.020		75	0.046	
17	0.020	ND	76	0.010	ND
18	1.1	Outlier	77	0.040	
19	0.050	ND	78	0.073	Outlier,ND
21	0.016		80	0.020	ND
22	0.018		83	0.025	
23	0.020		84	0.41	Outlier,ND
24	0.015		85	0.049	
25	0.013		86	0.022	
26	0.029		87	0.020	
27	0.047		90	0.056	Outlier
29	0.022		91	0.050	
30	0.027		92	0.034	
31	0.19	Outlier	93	0.035	
32	0.040	ND	94	0.020	ND
33	0.028		95	0.45	Outlier,ND
34	0.018		96	0.089	Outlier
36	0.014		97	0.030	ND
39	0.015		98	0.050	ND
40	0.030	ND	100	0.040	ND
43	0.10	Outlier,ND			
44	0.18	Outlier,ND			
47	0.073	Outlier			
48	0.020				
49	0.020				
50	0.027	ND			
51	0.030				
53	0.073	Outlier			
54	0.046				
55	0.010	ND			
56	0.024				
57	0.16	Outlier			
58	0.020				
59	0.020	ND			
60	0.015				
61	0.049	ND			
62	0.028				

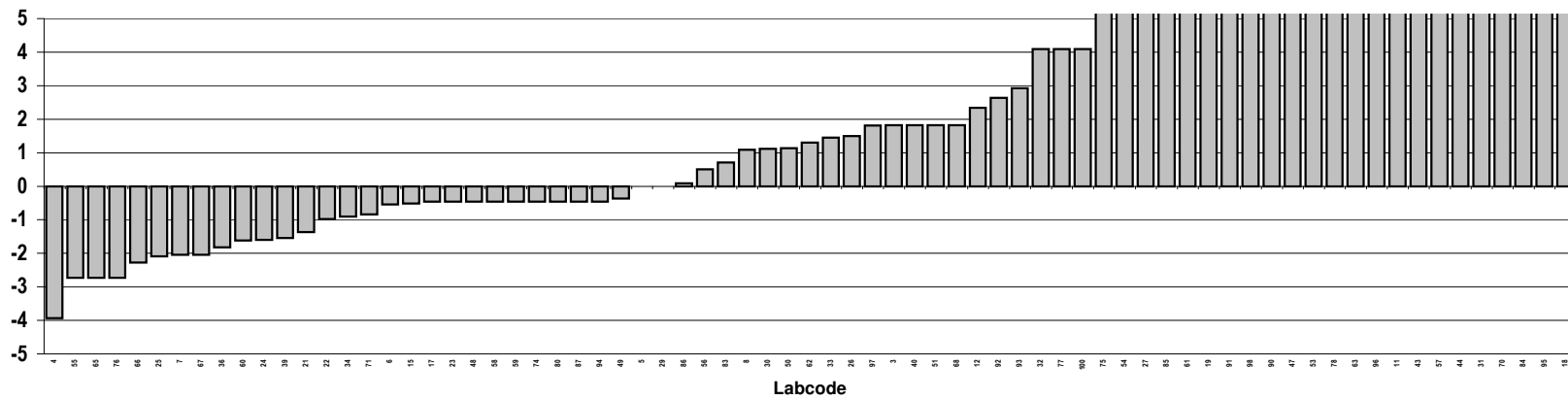
**Consensus statistics**

Consensus median, pg/g	0.022
Median all values pg/g	0.028
Consensus mean, pg/g	0.026
Standard deviation, pg/g	0.012
Relative standard deviation, %	46
No. of values reported	73
No. of values removed	15
No. of reported non-detects	24

1,2,3,4,7,8,9 HpCDF



Z-score: 1,2,3,4,7,8,9 HpCDF



## Mozzarella Cheese

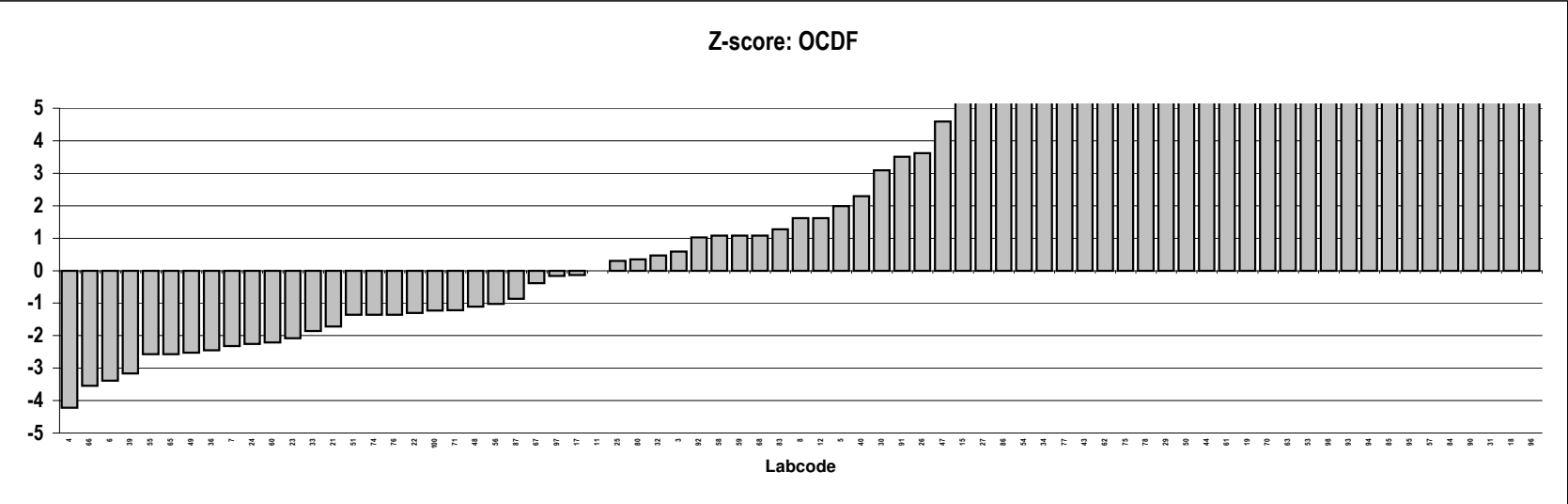
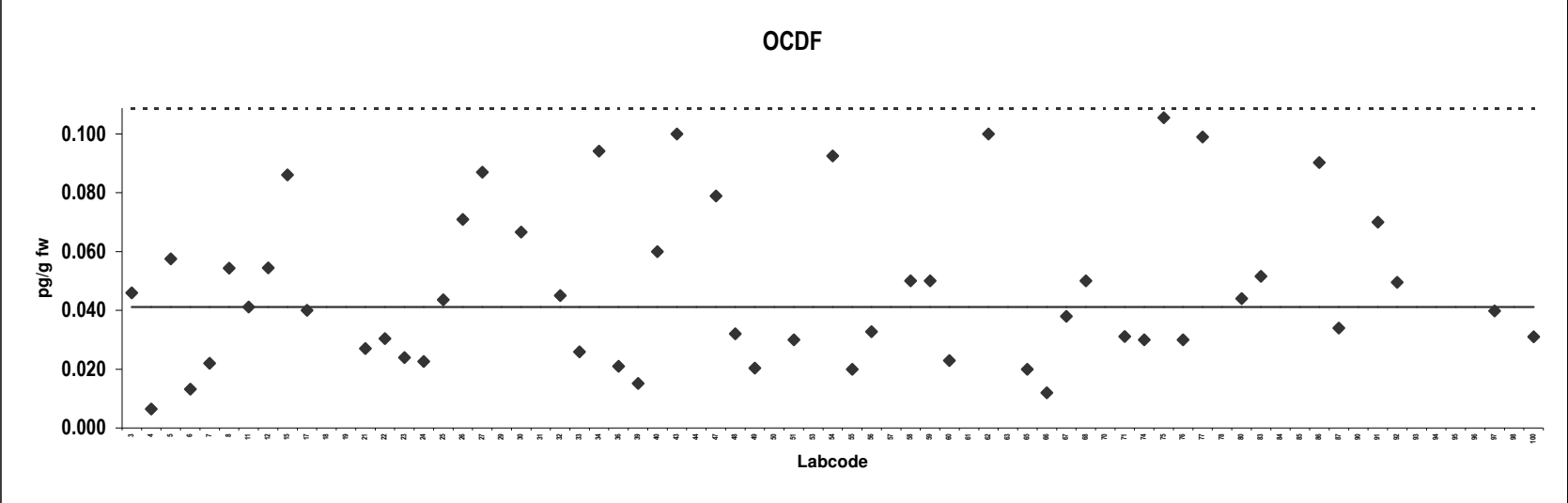
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.046	ND	63	0.21	Outlier
4	0.0064	ND	65	0.020	
5	0.058		66	0.012	
6	0.013		67	0.038	
7	0.022		68	0.050	ND
8	0.054		70	0.20	Outlier,ND
11	0.041	ND	71	0.031	
12	0.054		74	0.030	ND
15	0.086		75	0.11	
17	0.040	ND	76	0.030	ND
18	2.6	Outlier	77	0.099	
19	0.20	Outlier,ND	78	0.12	Outlier,ND
21	0.027		80	0.044	
22	0.030		83	0.052	
23	0.024		84	0.70	Outlier,ND
24	0.023		85	0.34	Outlier
25	0.044		86	0.090	
26	0.071		87	0.034	
27	0.087		90	0.83	Outlier
29	0.12	Outlier	91	0.070	
30	0.067		92	0.050	
31	2.5	Outlier	93	0.28	Outlier
32	0.045	ND	94	0.32	Outlier
33	0.026		95	0.40	Outlier,ND
34	0.094		96	3.3	Outlier
36	0.021		97	0.040	ND
39	0.015		98	0.25	Outlier,ND
40	0.060	ND	100	0.031	
43	0.10	ND			
44	0.16	Outlier,ND			
47	0.079				
48	0.032				
49	0.020				
50	0.13	Outlier,ND			
51	0.030				
53	0.22	Outlier			
54	0.093				
55	0.020	ND			
56	0.033				
57	0.50	Outlier			
58	0.050	ND			
59	0.050	ND			
60	0.023				
61	0.20	Outlier,ND			
62	0.10	ND			

### Consensus statistics

Consensus median, pg/g	0.041
Median all values pg/g	0.054
Consensus mean, pg/g	0.047
Standard deviation, pg/g	0.027
Relative standard deviation, %	57
No. of values reported	73
No. of values removed	20
No. of reported non-detects	24





## Mozzarella Cheese

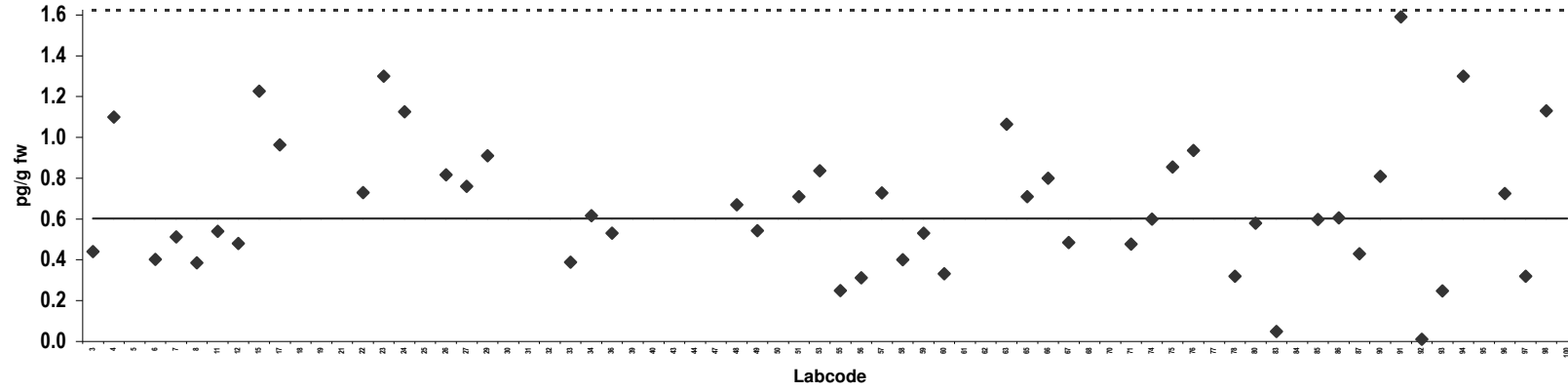
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.44		65	0.71	
4	1.1		66	0.80	
5	6.6	Outlier	67	0.49	
6	0.40		68	4.0	Outlier,ND
7	0.51		70	3.1	Outlier
8	0.39		71	0.48	
11	0.54		74	0.60	
12	0.48		75	0.85	
15	1.2		76	0.94	
17	0.96		77	2.6	Outlier
18	3.3	Outlier	78	0.32	
19	2.0	Outlier,ND	80	0.58	
21	2.1	Outlier	83	0.049	ND
22	0.73		84	2.5	Outlier
23	1.3		85	0.60	
24	1.1		86	0.61	
25	2.9	Outlier	87	0.43	
26	0.82		90	0.81	
27	0.76		91	1.6	
29	0.91		92	0.010	ND
30	2.9	Outlier	93	0.25	
31	5.3	Outlier	94	1.3	
32	4.4	Outlier	95	9.5	Outlier,ND
33	0.39		96	0.73	
34	0.62		97	0.32	ND
36	0.53		98	1.1	ND
39	1.8	Outlier,ND	100	2.1	Outlier
40	5.4	Outlier			
43	19	Outlier			
44	2.0	Outlier,ND			
47	14	Outlier			
48	0.67				
49	0.54				
50	1.7	Outlier			
51	0.71				
53	0.84				
55	0.25				
56	0.31				
57	0.73				
58	0.40				
59	0.53				
60	0.33				
61	2.2	Outlier			
62	2.0	Outlier,ND			
63	1.1				

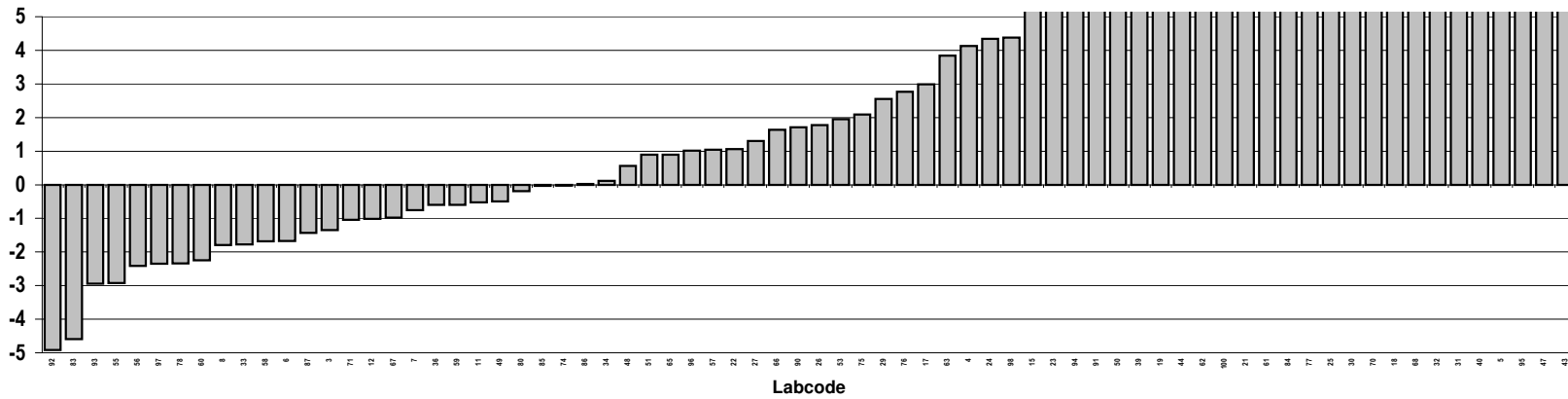
### Consensus statistics

Consensus median, pg/g	0.60
Median all values pg/g	0.81
Consensus mean, pg/g	0.66
Standard deviation, pg/g	0.33
Relative standard deviation, %	50
No. of values reported	72
No. of values removed	22
No. of reported non-detects	10

### PCB 77



### Z-score: PCB 77



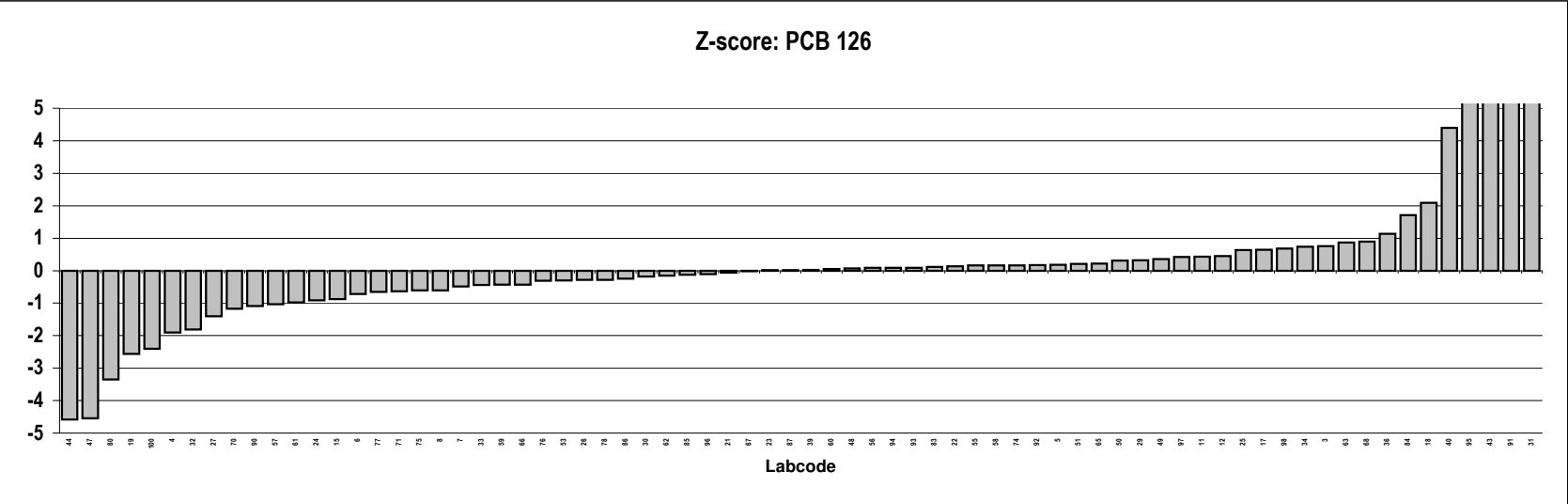
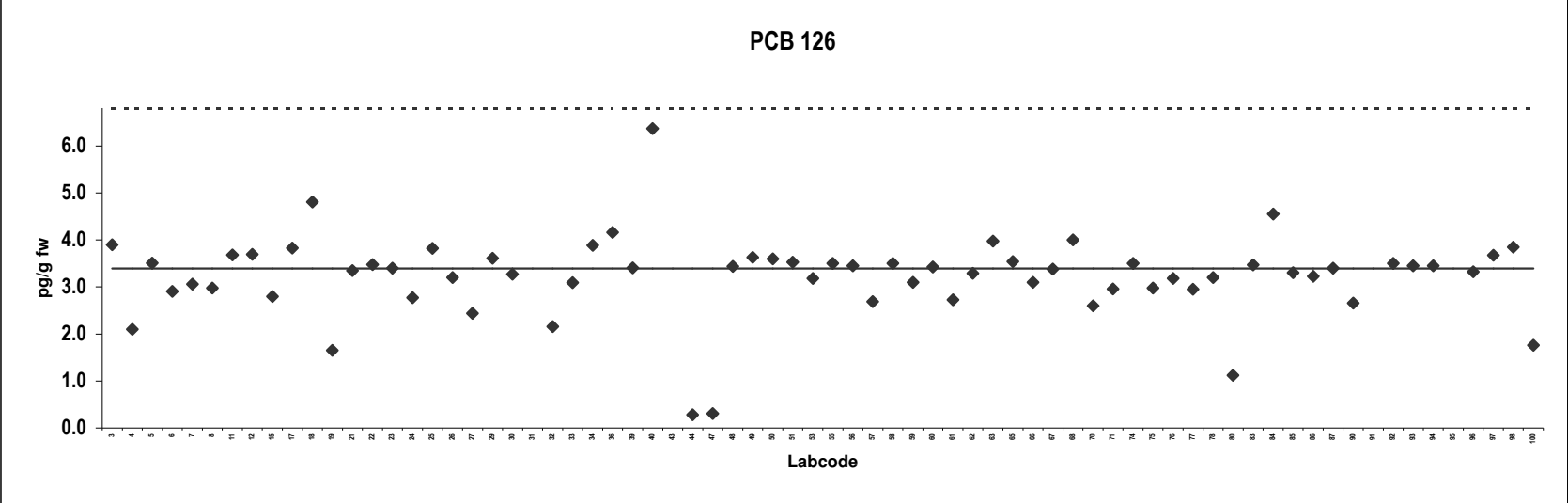
## Mozzarella Cheese

Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	3.9		65	3.5	
4	2.1		66	3.1	
5	3.5		67	3.4	
6	2.9		68	4.0	ND
7	3.1		70	2.6	
8	3.0		71	3.0	
11	3.7		74	3.5	
12	3.7		75	3.0	
15	2.8		76	3.2	
17	3.8		77	3.0	
18	4.8		78	3.2	
19	1.7		80	1.1	
21	3.4		83	3.5	
22	3.5		84	4.6	
23	3.4		85	3.3	
24	2.8		86	3.2	
25	3.8		87	3.4	
26	3.2		90	2.7	
27	2.4		91	11	Outlier
29	3.6		92	3.5	
30	3.3		93	3.5	
31	13	Outlier	94	3.5	
32	2.2		95	9.5	Outlier,ND
33	3.1		96	3.3	
34	3.9		97	3.7	
36	4.2		98	3.9	
39	3.4		100	1.8	
40	6.4				
43	9.8	Outlier			
44	0.28	ND			
47	0.31				
48	3.4				
49	3.6				
50	3.6				
51	3.5				
53	3.2				
55	3.5				
56	3.4				
57	2.7				
58	3.5				
59	3.1				
60	3.4				
61	2.7				
62	3.3				
63	4.0				

### Consensus statistics

Consensus median, pg/g	3.4
Median all values pg/g	3.4
Consensus mean, pg/g	3.2
Standard deviation, pg/g	0.88
Relative standard deviation, %	27
No. of values reported	72
No. of values removed	4
No. of reported non-detects	3



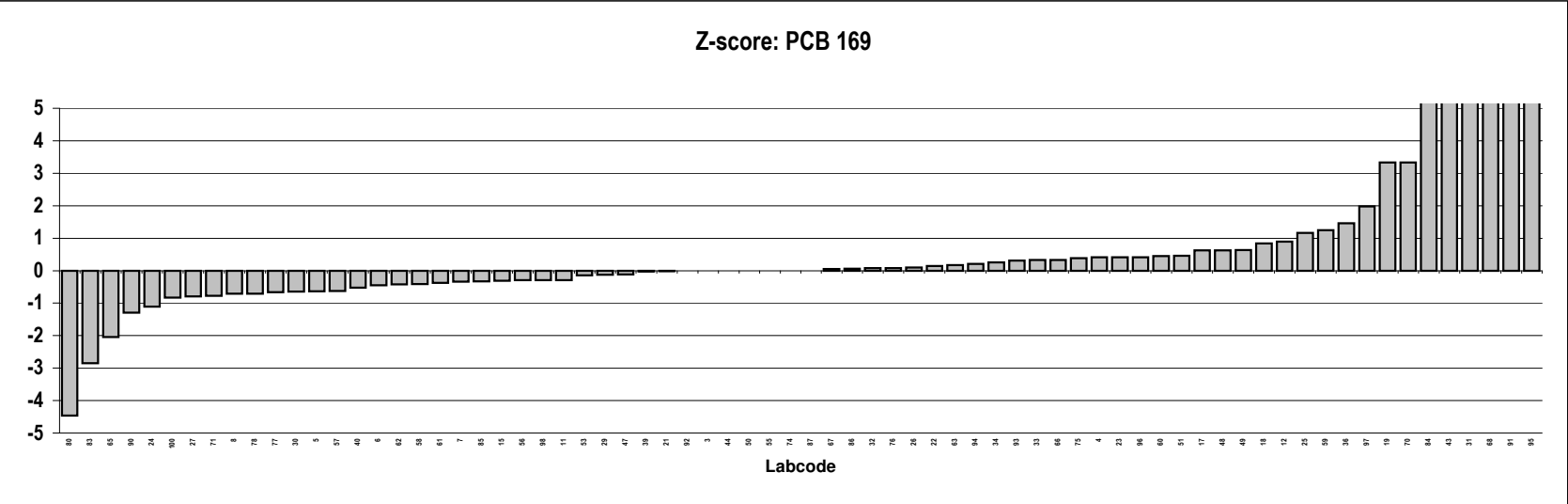
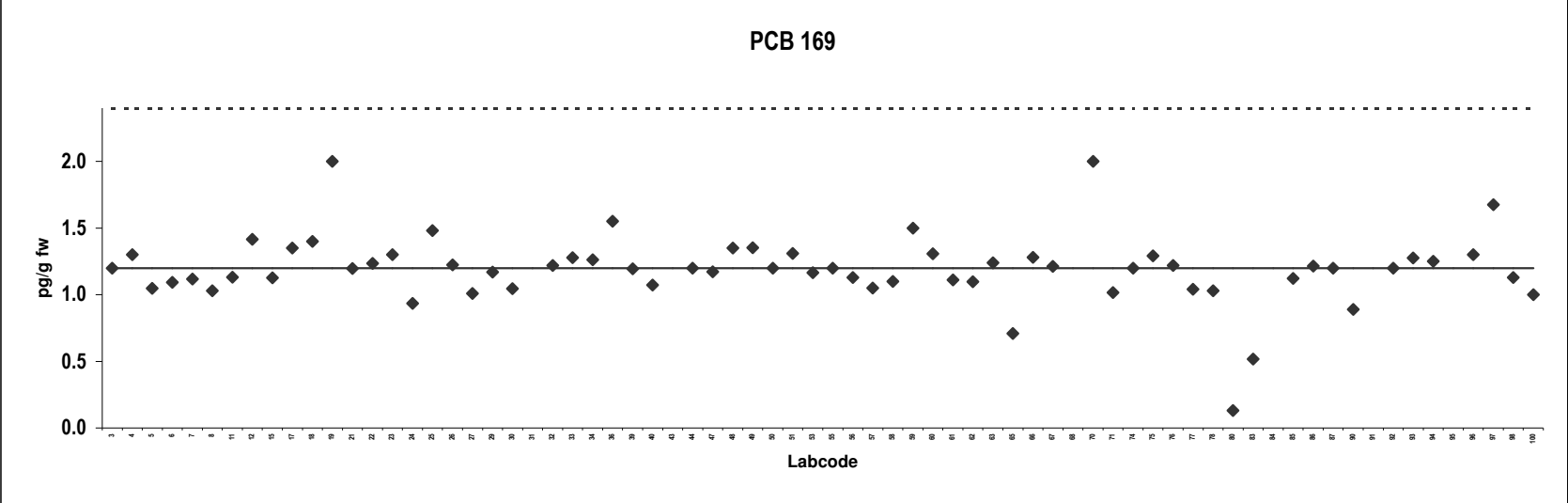
## Mozzarella Cheese

Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	1.2		65	0.71	
4	1.3		66	1.3	
5	1.0		67	1.2	
6	1.1		68	4.0	Outlier,ND
7	1.1		70	2.0	ND
8	1.0		71	1.0	
11	1.1		74	1.2	
12	1.4		75	1.3	
15	1.1		76	1.2	
17	1.4		77	1.0	
18	1.4		78	1.0	
19	2.0	ND	80	0.13	
21	1.2		83	0.52	ND
22	1.2		84	3.0	Outlier
23	1.3		85	1.1	
24	0.93		86	1.2	
25	1.5		87	1.2	
26	1.2		90	0.89	
27	1.0		91	4.0	Outlier
29	1.2		92	1.2	
30	1.0		93	1.3	
31	3.9	Outlier	94	1.3	
32	1.2		95	9.5	Outlier,ND
33	1.3		96	1.3	
34	1.3		97	1.7	ND
36	1.6		98	1.1	ND
39	1.2		100	1.0	
40	1.1				
43	3.7	Outlier			
44	1.2	ND			
47	1.2				
48	1.4				
49	1.4				
50	1.2				
51	1.3				
53	1.2				
55	1.2				
56	1.1				
57	1.1				
58	1.1				
59	1.5				
60	1.3				
61	1.1				
62	1.1				
63	1.2				

### Consensus statistics

Consensus median, pg/g	1.2
Median all values pg/g	1.2
Consensus mean, pg/g	1.2
Standard deviation, pg/g	0.26
Relative standard deviation, %	22
No. of values reported	72
No. of values removed	6
No. of reported non-detects	8



## Mozzarella Cheese

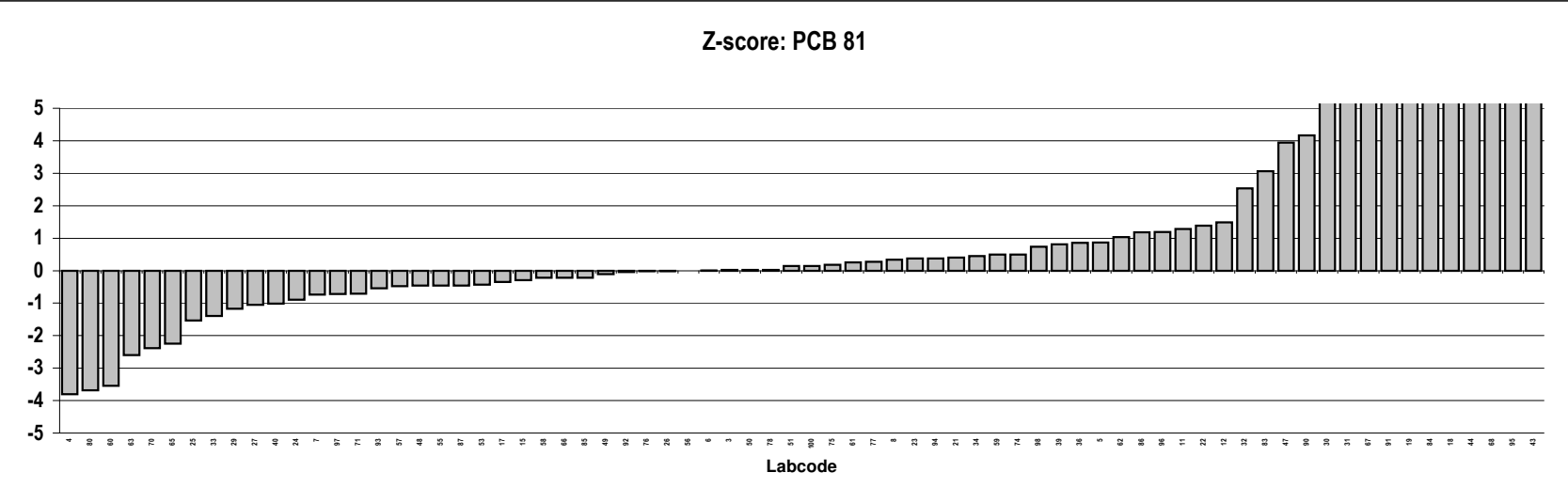
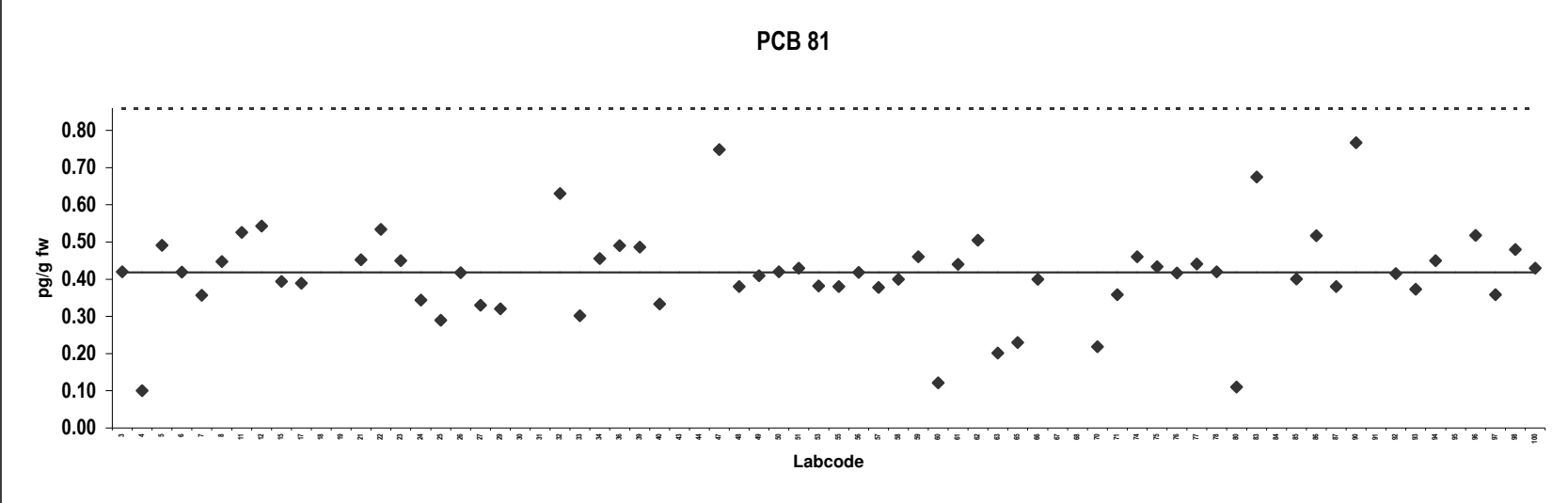
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
3	0.42		65	0.23	
4	0.10	ND	66	0.40	
5	0.49		67	1.2	Outlier
6	0.42		68	4.0	Outlier,ND
7	0.36		70	0.22	
8	0.45		71	0.36	
11	0.53		74	0.46	
12	0.54		75	0.43	
15	0.39		76	0.42	
17	0.39		77	0.44	
18	2.7	Outlier	78	0.42	
19	2.0	Outlier,ND	80	0.11	
21	0.45		83	0.67	
22	0.53		84	2.7	Outlier,ND
23	0.45		85	0.40	
24	0.34		86	0.52	
25	0.29		87	0.38	
26	0.42		90	0.77	
27	0.33		91	1.3	Outlier
29	0.32		92	0.42	
30	0.93	Outlier	93	0.37	
31	1.1	Outlier	94	0.45	
32	0.63	ND	95	9.5	Outlier,ND
33	0.30		96	0.52	
34	0.46		97	0.36	ND
36	0.49		98	0.48	
39	0.49		100	0.43	
40	0.33				
43	10	Outlier			
44	3.0	Outlier,ND			
47	0.75				
48	0.38				
49	0.41				
50	0.42				
51	0.43				
53	0.38				
55	0.38				
56	0.42				
57	0.38				
58	0.40				
59	0.46				
60	0.12				
61	0.44				
62	0.50				
63	0.20	ND			

### Consensus statistics

Consensus median, pg/g	0.42
Median all values pg/g	0.43
Consensus mean, pg/g	0.41
Standard deviation, pg/g	0.12
Relative standard deviation, %	30
No. of values reported	72
No. of values removed	11
No. of reported non-detects	9





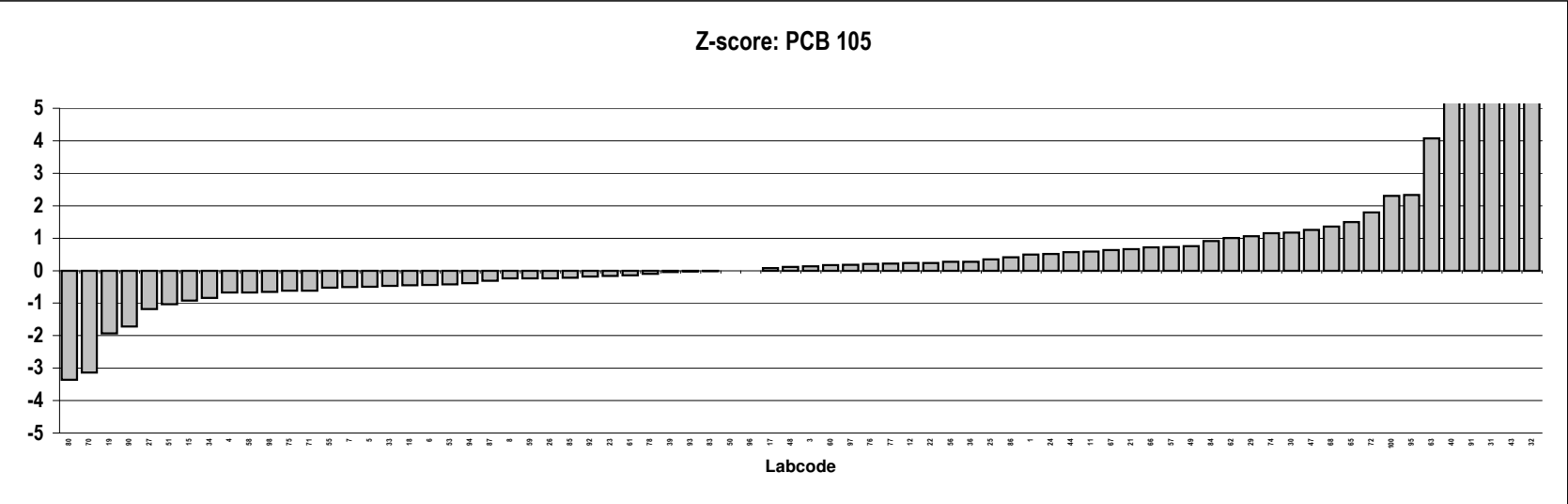
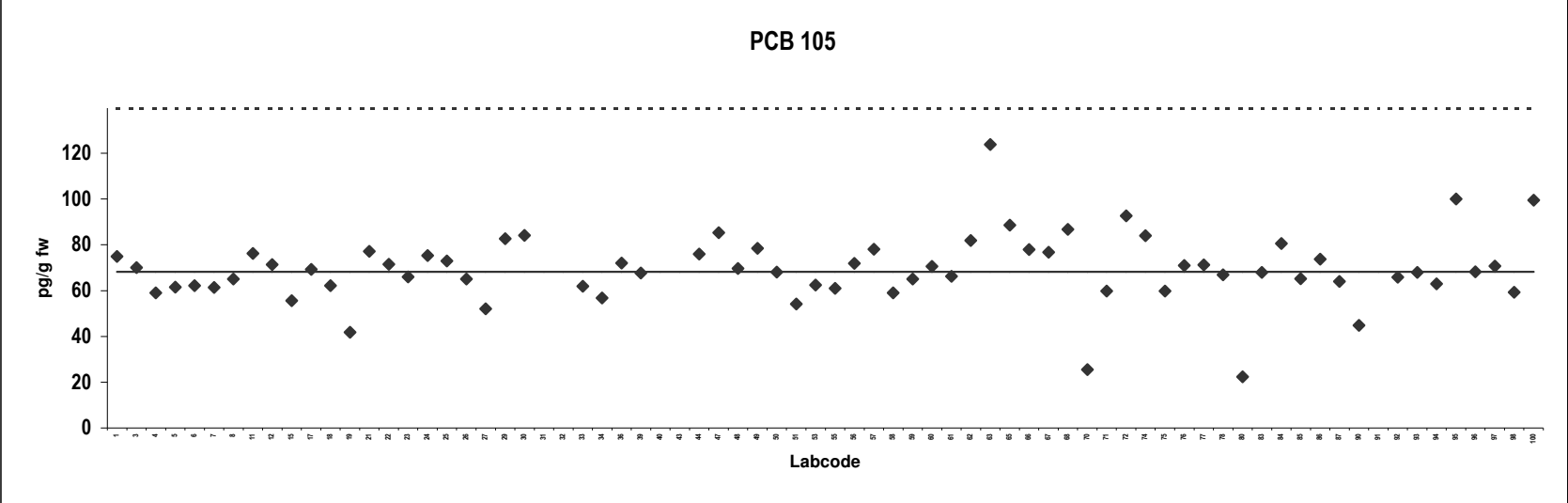
## Mozzarella Cheese

Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	75		63	124	
3	70		65	89	
4	59		66	78	
5	61		67	77	
6	62		68	87	
7	61		70	25	
8	65		71	60	
11	76		72	93	
12	71		74	84	
15	56		75	60	
17	69		76	71	
18	62		77	71	
19	42		78	67	
21	77		80	22	
22	71		83	68	
23	66		84	81	
24	75		85	65	
25	73		86	74	
26	65		87	64	
27	52		90	45	
29	83		91	238	Outlier
30	84		92	66	
31	255	Outlier	93	68	
32	298	Outlier	94	63	
33	62		95	100	
34	57		96	68	
36	72		97	71	
39	68		98	59	
40	167	Outlier	100	100	
43	275	Outlier			
44	76				
47	85				
48	70				
49	78				
50	68				
51	54				
53	62				
55	61				
56	72				
57	78				
58	59				
59	65				
60	71				
61	66				
62	82				

### Consensus statistics

Consensus median, pg/g	68
Median all values pg/g	70
Consensus mean, pg/g	69
Standard deviation, pg/g	15
Relative standard deviation, %	22
No. of values reported	74
No. of values removed	5
No. of reported non-detects	0



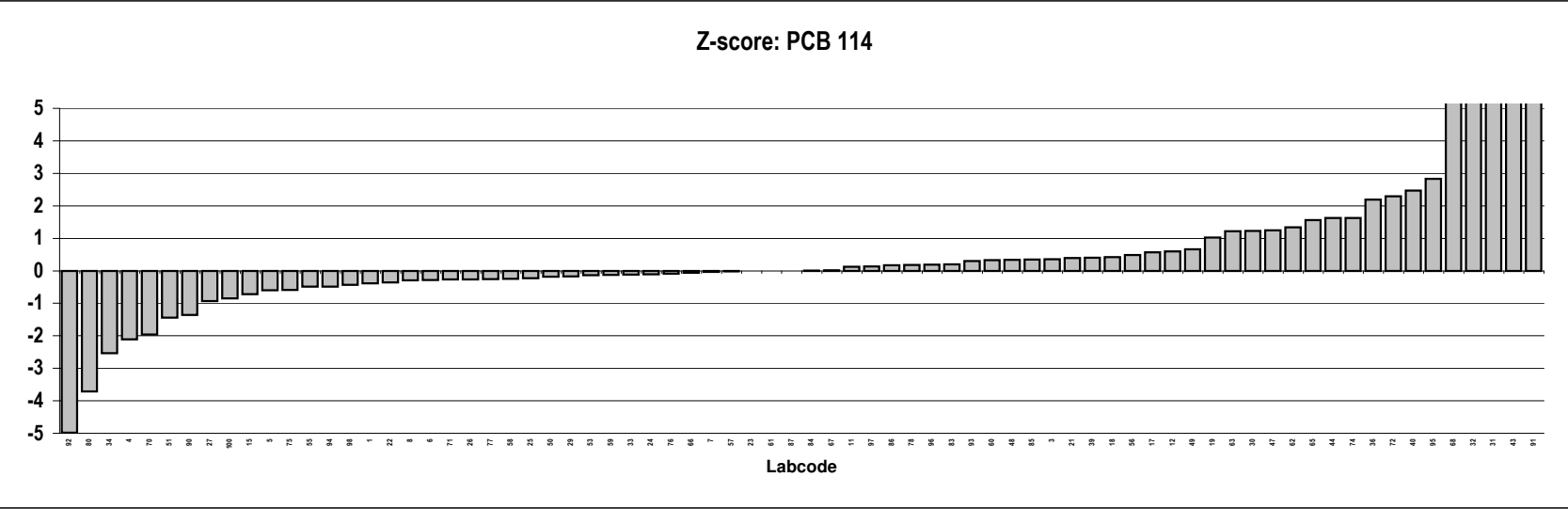
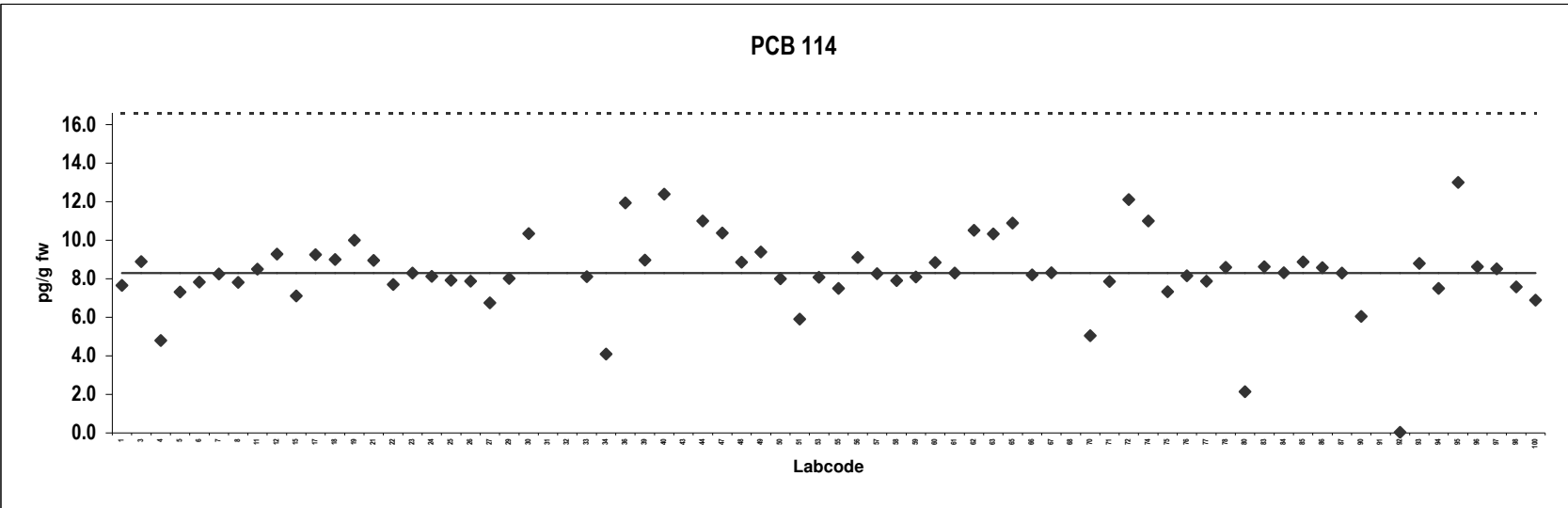
## Mozzarella Cheese

Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	7.7		63	10	
3	8.9		65	11	
4	4.8		66	8.2	
5	7.3	ND	67	8.3	
6	7.8		68	20	Outlier
7	8.3		70	5.1	
8	7.8		71	7.9	
11	8.5		72	12	ND
12	9.3		74	11	
15	7.1		75	7.3	
17	9.3		76	8.2	
18	9.0		77	7.9	
19	10	ND	78	8.6	
21	9.0		80	2.1	
22	7.7		83	8.6	
23	8.3		84	8.3	
24	8.1		85	8.9	
25	7.9		86	8.6	
26	7.9		87	8.3	
27	6.8		90	6.1	
29	8.0		91	36	Outlier
30	10		92	0.025	ND
31	32	Outlier	93	8.8	
32	24	Outlier	94	7.5	
33	8.1		95	13	
34	4.1		96	8.6	
36	12		97	8.5	
39	9.0		98	7.6	
40	12		100	6.9	
43	35	Outlier			
44	11				
47	10	ND			
48	8.9				
49	9.4				
50	8.0				
51	5.9				
53	8.1				
55	7.5				
56	9.1				
57	8.3				
58	7.9				
59	8.1				
60	8.8				
61	8.3				
62	11				

### Consensus statistics

Consensus median, pg/g	8.3
Median all values pg/g	8.3
Consensus mean, pg/g	8.3
Standard deviation, pg/g	2.0
Relative standard deviation, %	25
No. of values reported	74
No. of values removed	5
No. of reported non-detects	5



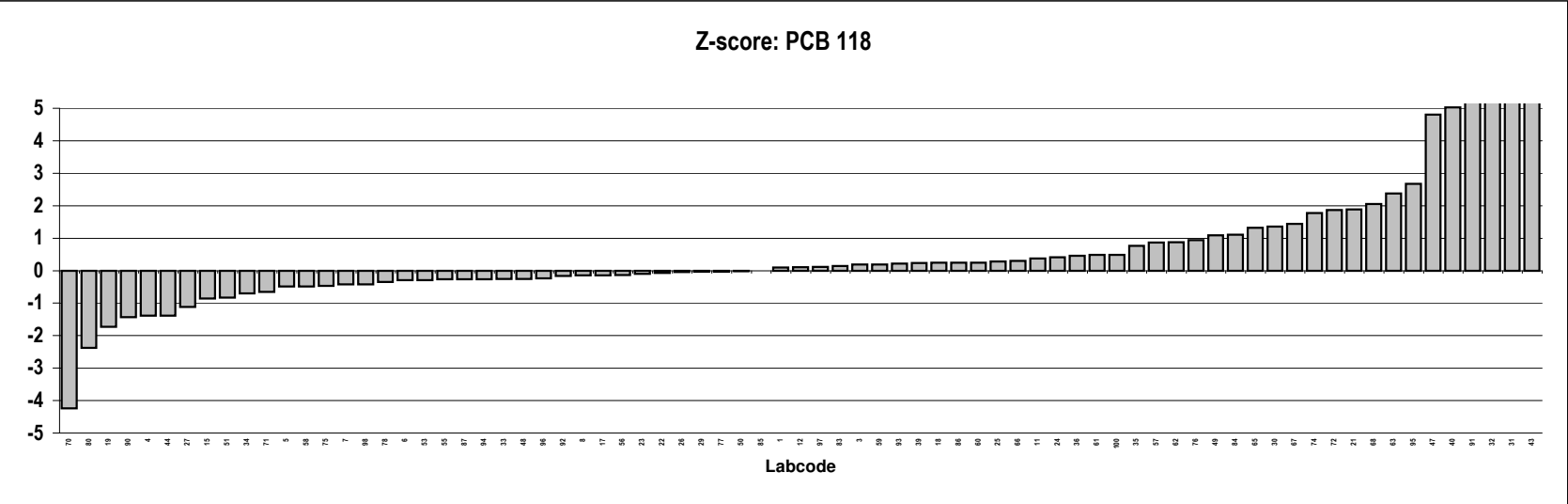
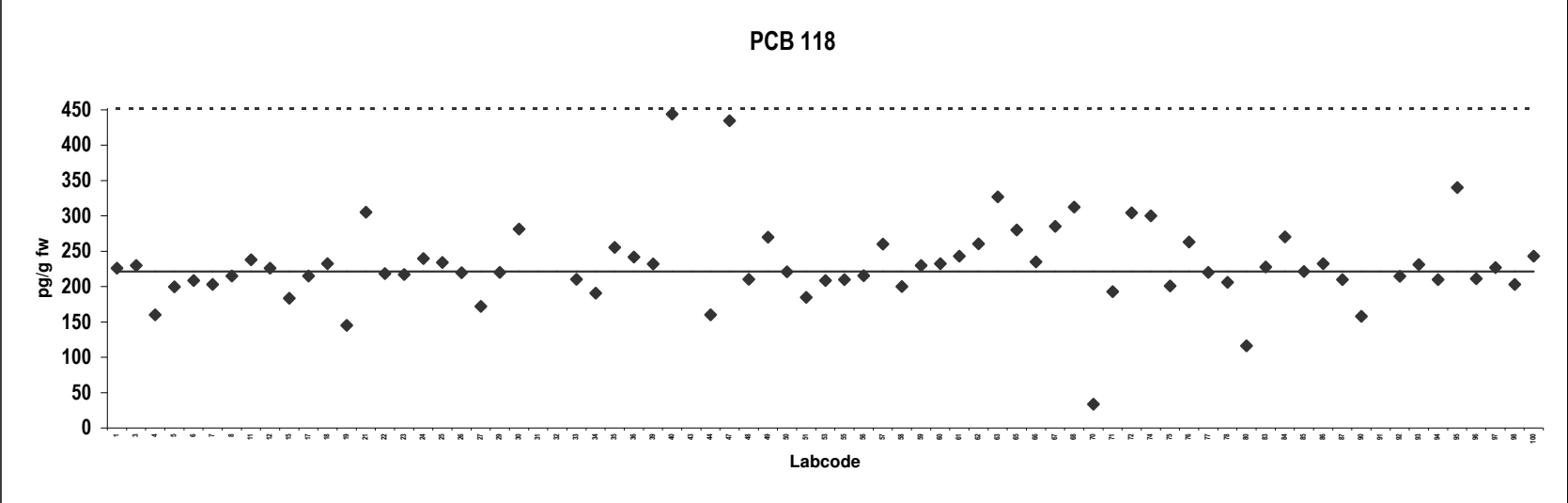
## Mozzarella Cheese

Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	226		62	260	
3	230		63	327	
4	160		65	280	
5	200		66	235	
6	209		67	285	
7	203		68	312	
8	215		70	34	
11	238		71	193	
12	226		72	304	
15	183		74	300	
17	215		75	201	
18	232		76	263	
19	145		77	220	
21	305		78	206	
22	218		80	116	
23	217		83	228	
24	240		84	270	
25	234		85	222	
26	220		86	232	
27	172		87	210	
29	220		90	158	
30	281		91	783	Outlier
31	859	Outlier	92	214	
32	819	Outlier	93	231	
33	210		94	210	
34	191		95	340	
35	256		96	211	
36	242		97	227	
39	232		98	203	
40	444		100	243	
43	862	Outlier			
44	160				
47	434				
48	210				
49	270				
50	221				
51	185				
53	209				
55	210				
56	216				
57	260				
58	200				
59	230				
60	233				
61	243				

### Consensus statistics

Consensus median, pg/g	222
Median all values pg/g	226
Consensus mean, pg/g	231
Standard deviation, pg/g	59
Relative standard deviation, %	25
No. of values reported	75
No. of values removed	4
No. of reported non-detects	0



## Mozzarella Cheese

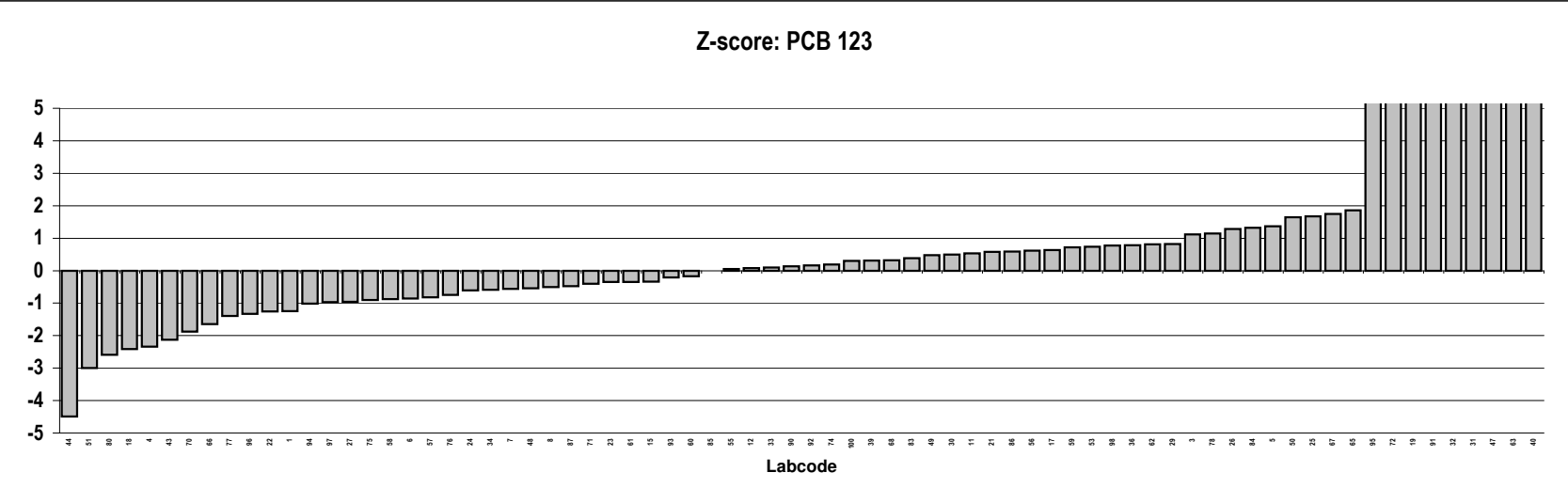
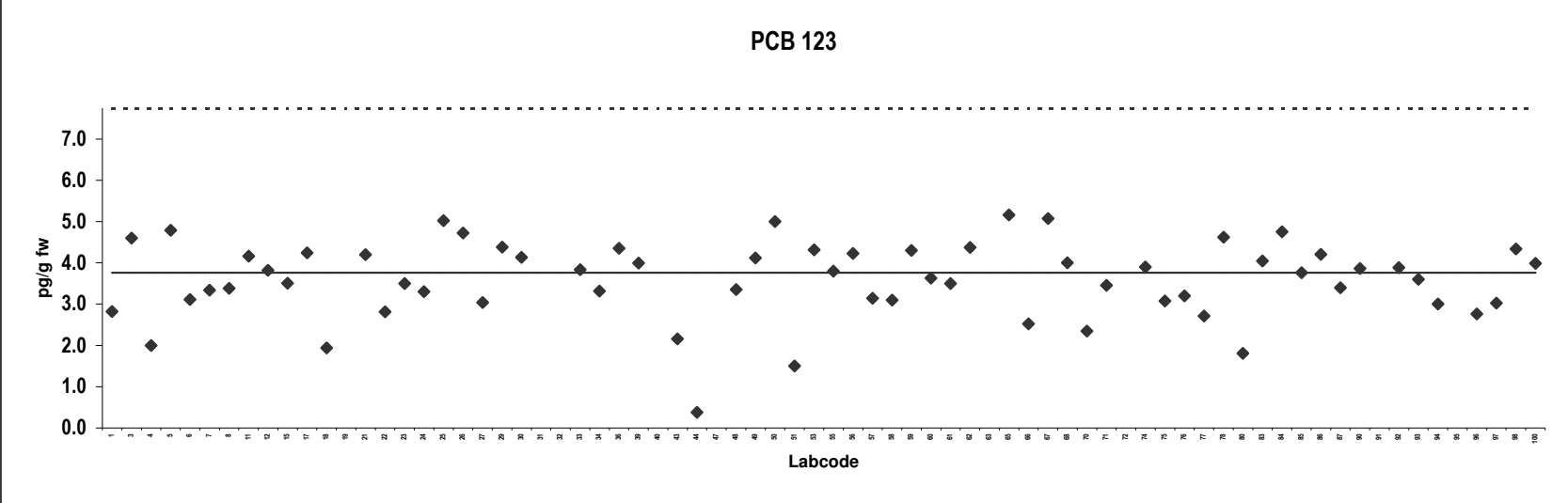
Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.8	ND	63	159	Outlier
3	4.6		65	5.2	
4	2.0		66	2.5	
5	4.8	ND	67	5.1	
6	3.1		68	4.0	ND
7	3.3		70	2.3	
8	3.4		71	3.5	
11	4.2		72	9.7	Outlier,ND
12	3.8		74	3.9	
15	3.5		75	3.1	
17	4.2		76	3.2	
18	1.9		77	2.7	
19	10	Outlier,ND	78	4.6	ND
21	4.2		80	1.8	
22	2.8		83	4.0	
23	3.5		84	4.8	ND
24	3.3		85	3.8	
25	5.0		86	4.2	
26	4.7		87	3.4	
27	3.0		90	3.9	
29	4.4		91	11	Outlier
30	4.1		92	3.9	
31	18	Outlier	93	3.6	
32	16	Outlier	94	3.0	
33	3.8		95	9.5	Outlier,ND
34	3.3	ND	96	2.8	
36	4.4		97	3.0	
39	4.0		98	4.3	
40	425	Outlier	100	4.0	
43	2.2				
44	0.38	ND			
47	43	Outlier			
48	3.4				
49	4.1				
50	5.0				
51	1.5	ND			
53	4.3				
55	3.8				
56	4.2				
57	3.1				
58	3.1				
59	4.3				
60	3.6				
61	3.5				
62	4.4				

### Consensus statistics

Consensus median, pg/g	3.8
Median all values pg/g	3.9
Consensus mean, pg/g	3.6
Standard deviation, pg/g	0.93
Relative standard deviation, %	26
No. of values reported	74
No. of values removed	9
No. of reported non-detects	11





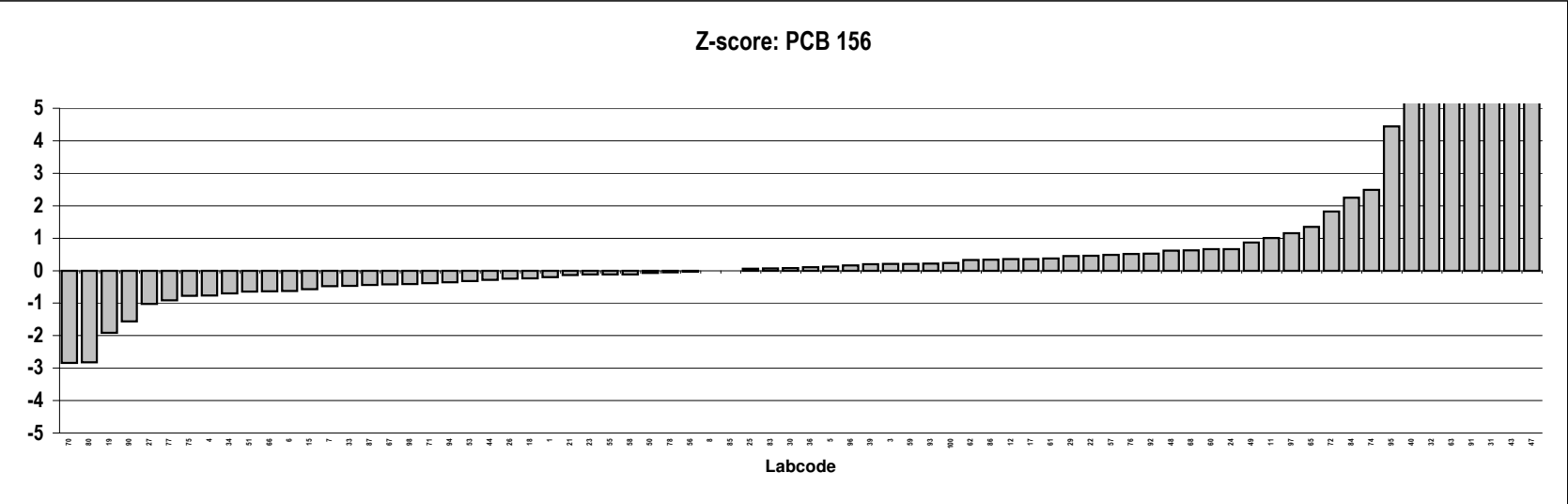
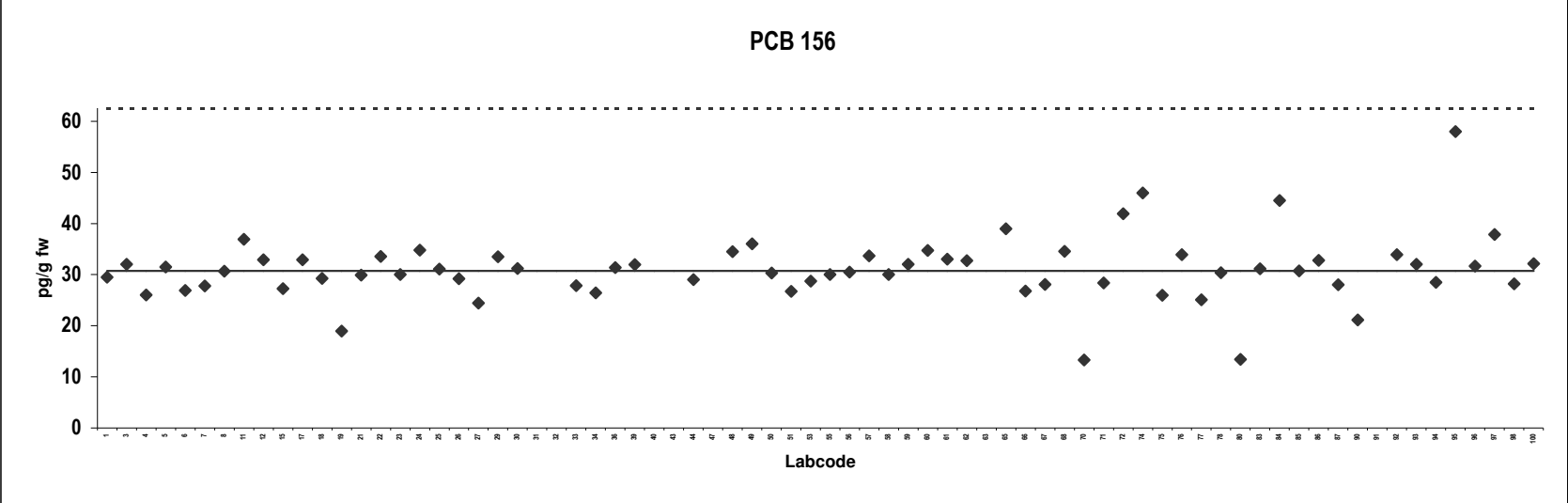
## Mozzarella Cheese

Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	30		63	84	Outlier
3	32		65	39	
4	26		66	27	
5	31		67	28	
6	27		68	35	
7	28		70	13	
8	31		71	28	
11	37		72	42	
12	33		74	46	
15	27		75	26	
17	33		76	34	
18	29		77	25	
19	19		78	30	
21	30		80	13	
22	34		83	31	
23	30		84	45	
24	35		85	31	
25	31		86	33	
26	29		87	28	
27	24		90	21	
29	34		91	110	Outlier
30	31		92	34	
31	111	Outlier	93	32	
32	70	Outlier	94	29	
33	28		95	58	
34	26		96	32	
36	31		97	38	
39	32		98	28	
40	69	Outlier	100	32	
43	116	Outlier			
44	29				
47	215	Outlier			
48	34				
49	36				
50	30				
51	27				
53	29				
55	30				
56	31				
57	34				
58	30				
59	32				
60	35				
61	33				
62	33				

### Consensus statistics

Consensus median, pg/g	31
Median all values pg/g	31
Consensus mean, pg/g	31
Standard deviation, pg/g	6.4
Relative standard deviation, %	21
No. of values reported	74
No. of values removed	7
No. of reported non-detects	0



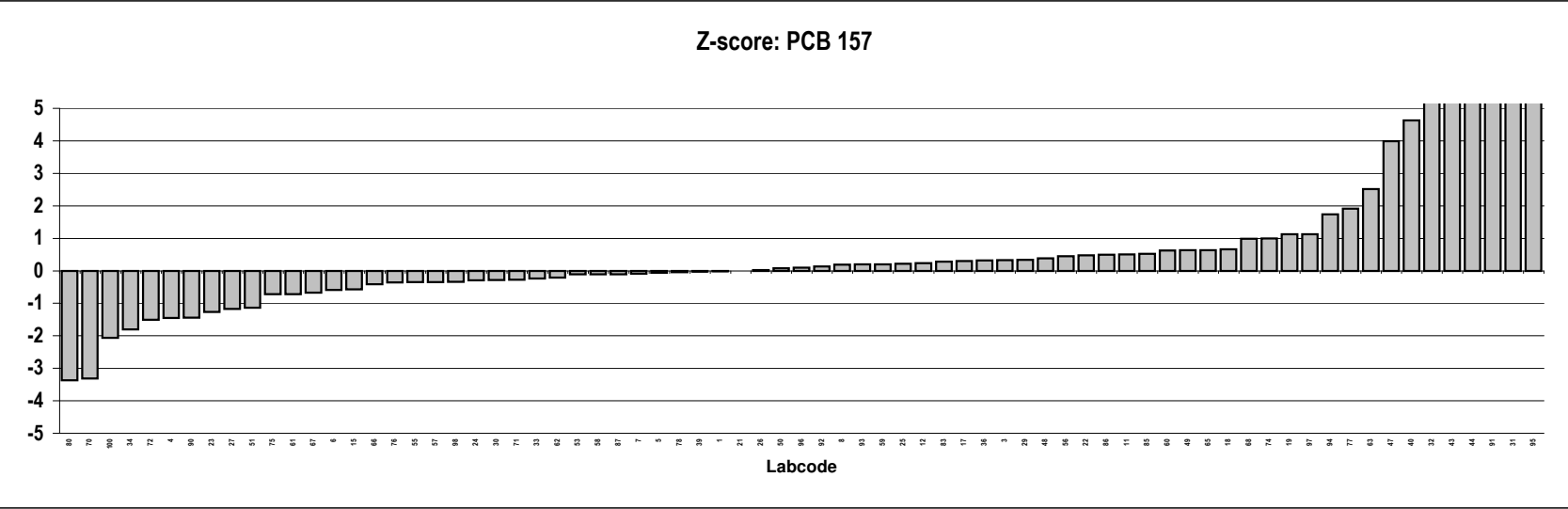
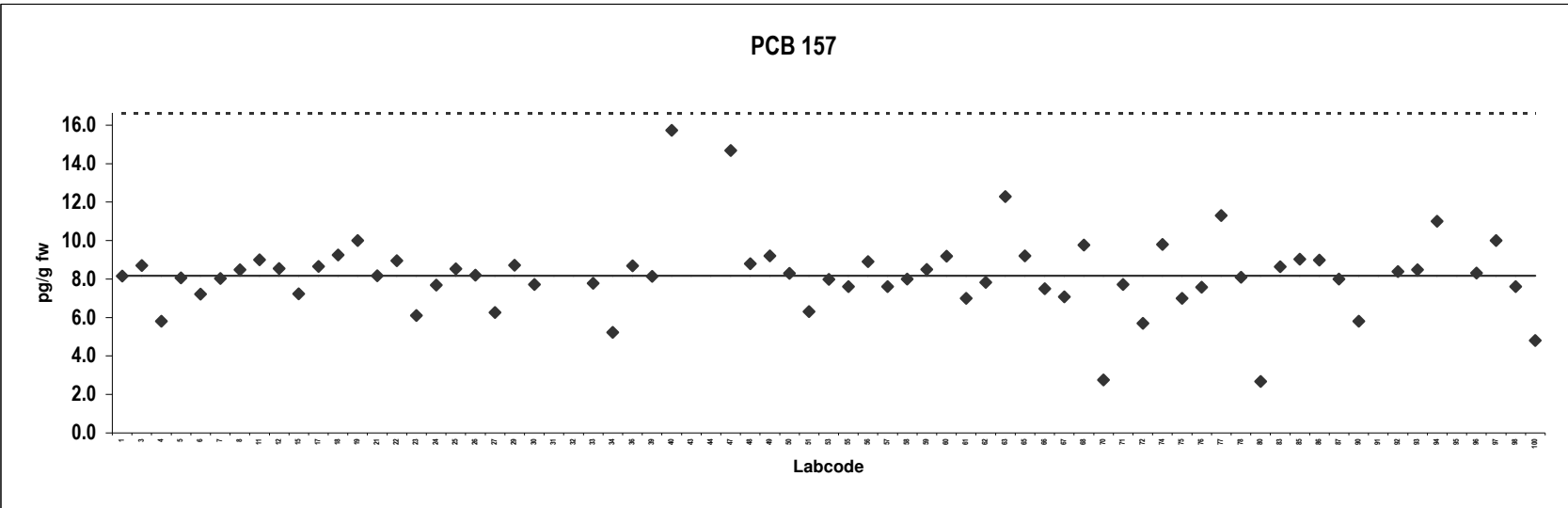
## Mozzarella Cheese

Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	8.2		63	12	
3	8.7		65	9.2	
4	5.8		66	7.5	
5	8.1	ND	67	7.1	
6	7.2		68	9.8	
7	8.0		70	2.8	
8	8.5		71	7.7	
11	9.0		72	5.7	ND
12	8.5		74	9.8	
15	7.2		75	7.0	
17	8.7		76	7.6	
18	9.2		77	11	
19	10	ND	78	8.1	
21	8.2		80	2.7	
22	8.9		83	8.6	
23	6.1		85	9.0	
24	7.7		86	9.0	
25	8.5		87	8.0	
26	8.2		90	5.8	
27	6.3		91	30	Outlier
29	8.7		92	8.4	
30	7.7		93	8.5	
31	31	Outlier	94	11	
32	19	Outlier	95	58	Outlier
33	7.8		96	8.3	
34	5.2		97	10	
36	8.7		98	7.6	
39	8.1		100	4.8	
40	16				
43	28	Outlier			
44	30	Outlier			
47	15				
48	8.8				
49	9.2				
50	8.3				
51	6.3				
53	8.0				
55	7.6				
56	8.9				
57	7.6				
58	8.0				
59	8.5				
60	9.2				
61	7.0				
62	7.8				

### Consensus statistics

Consensus median, pg/g	8.2
Median all values pg/g	8.3
Consensus mean, pg/g	8.2
Standard deviation, pg/g	2.0
Relative standard deviation, %	25
No. of values reported	73
No. of values removed	6
No. of reported non-detects	3



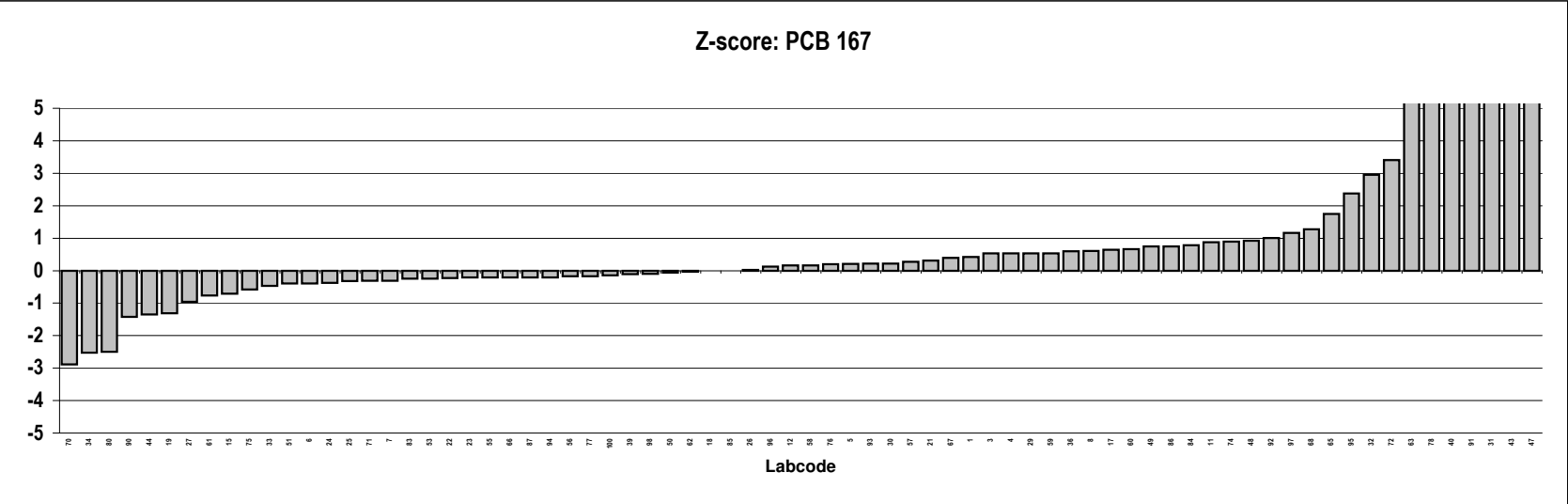
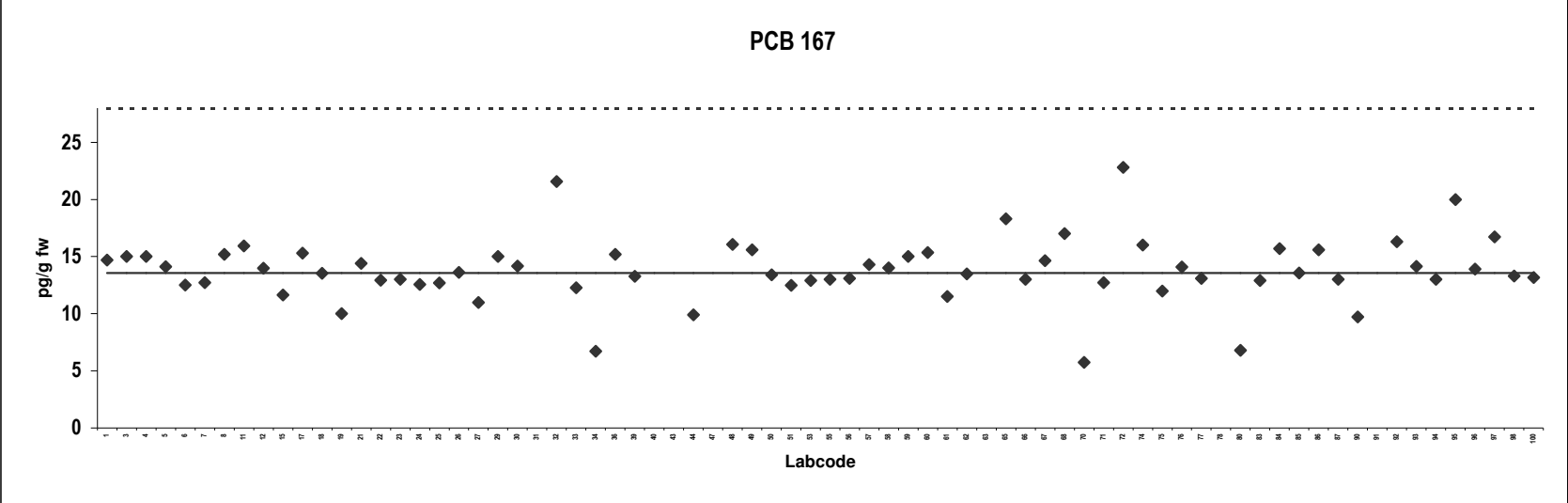
## Mozzarella Cheese

Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	15		63	29	Outlier
3	15		65	18	
4	15		66	13	
5	14	ND	67	15	
6	13		68	17	
7	13		70	5.7	
8	15		71	13	
11	16		72	23	
12	14		74	16	
15	12		75	12	
17	15		76	14	
18	14		77	13	
19	10	ND	78	36	Outlier
21	14		80	6.8	
22	13		83	13	
23	13		84	16	
24	13		85	14	
25	13		86	16	
26	14		87	13	
27	11		90	9.7	
29	15		91	49	Outlier
30	14		92	16	
31	53	Outlier	93	14	
32	22		94	13	
33	12		95	20	
34	6.7		96	14	
36	15		97	17	
39	13		98	13	
40	36	Outlier	100	13	
43	55	Outlier			
44	9.9				
47	89	Outlier			
48	16				
49	16				
50	13				
51	12				
53	13				
55	13				
56	13				
57	14				
58	14				
59	15				
60	15				
61	12				
62	13				

### Consensus statistics

Consensus median, pg/g	14
Median all values pg/g	14
Consensus mean, pg/g	14
Standard deviation, pg/g	2.8
Relative standard deviation, %	20
No. of values reported	74
No. of values removed	7
No. of reported non-detects	2



## Mozzarella Cheese

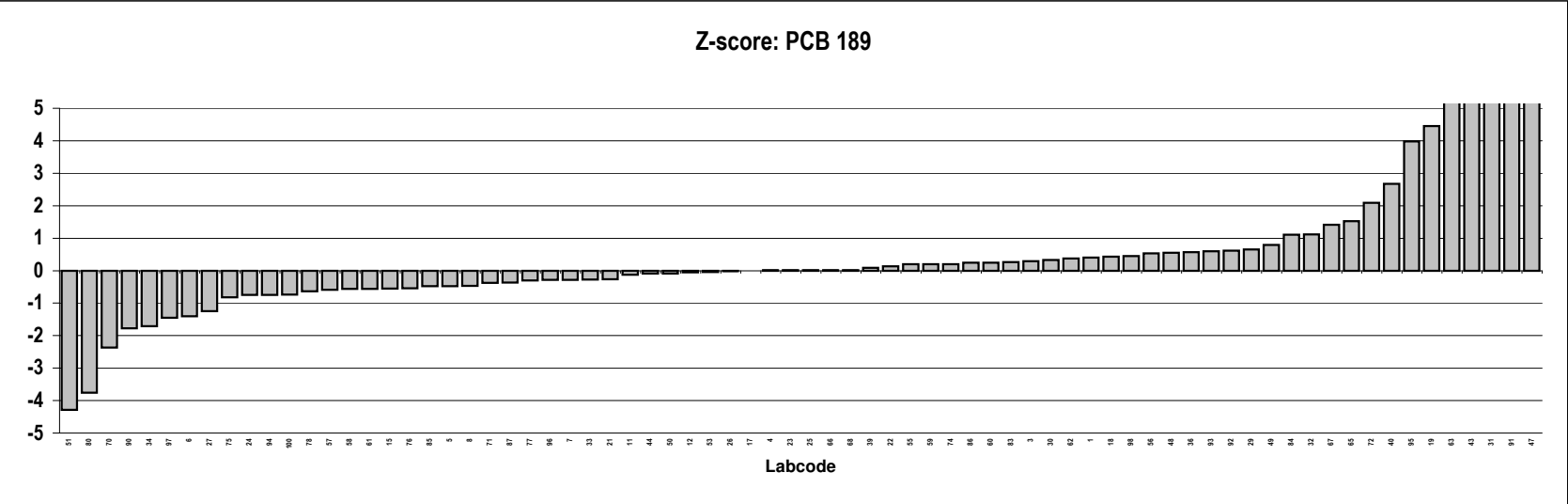
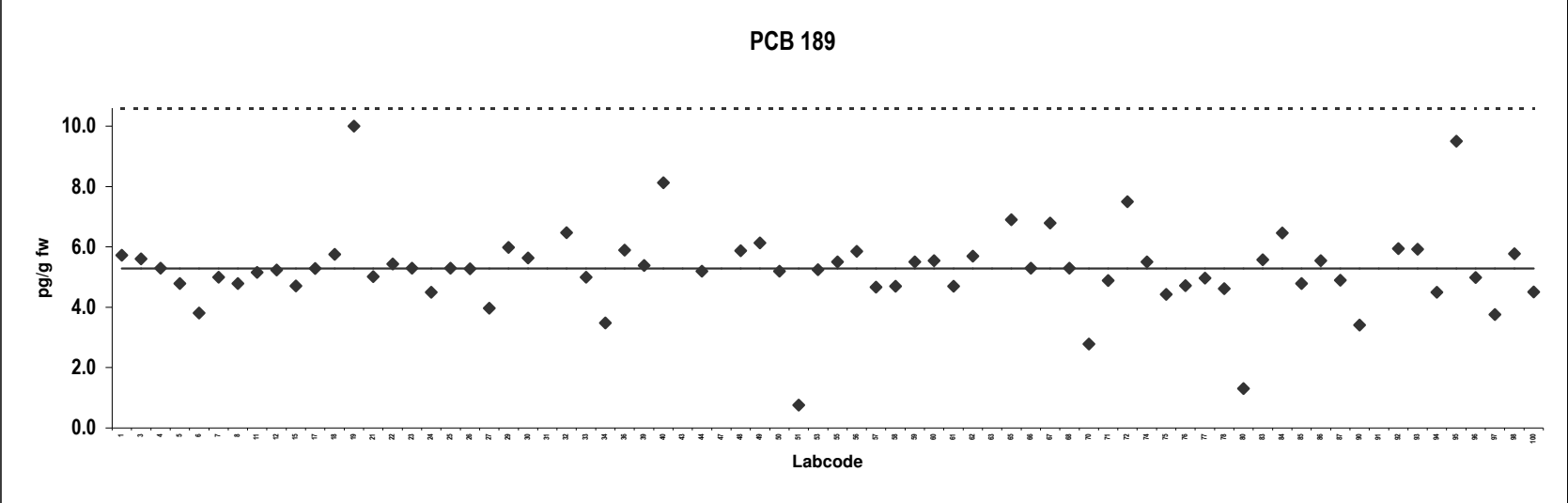
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.7		63	11	Outlier
3	5.6		65	6.9	
4	5.3		66	5.3	
5	4.8	ND	67	6.8	
6	3.8		68	5.3	
7	5.0		70	2.8	
8	4.8		71	4.9	
11	5.2		72	7.5	ND
12	5.2		74	5.5	
15	4.7		75	4.4	
17	5.3		76	4.7	
18	5.7		77	5.0	
19	10	ND	78	4.6	ND
21	5.0		80	1.3	
22	5.4		83	5.6	
23	5.3		84	6.5	
24	4.5		85	4.8	
25	5.3		86	5.5	
26	5.3		87	4.9	
27	4.0		90	3.4	
29	6.0		91	19	Outlier
30	5.6		92	5.9	
31	18	Outlier	93	5.9	
32	6.5		94	4.5	
33	5.0		95	9.5	ND
34	3.5		96	5.0	
36	5.9		97	3.8	
39	5.4		98	5.8	
40	8.1		100	4.5	
43	15	Outlier			
44	5.2				
47	37	Outlier			
48	5.9				
49	6.1				
50	5.2				
51	0.76	ND			
53	5.2				
55	5.5				
56	5.9				
57	4.7				
58	4.7				
59	5.5				
60	5.5				
61	4.7				
62	5.7				

### Consensus statistics

Consensus median, pg/g	5.3
Median all values pg/g	5.3
Consensus mean, pg/g	5.3
Standard deviation, pg/g	1.4
Relative standard deviation, %	26
No. of values reported	74
No. of values removed	5
No. of reported non-detects	6





## Mozzarella Cheese

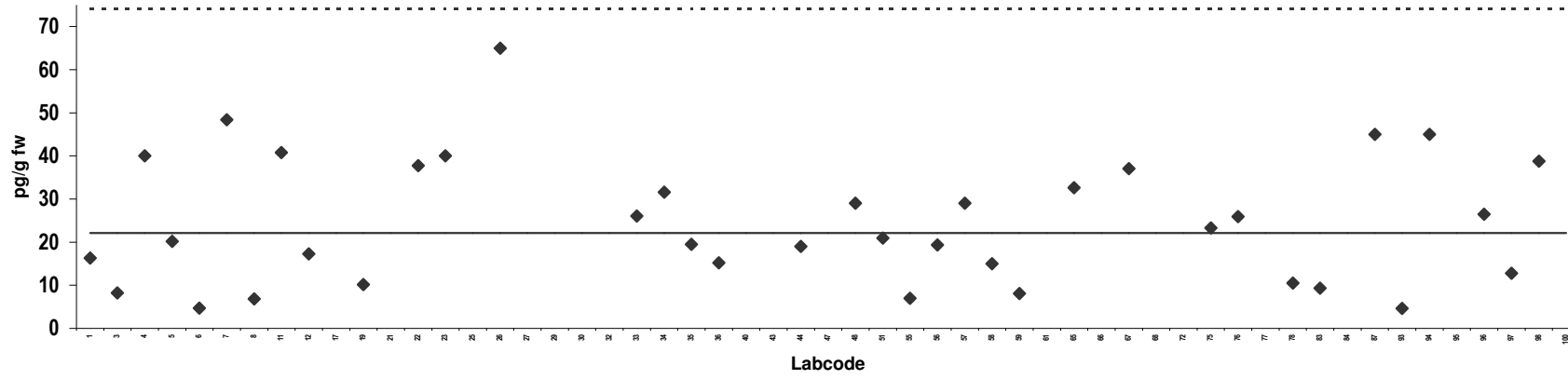
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	16		83	9.3	
3	8.2		84	109	Outlier
4	40		87	45	
5	20	ND	93	4.7	
6	4.7		94	45	
7	48		95	95	Outlier,ND
8	6.8		96	27	
11	41		97	13	
12	17		98	39	
17	117	Outlier	100	86	Outlier
19	10				
21	76	Outlier			
22	38				
23	40				
25	170	Outlier			
26	65				
27	80	Outlier			
29	91	Outlier			
30	165	Outlier			
32	163	Outlier			
33	26				
34	32				
35	19				
36	15				
40	135	Outlier			
43	1611	Outlier			
44	19				
47	86	Outlier			
48	29				
51	21				
55	7.0				
56	19				
57	29				
58	15				
59	8.1				
61	120	Outlier			
65	33				
66	80	Outlier			
67	37				
68	314	Outlier			
72	236	Outlier			
75	23				
76	26				
77	128	Outlier,ND			
78	11				

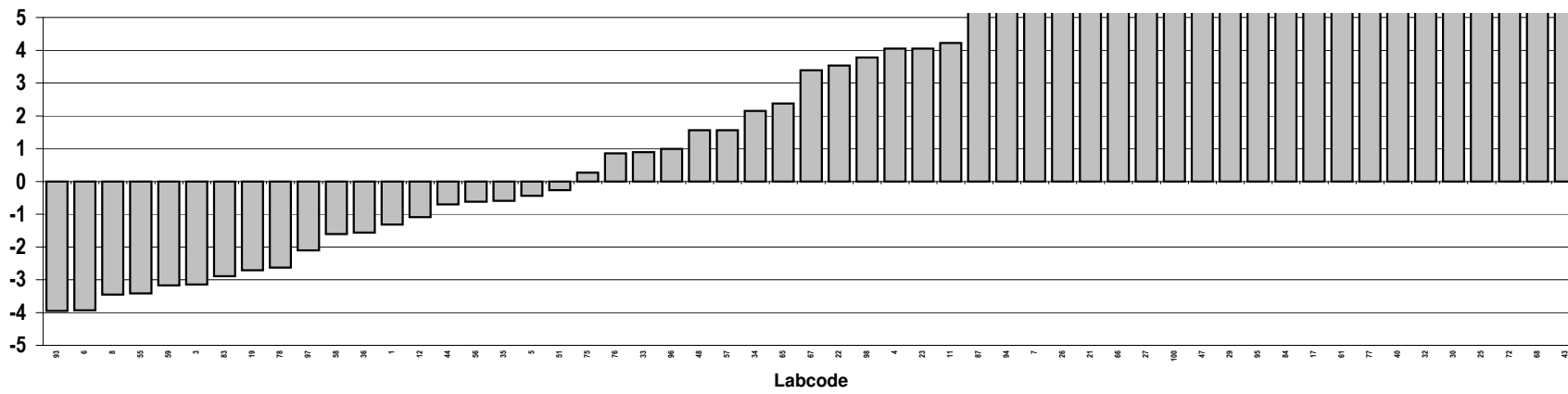
### Consensus statistics

Consensus median, pg/g	22
Median all values pg/g	37
Consensus mean, pg/g	25
Standard deviation, pg/g	15
Relative standard deviation, %	59
No. of values reported	55
No. of values removed	18
No. of reported non-detects	3

### CB 28



### Z-score: CB 28



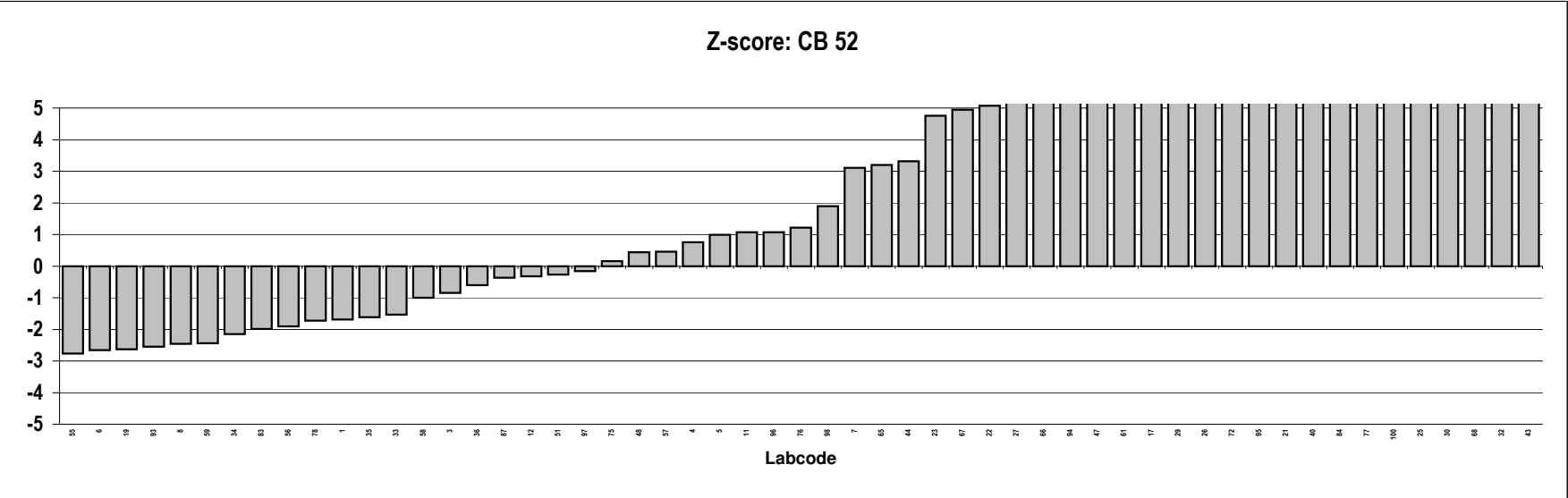
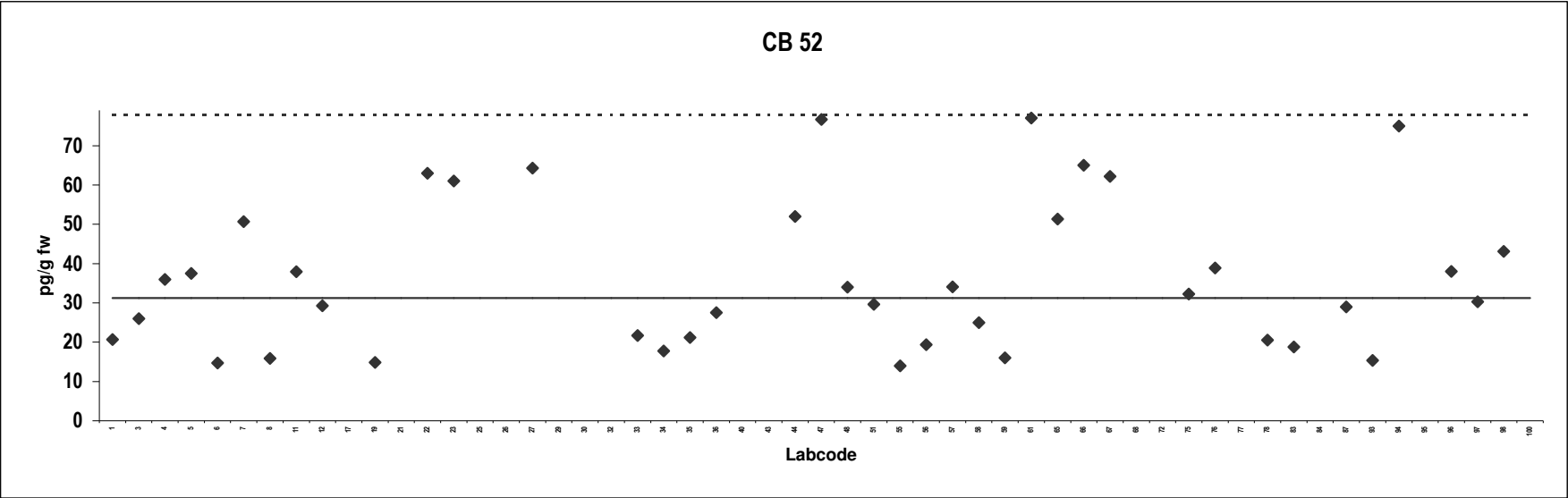
## Mozzarella Cheese

Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	21		83	19	
3	26		84	117	Outlier
4	36		87	29	
5	37		93	15	
6	15		94	75	
7	51		95	95	Outlier,ND
8	16		96	38	
11	38		97	30	
12	29		98	43	
17	80	Outlier	100	179	Outlier
19	15				
21	97	Outlier			
22	63				
23	61				
25	179	Outlier			
26	88	Outlier			
27	64				
29	85	Outlier			
30	247	Outlier			
32	432	Outlier			
33	22				
34	18				
35	21				
36	28				
40	105	Outlier			
43	1565	Outlier			
44	52				
47	77				
48	34				
51	30				
55	14				
56	19				
57	34				
58	25				
59	16				
61	77				
65	51				
66	65				
67	62				
68	261	Outlier			
72	92	Outlier			
75	32				
76	39				
77	128	Outlier,ND			
78	21				

### Consensus statistics

Consensus median, pg/g	31
Median all values pg/g	39
Consensus mean, pg/g	36
Standard deviation, pg/g	19
Relative standard deviation, %	52
No. of values reported	55
No. of values removed	15
No. of reported non-detects	2



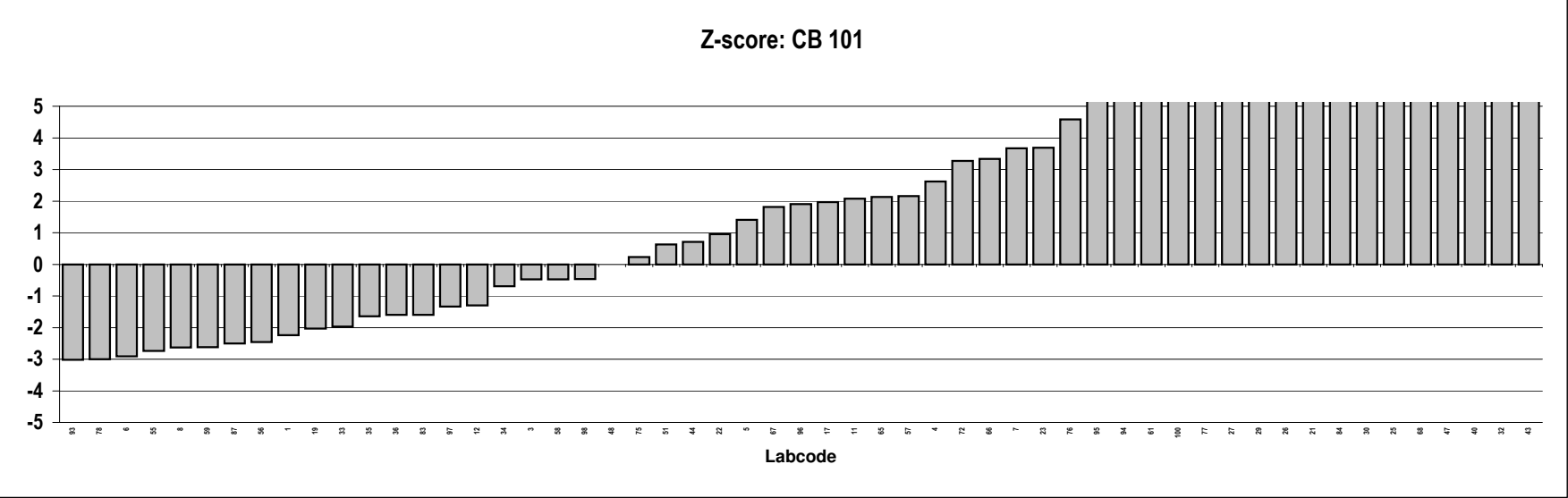
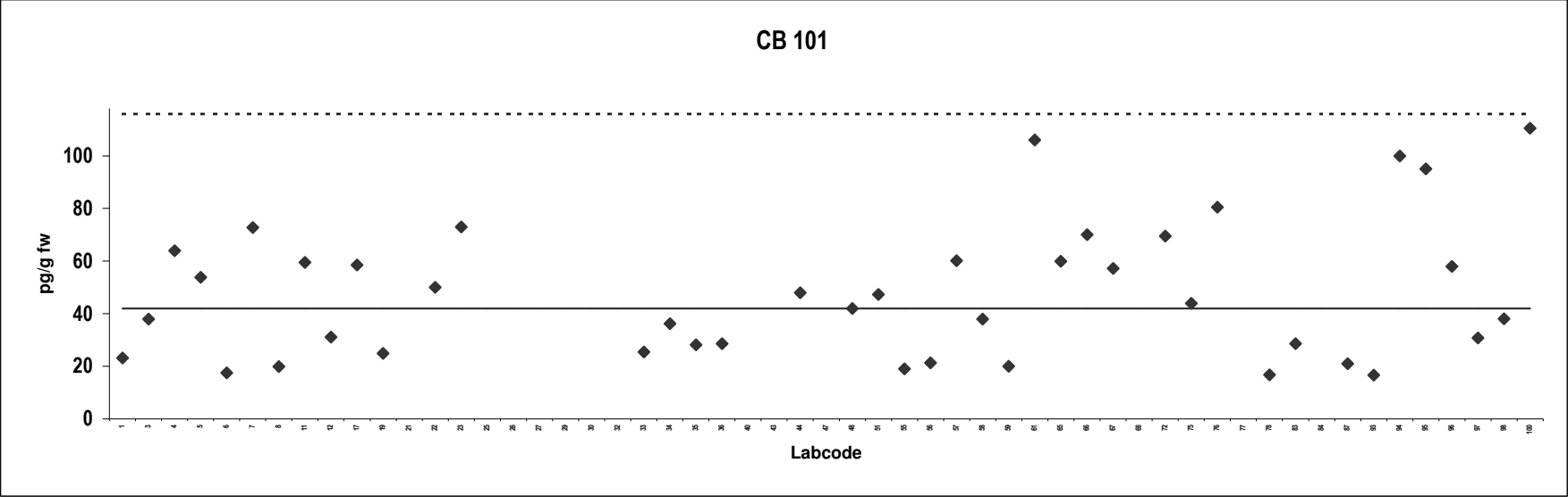
# Mozzarella Cheese

Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	23		83	29	
3	38		84	191	Outlier
4	64		87	21	
5	54		93	17	
6	18		94	100	
7	73		95	95	ND
8	20		96	58	
11	59		97	31	
12	31		98	38	
17	59		100	111	
19	25				
21	170	Outlier			
22	50				
23	73				
25	261	Outlier			
26	151	Outlier			
27	129	Outlier			
29	131	Outlier			
30	237	Outlier			
32	635	Outlier			
33	25				
34	36				
35	28				
36	29				
40	529	Outlier			
43	672	Outlier			
44	48				
47	493	Outlier			
48	42				
51	47				
55	19				
56	21				
57	60				
58	38				
59	20				
61	106				
65	60				
66	70				
67	57				
68	387	Outlier			
72	69				
75	44				
76	81				
77	128	Outlier,ND			
78	17				

## Consensus statistics

Consensus median, pg/g	42
Median all values pg/g	58
Consensus mean, pg/g	48
Standard deviation, pg/g	26
Relative standard deviation, %	54
No. of values reported	55
No. of values removed	13
No. of reported non-detects	2



## Mozzarella Cheese

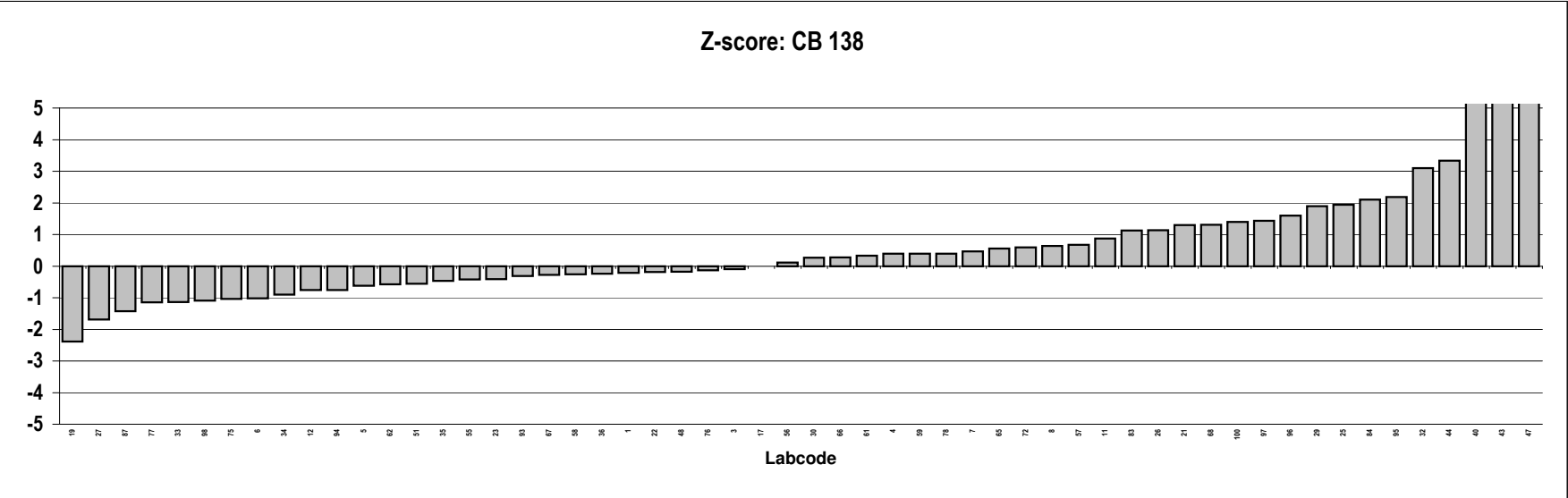
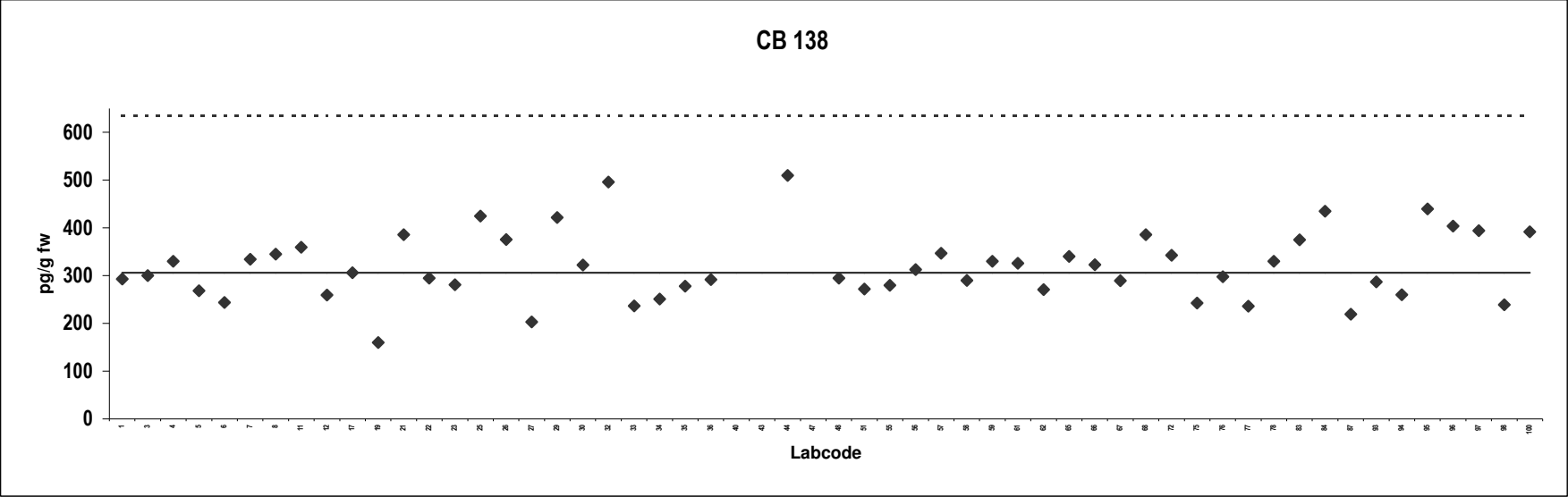
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	293		78	330	
3	300		83	375	
4	330		84	435	
5	268		87	219	
6	244		93	287	
7	334		94	260	
8	345		95	440	
11	359		96	404	
12	260		97	394	
17	306		98	239	
19	160		100	392	
21	386				
22	294				
23	281				
25	425				
26	376				
27	203				
29	422				
30	322				
32	496				
33	237				
34	251				
35	278				
36	292				
40	900	Outlier			
43	1072	Outlier			
44	510				
47	3522	Outlier			
48	295				
51	272				
55	280				
56	313				
57	347				
58	290				
59	330				
61	326				
62	271				
65	340				
66	323				
67	289				
68	386				
72	342				
75	243				
76	298				
77	236				

### Consensus statistics

Consensus median, pg/g	306
Median all values pg/g	318
Consensus mean, pg/g	319
Standard deviation, pg/g	72
Relative standard deviation, %	22
No. of values reported	56
No. of values removed	3
No. of reported non-detects	0





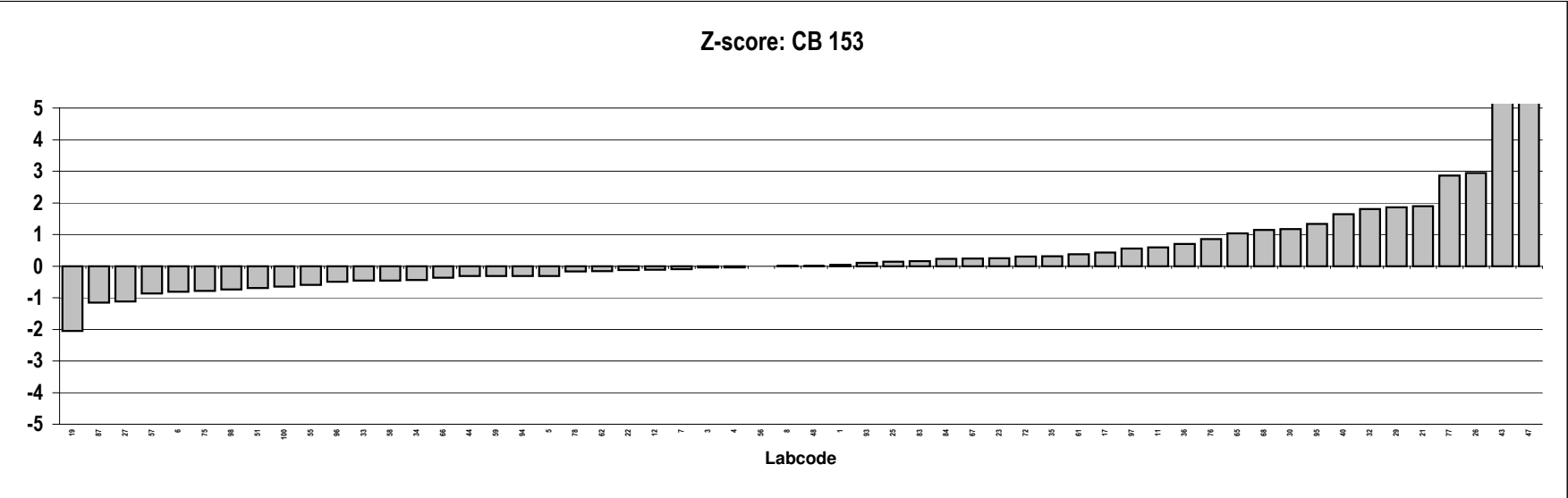
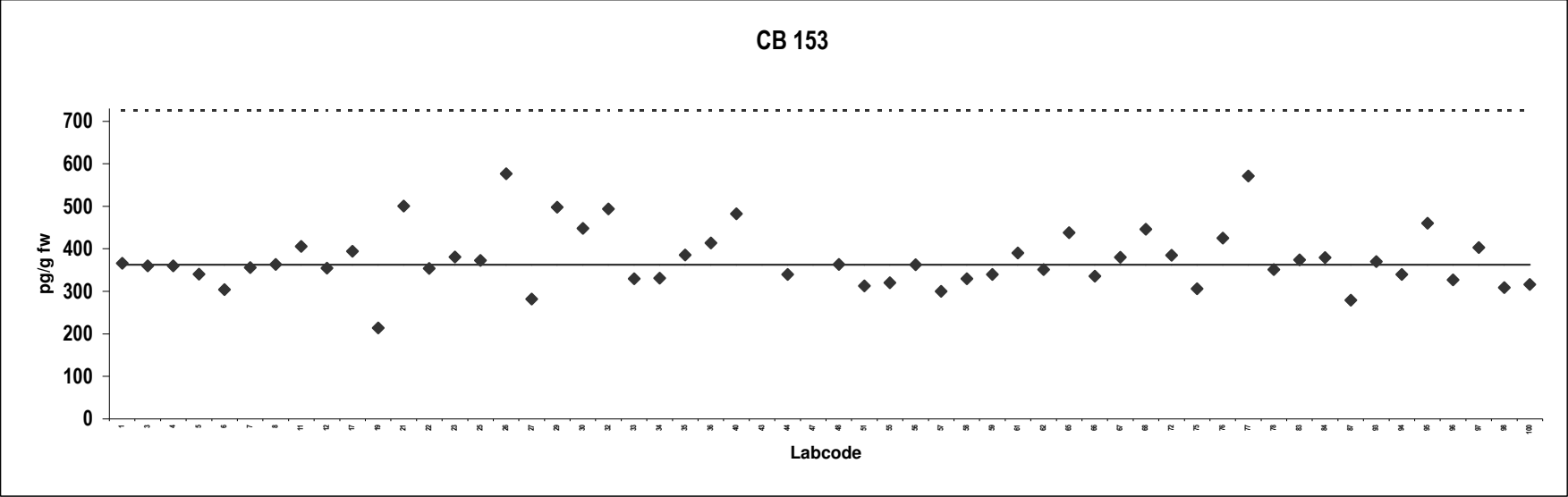
## Mozzarella Cheese

Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	366		78	351	
3	360		83	374	
4	360		84	380	
5	340		87	279	
6	304		93	370	
7	356		94	340	
8	363		95	460	
11	406		96	327	
12	355		97	403	
17	394		98	309	
19	214		100	316	
21	501				
22	354				
23	381				
25	373				
26	577				
27	282				
29	498				
30	448				
32	494				
33	329				
34	331				
35	385				
36	414				
40	482				
43	1719	Outlier			
44	340				
47	3034	Outlier			
48	363				
51	313				
55	320				
56	363				
57	300				
58	330				
59	340				
61	390				
62	351				
65	438				
66	336				
67	380				
68	446				
72	385				
75	306				
76	425				
77	571				

### Consensus statistics

Consensus median, pg/g	363
Median all values pg/g	363
Consensus mean, pg/g	375
Standard deviation, pg/g	69
Relative standard deviation, %	19
No. of values reported	56
No. of values removed	2
No. of reported non-detects	0



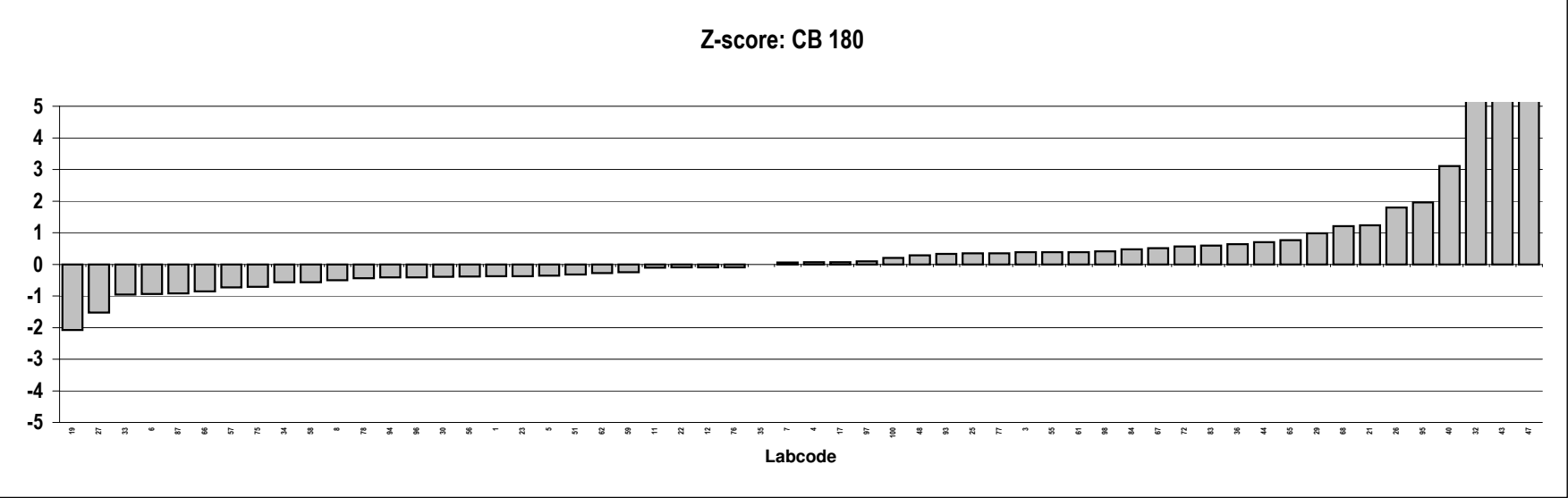
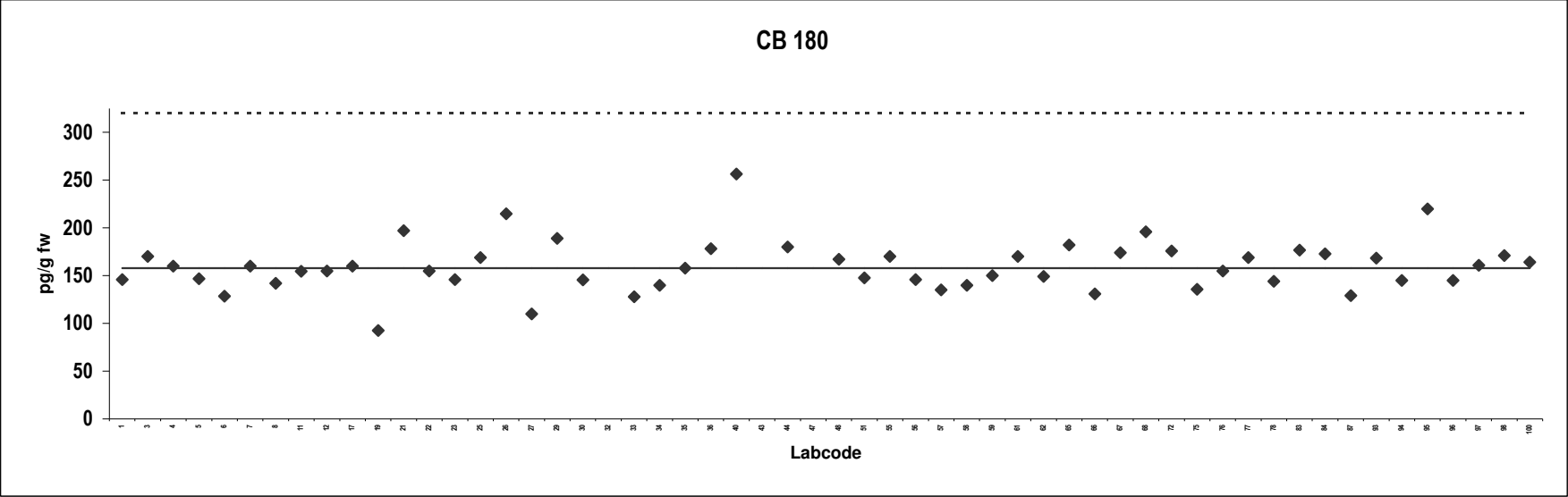
## Mozzarella Cheese

Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	146		78	144	
3	170		83	177	
4	160		84	173	
5	147		87	129	
6	128		93	168	
7	160		94	145	
8	142		95	220	
11	155		96	145	
12	155		97	161	
17	160		98	171	
19	92		100	164	
21	197				
22	155				
23	146				
25	169				
26	215				
27	110				
29	189				
30	146				
32	385	Outlier			
33	128				
34	140				
35	158				
36	178				
40	256				
43	615	Outlier			
44	180				
47	2741	Outlier			
48	167				
51	148				
55	170				
56	146				
57	135				
58	140				
59	150				
61	170				
62	149				
65	182				
66	131				
67	174				
68	196				
72	176				
75	136				
76	155				
77	169				

### Consensus statistics

Consensus median, pg/g	158
Median all values pg/g	160
Consensus mean, pg/g	160
Standard deviation, pg/g	27
Relative standard deviation, %	17
No. of values reported	56
No. of values removed	3
No. of reported non-detects	0



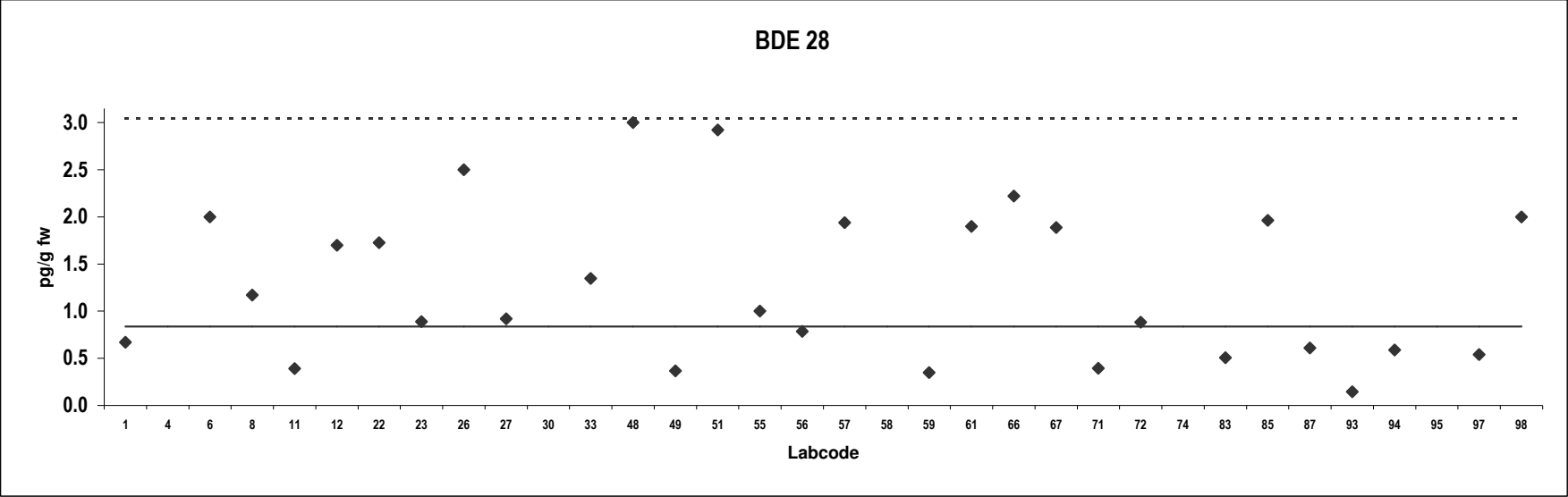
## Mozzarella Cheese

Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.67				
4	120	Outlier			
6	2.0	ND			
8	1.2				
11	0.39				
12	1.7	ND			
22	1.7				
23	0.89				
26	2.5				
27	0.92				
30	5.8	Outlier			
33	1.3				
48	3.0	ND			
49	0.37				
51	2.9	ND			
55	1.0				
56	0.79				
57	1.9				
58	5.0	Outlier,ND			
59	0.35				
61	1.9				
66	2.2				
67	1.9				
71	0.40				
72	0.88	ND			
74	20	Outlier,ND			
83	0.51				
85	2.0	ND			
87	0.61				
93	0.15				
94	0.59				
95	10	Outlier			
97	0.54				
98	2.0	ND			

### Consensus statistics

Consensus median, pg/g	0.84
Median all values pg/g	1.5
Consensus mean, pg/g	1.3
Standard deviation, pg/g	0.82
Relative standard deviation, %	64
No. of values reported	34
No. of values removed	5
No. of reported non-detects	9



## Mozzarella Cheese

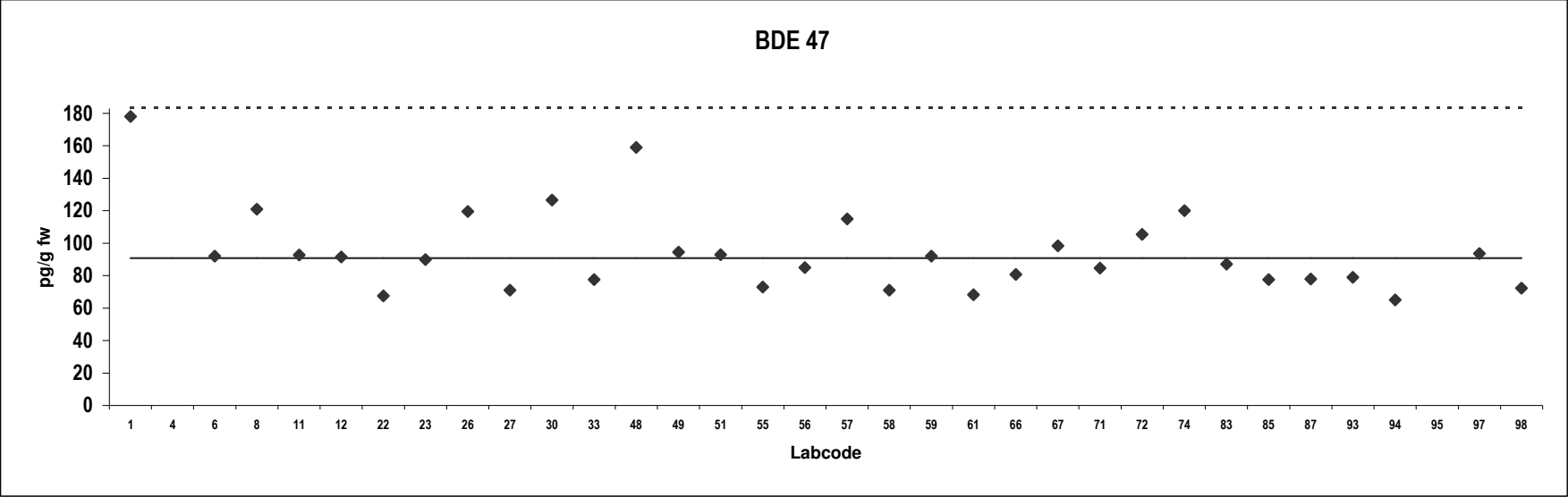
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	178				
4	3300	Outlier			
6	92				
8	121				
11	93				
12	92				
22	67				
23	90				
26	120				
27	71				
30	127				
33	78				
48	159				
49	94				
51	93				
55	73				
56	85				
57	115				
58	71				
59	92				
61	68				
66	81				
67	98				
71	85				
72	105				
74	120				
83	87				
85	78				
87	78				
93	79				
94	65				
95	690	Outlier			
97	94				
98	72				

### Consensus statistics

Consensus median, pg/g	91
Median all values pg/g	92
Consensus mean, pg/g	94
Standard deviation, pg/g	26
Relative standard deviation, %	27
No. of values reported	34
No. of values removed	2
No. of reported non-detects	0





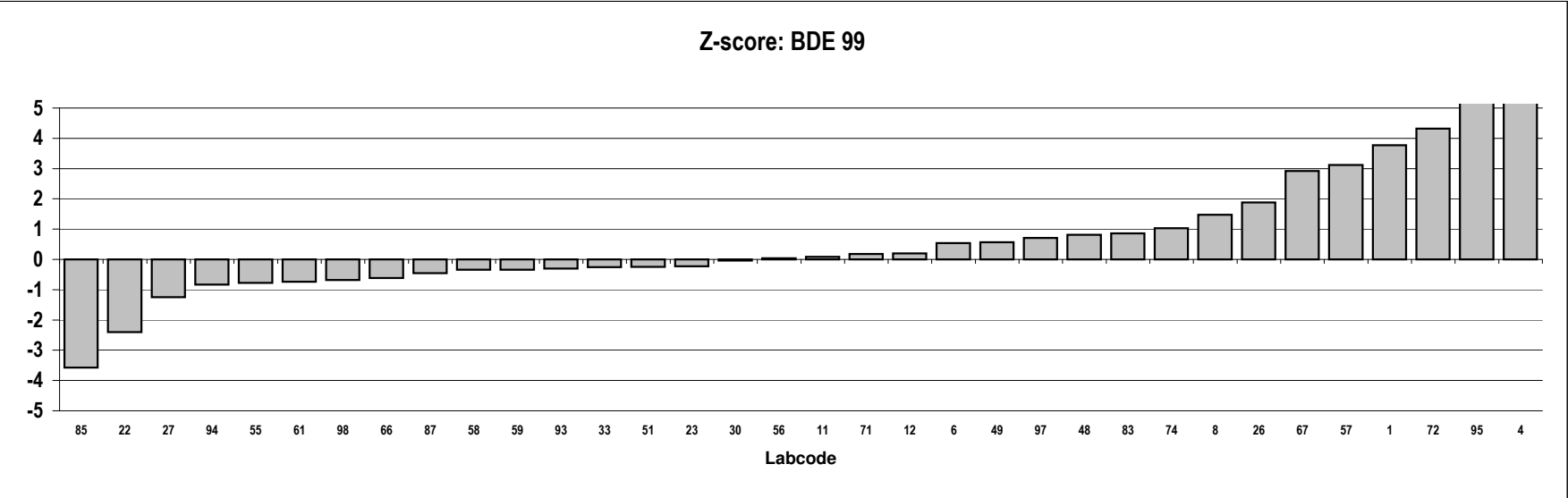
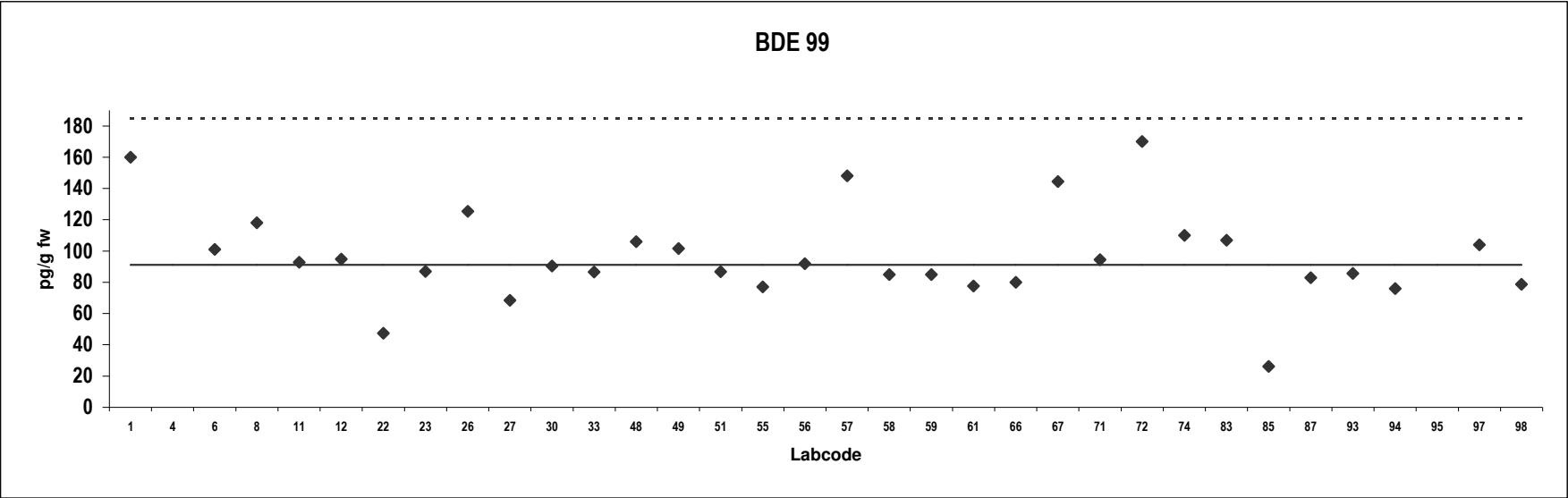
## Mozzarella Cheese

Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	160				
4	850	Outlier			
6	101				
8	118				
11	93				
12	95				
22	47				
23	87				
26	125				
27	68				
30	90				
33	87				
48	106				
49	102				
51	87				
55	77				
56	92				
57	148				
58	85				
59	85				
61	78				
66	80				
67	144				
71	94				
72	170				
74	110				
83	107				
85	26				
87	83				
93	86				
94	76				
95	650	Outlier			
97	104				
98	79				

### Consensus statistics

Consensus median, pg/g	91
Median all values pg/g	92
Consensus mean, pg/g	97
Standard deviation, pg/g	30
Relative standard deviation, %	31
No. of values reported	34
No. of values removed	2
No. of reported non-detects	0



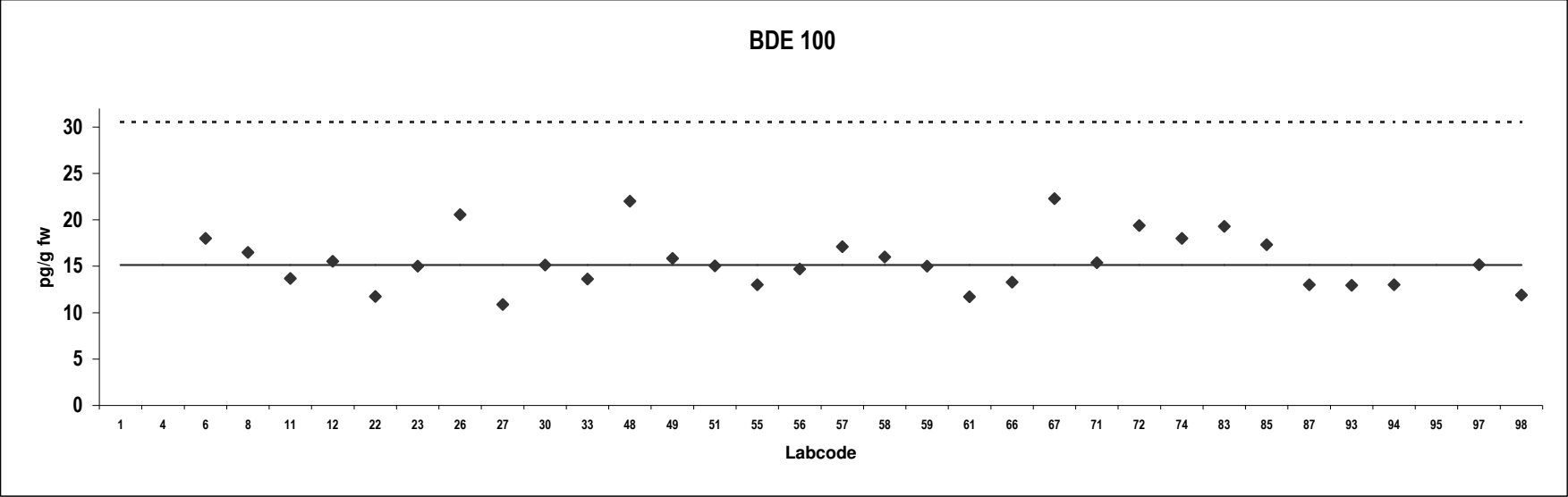
## Mozzarella Cheese

Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	33	Outlier			
4	770	Outlier			
6	18				
8	17				
11	14				
12	16				
22	12				
23	15				
26	21				
27	11				
30	15				
33	14				
48	22				
49	16				
51	15				
55	13				
56	15				
57	17				
58	16				
59	15				
61	12				
66	13				
67	22				
71	15				
72	19				
74	18				
83	19				
85	17				
87	13				
93	13				
94	13				
95	170	Outlier			
97	15				
98	12				

### Consensus statistics

Consensus median, pg/g	15
Median all values pg/g	15
Consensus mean, pg/g	16
Standard deviation, pg/g	3.0
Relative standard deviation, %	19
No. of values reported	34
No. of values removed	3
No. of reported non-detects	0



## Mozzarella Cheese

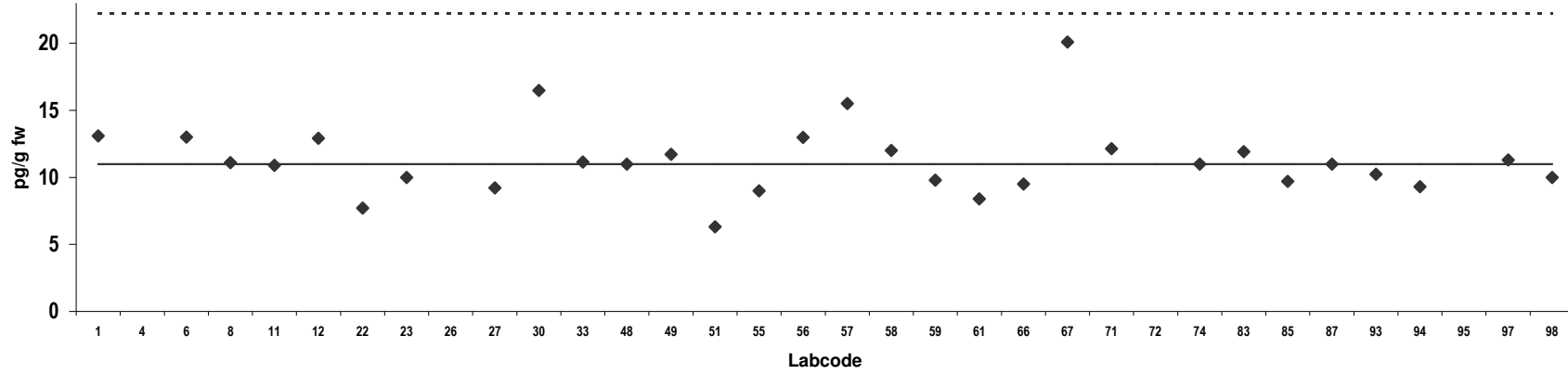
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	13				
4	200	Outlier			
6	13				
8	11				
11	11				
12	13				
22	7.7				
23	10				
26	179	Outlier			
27	9.2				
30	16				
33	11				
48	11				
49	12				
51	6.3	ND			
55	9.0				
56	13				
57	16				
58	12				
59	9.8				
61	8.4				
66	9.5				
67	20				
71	12				
72	31	Outlier			
74	11				
83	12				
85	9.7				
87	11				
93	10				
94	9.3				
95	40	Outlier			
97	11				
98	10				

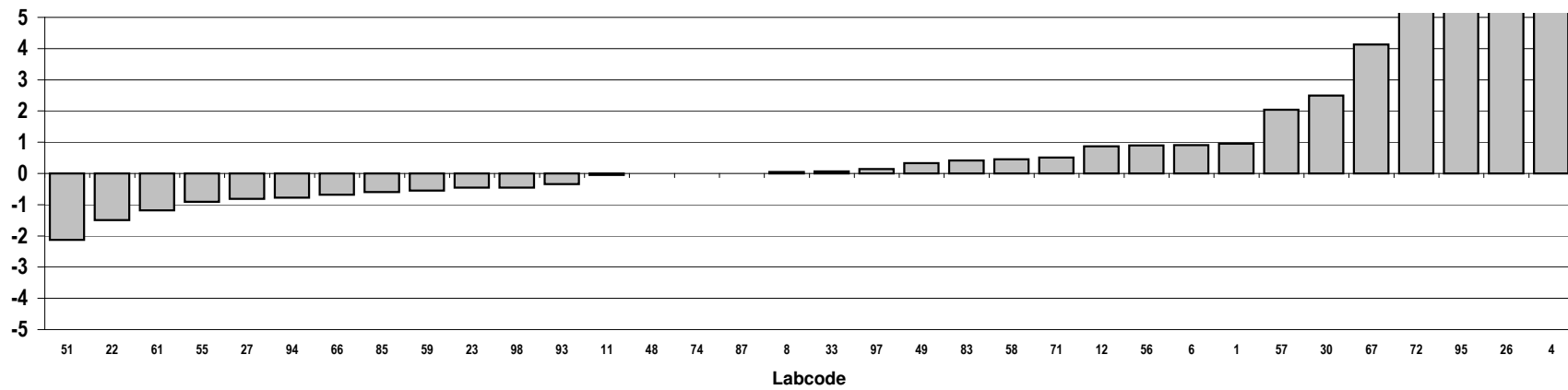
### Consensus statistics

Consensus median, pg/g	11
Median all values pg/g	11
Consensus mean, pg/g	11
Standard deviation, pg/g	2.7
Relative standard deviation, %	24
No. of values reported	34
No. of values removed	4
No. of reported non-detects	1

### BDE 153



### Z-score: BDE 153



## Mozzarella Cheese

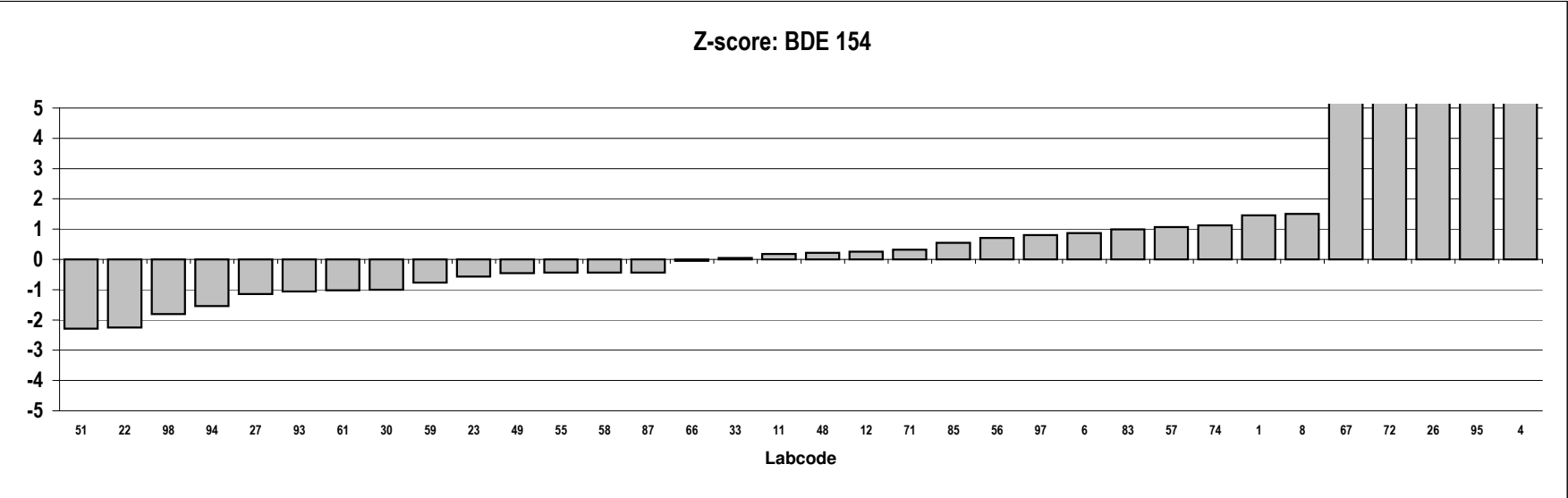
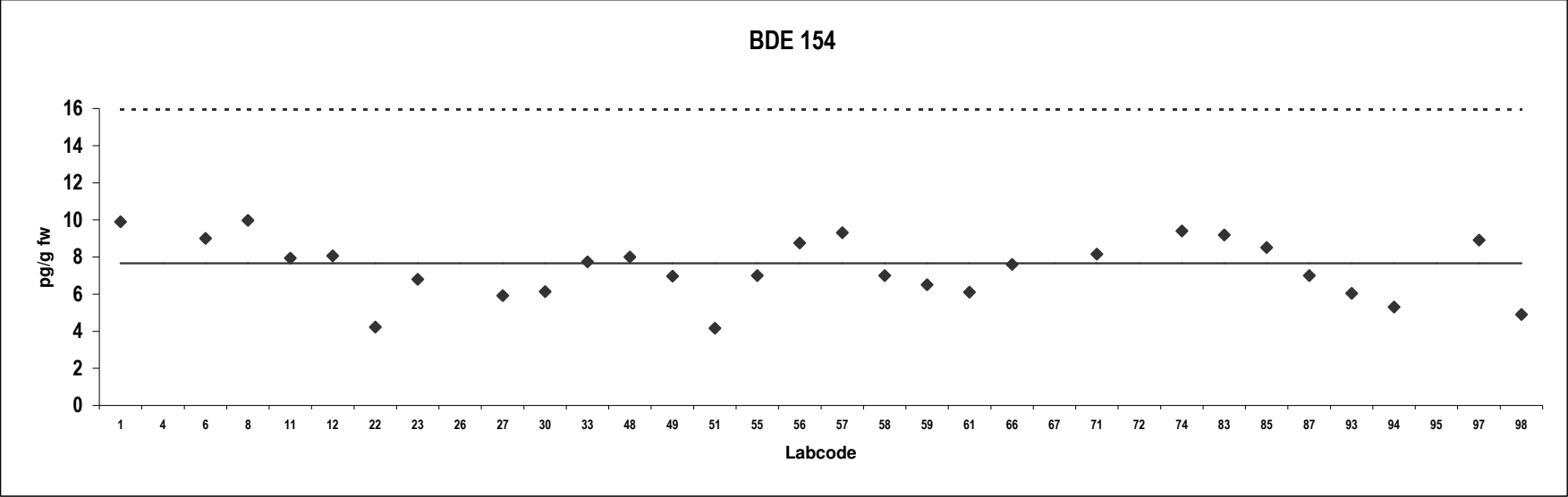
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	9.9				
4	430	Outlier			
6	9.0				
8	10				
11	7.9				
12	8.1				
22	4.2				
23	6.8				
26	48	Outlier			
27	5.9				
30	6.1				
33	7.7				
48	8.0				
49	7.0				
51	4.2	ND			
55	7.0				
56	8.8				
57	9.3				
58	7.0				
59	6.5				
61	6.1				
66	7.6				
67	16	Outlier			
71	8.2				
72	22	Outlier			
74	9.4				
83	9.2				
85	8.5				
87	7.0				
93	6.0				
94	5.3				
95	100	Outlier,ND			
97	8.9				
98	4.9				

### Consensus statistics

Consensus median, pg/g	7.7
Median all values pg/g	8.0
Consensus mean, pg/g	7.4
Standard deviation, pg/g	1.6
Relative standard deviation, %	22
No. of values reported	34
No. of values removed	5
No. of reported non-detects	2





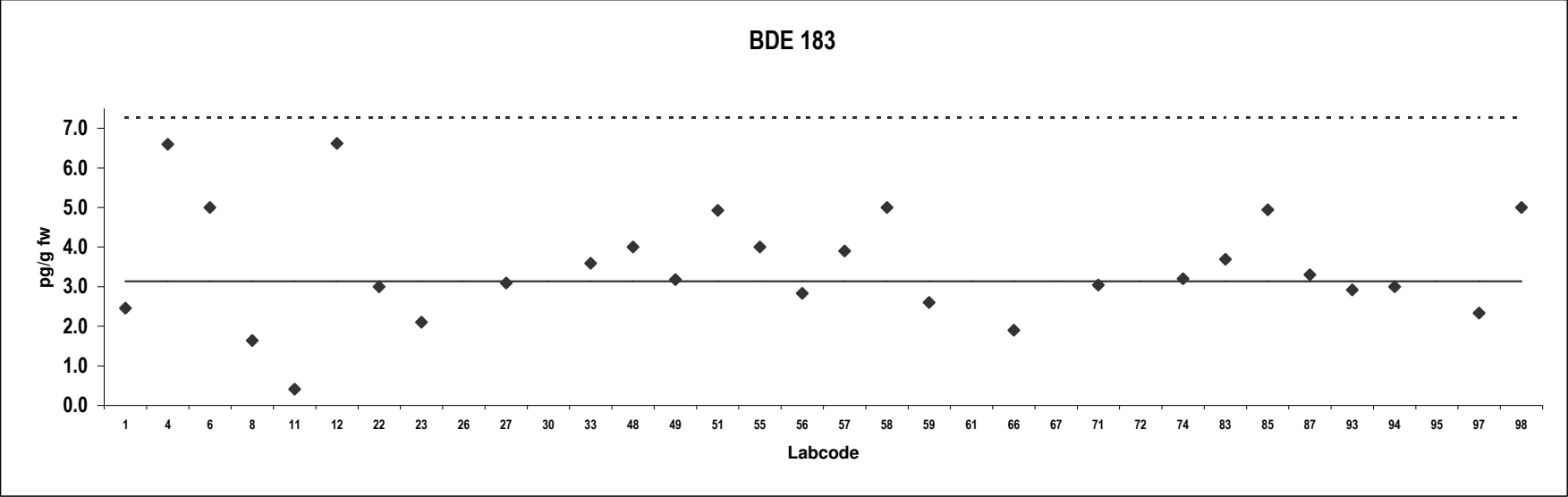
## Mozzarella Cheese

Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.5				
4	6.6				
6	5.0				
8	1.6	ND			
11	0.41				
12	6.6				
22	3.0	ND			
23	2.1				
26	688	Outlier			
27	3.1				
30	30	Outlier			
33	3.6				
48	4.0				
49	3.2				
51	4.9	ND			
55	4.0				
56	2.8				
57	3.9				
58	5.0	ND			
59	2.6				
61	17	Outlier,ND			
66	1.9				
67	14	Outlier			
71	3.0				
72	12	Outlier			
74	3.2				
83	3.7				
85	4.9	ND			
87	3.3				
93	2.9				
94	3.0				
95	10	Outlier,ND			
97	2.3				
98	5.0	ND			

### Consensus statistics

Consensus median, pg/g	3.1
Median all values pg/g	3.6
Consensus mean, pg/g	3.5
Standard deviation, pg/g	1.4
Relative standard deviation, %	40
No. of values reported	34
No. of values removed	6
No. of reported non-detects	8



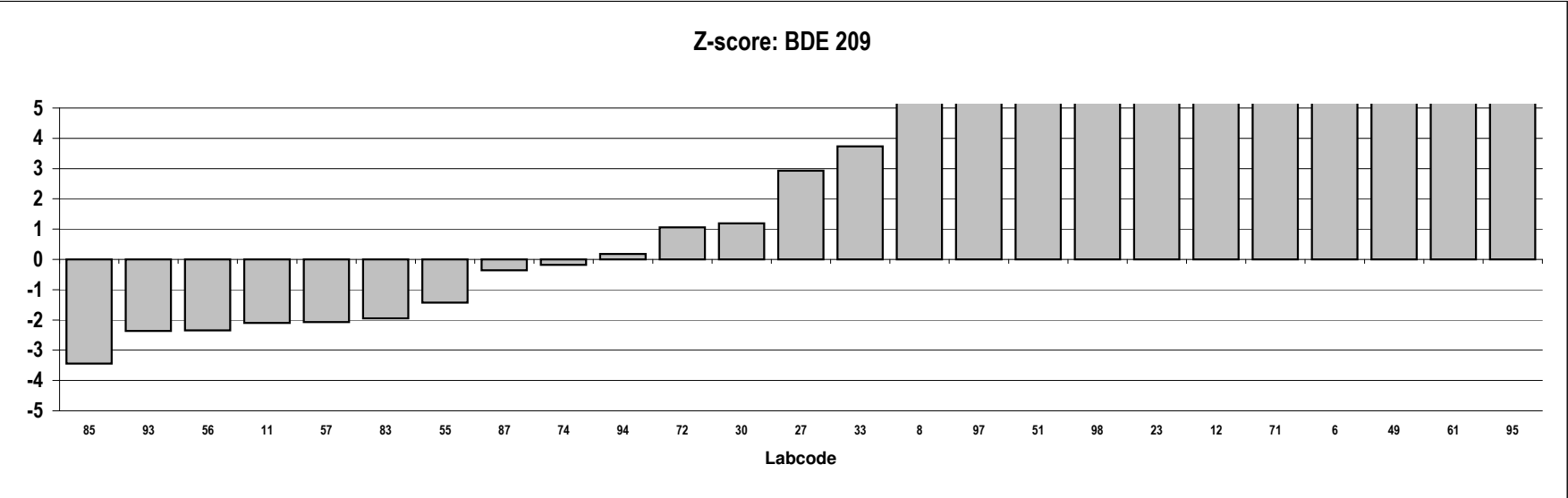
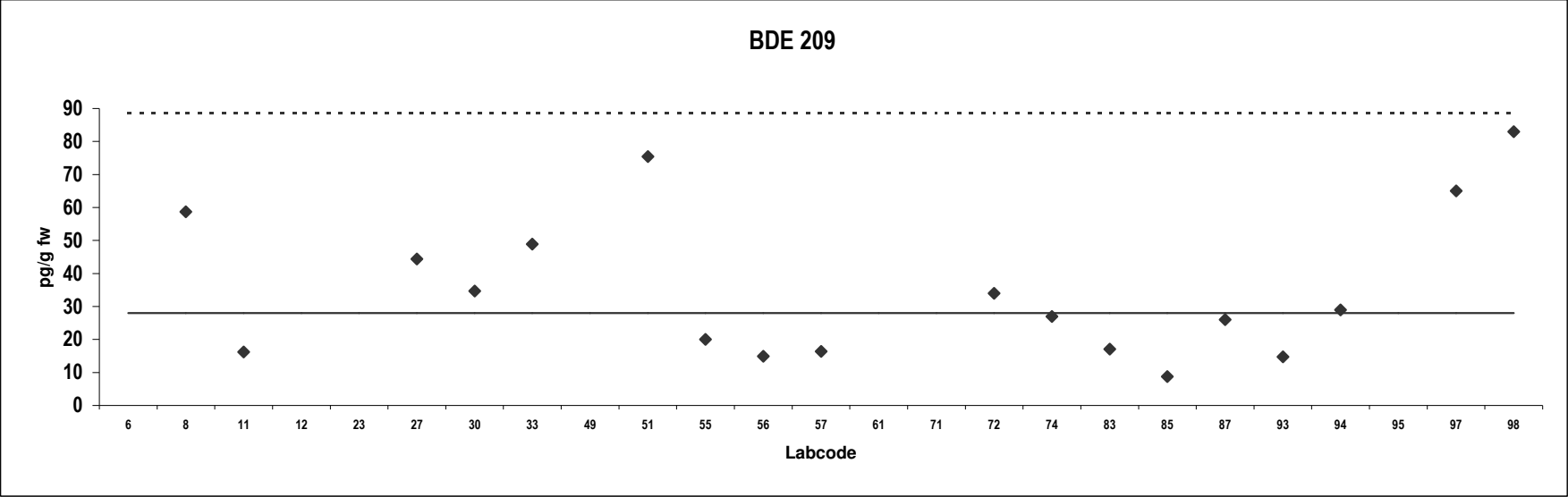
## Mozzarella Cheese

Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	300	Outlier,ND			
8	59				
11	16				
12	178	Outlier			
23	109	Outlier,ND			
27	44				
30	35				
33	49				
49	373	Outlier			
51	75				
55	20				
56	15				
57	16				
61	400	Outlier,ND			
71	297	Outlier			
72	34	ND			
74	27				
83	17				
85	8.7	ND			
87	26				
93	15				
94	29				
95	5000	Outlier,ND			
97	65				
98	83				

### Consensus statistics

Consensus median, pg/g	28
Median all values pg/g	44
Consensus mean, pg/g	35
Standard deviation, pg/g	23
Relative standard deviation, %	64
No. of values reported	25
No. of values removed	7
No. of reported non-detects	6



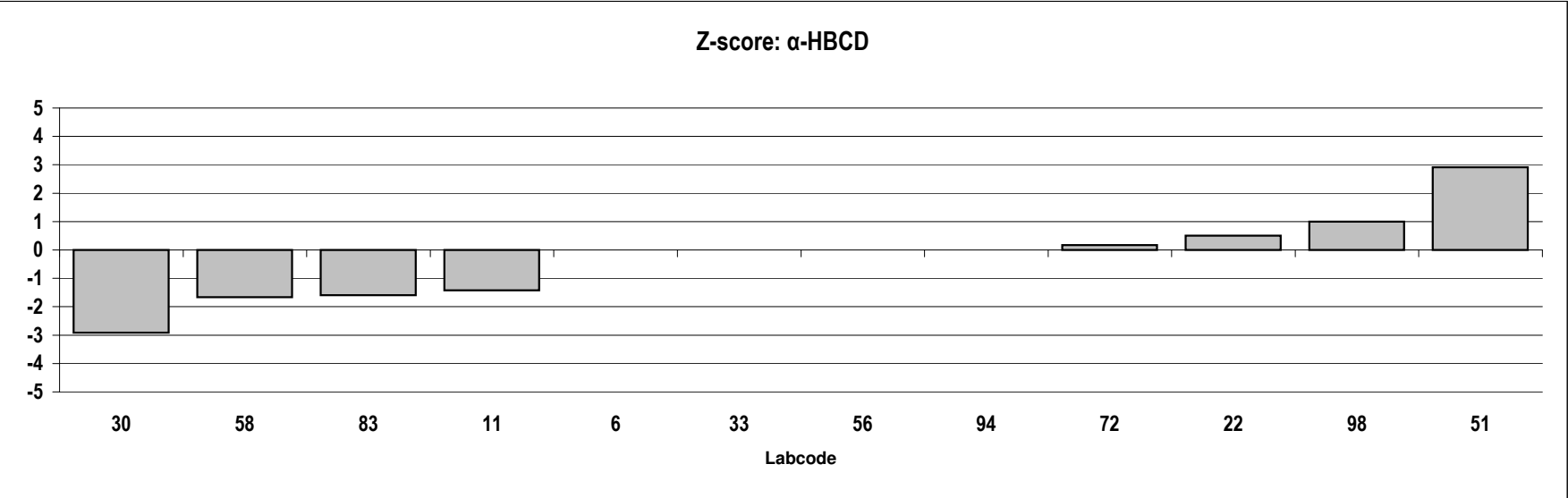
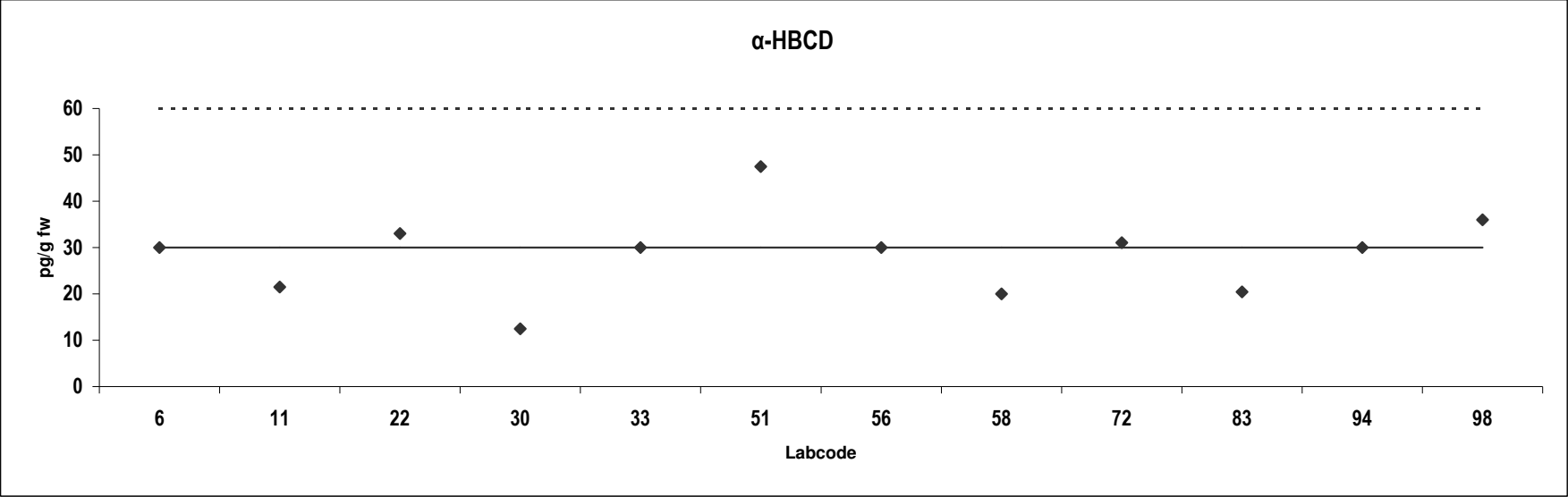
## Mozzarella Cheese

Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	30	ND			
11	21				
22	33				
30	13				
33	30	ND			
51	47	ND			
56	30	ND			
58	20	ND			
72	31				
83	20				
94	30				
98	36				

### Consensus statistics

Consensus median, pg/g	30
Median all values pg/g	30
Consensus mean, pg/g	28
Standard deviation, pg/g	9.0
Relative standard deviation, %	32
No. of values reported	12
No. of values removed	0
No. of reported non-detects	5



## Mozzarella Cheese

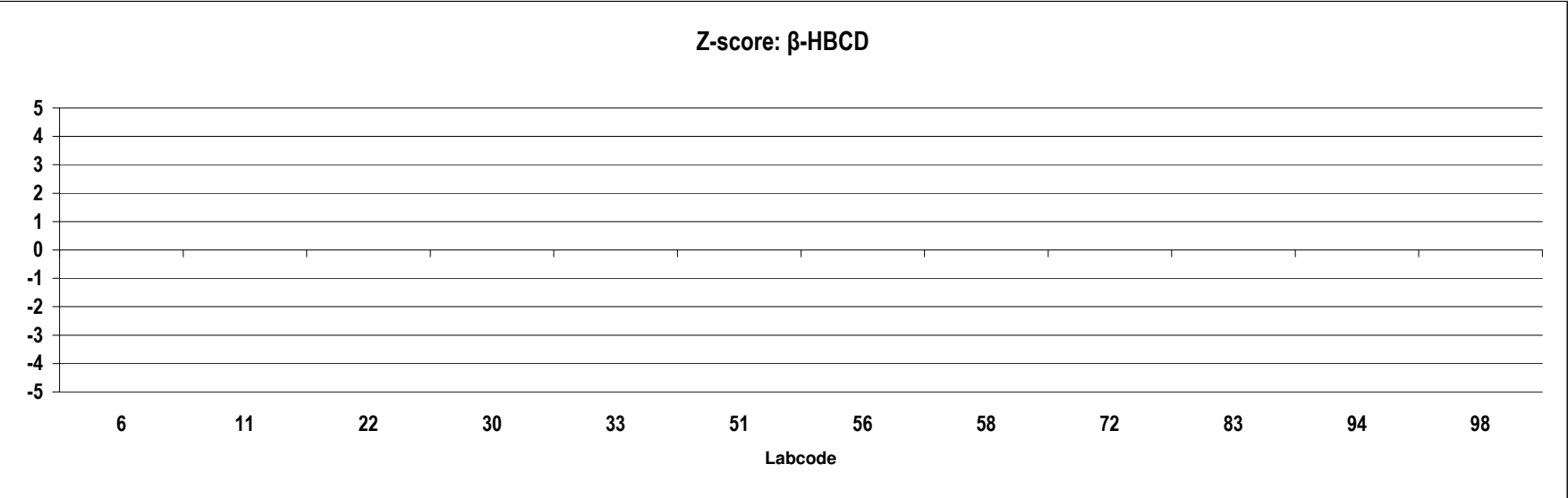
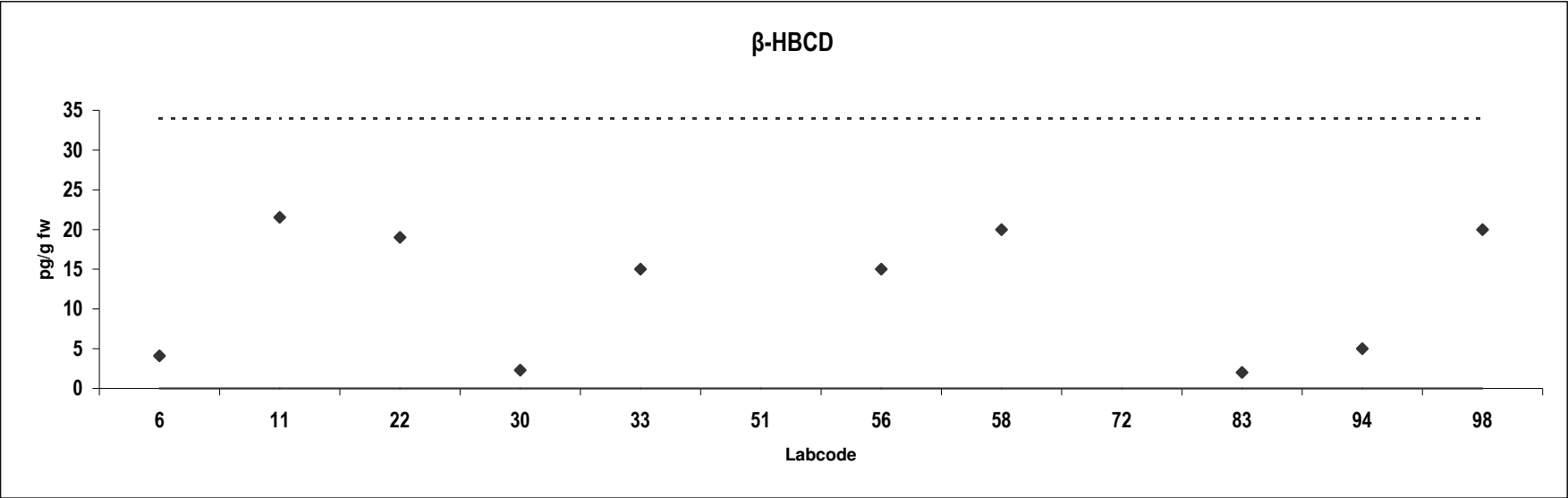
Congener:  $\beta$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	4.1	ND			
11	22	ND			
22	19	ND			
30	2.3	ND			
33	15	ND			
51	61	Outlier,ND			
56	15	ND			
58	20	ND			
72	55	Outlier,ND			
83	2.0	ND			
94	5.0	ND			
98	20	ND			

### Consensus statistics

Consensus median, pg/g	#NUM!
Median all values pg/g	17
Consensus mean, pg/g	12
Standard deviation, pg/g	8.1
Relative standard deviation, %	65
No. of values reported	12
No. of values removed	2
No. of reported non-detects	12





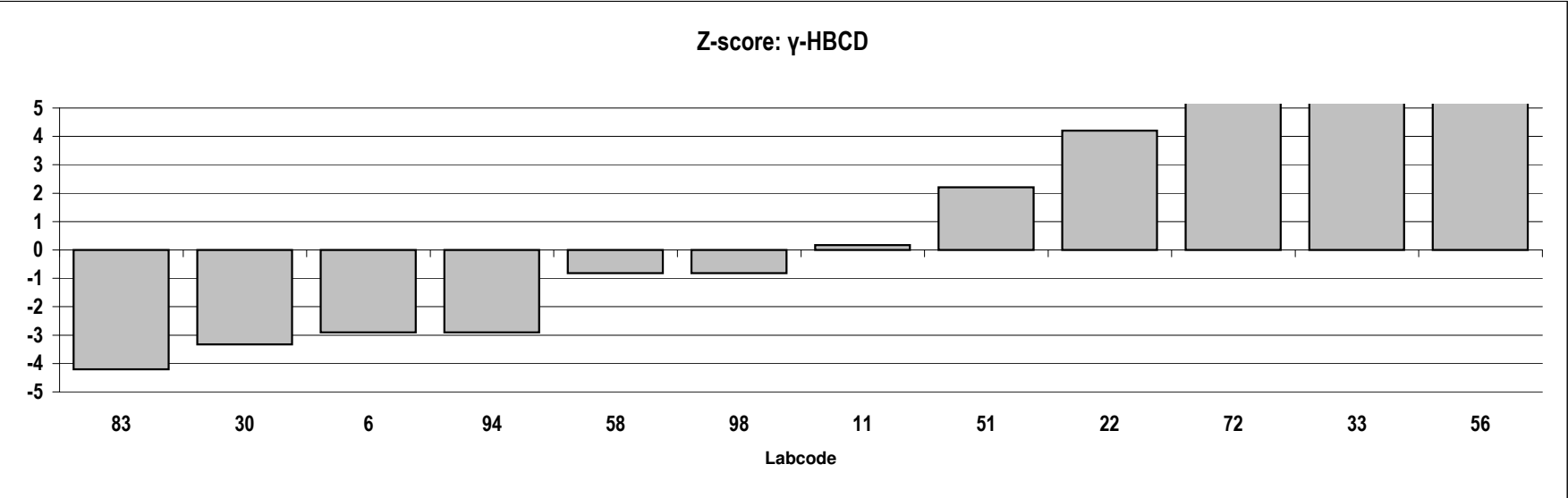
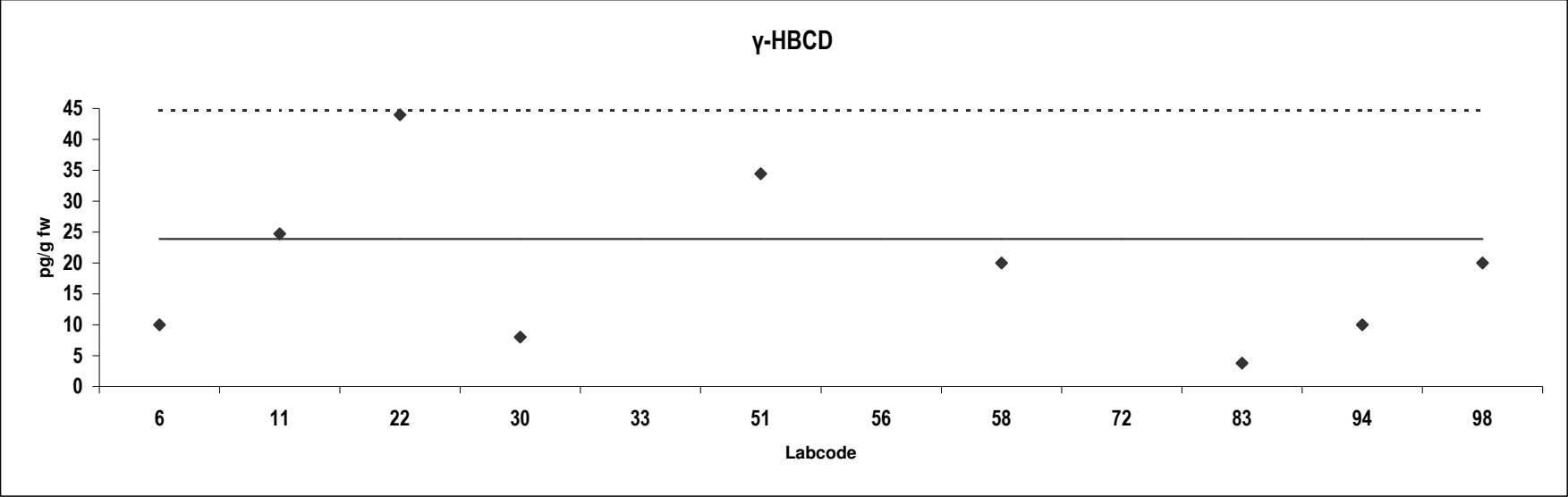
## Mozzarella Cheese

Congener:  $\gamma$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	10	ND			
11	25	ND			
22	44				
30	8.0	ND			
33	60	Outlier,ND			
51	34	ND			
56	60	Outlier,ND			
58	20	ND			
72	52	Outlier,ND			
83	3.8				
94	10	ND			
98	20	ND			

### Consensus statistics

Consensus median, pg/g	24
Median all values pg/g	22
Consensus mean, pg/g	19
Standard deviation, pg/g	13
Relative standard deviation, %	68
No. of values reported	12
No. of values removed	3
No. of reported non-detects	10



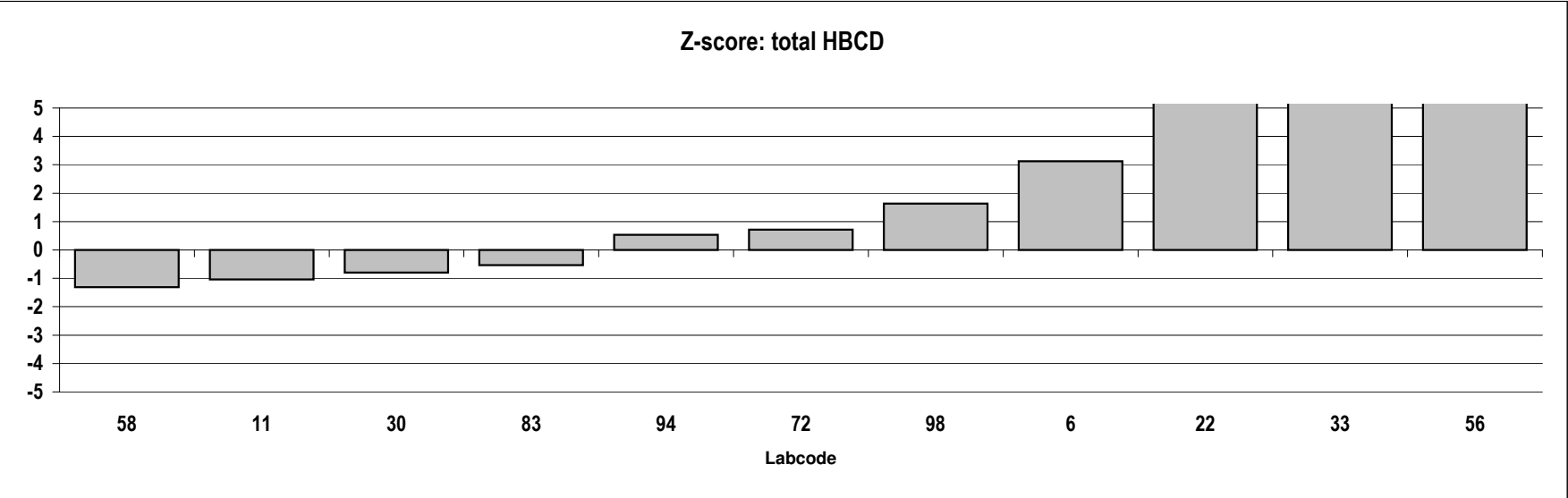
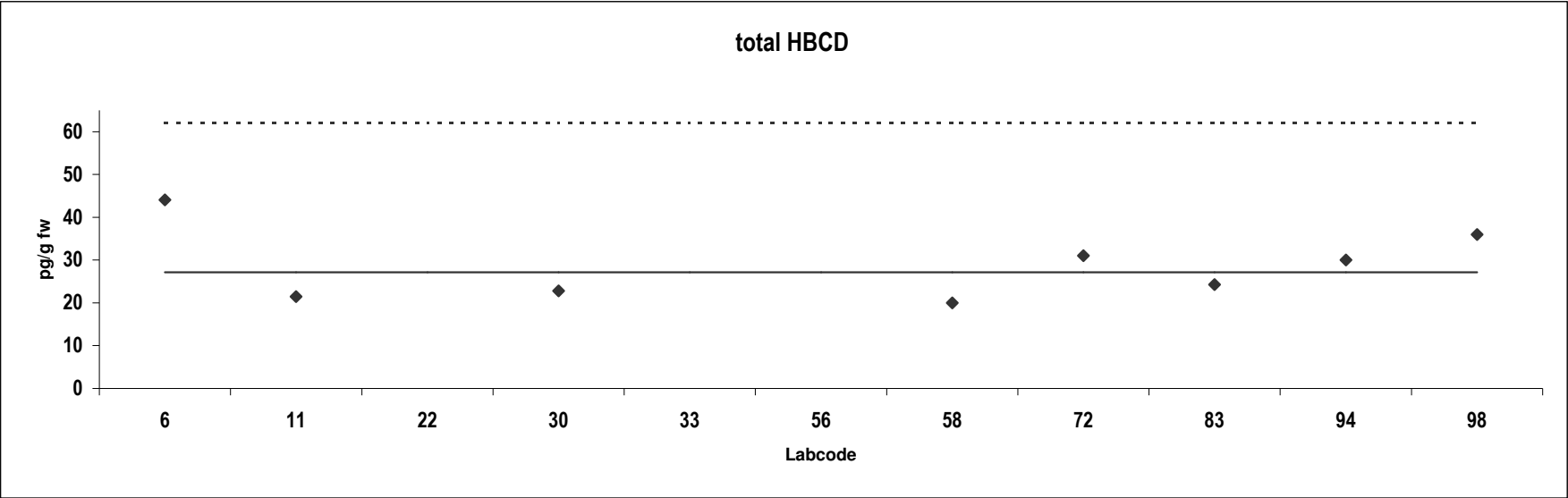
## Mozzarella Cheese

Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	44	ND			
11	21				
22	77	Outlier			
30	23				
33	105	Outlier,ND			
56	105	Outlier,ND			
58	20	ND			
72	31				
83	24				
94	30				
98	36				

### Consensus statistics

Consensus median, pg/g	27
Median all values pg/g	31
Consensus mean, pg/g	29
Standard deviation, pg/g	8.3
Relative standard deviation, %	29
No. of values reported	11
No. of values removed	3
No. of reported non-detects	4





## **Appendix 4:**

Presentation of results  
for egg





## Appendix 4: Presentation of results: Egg

### Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

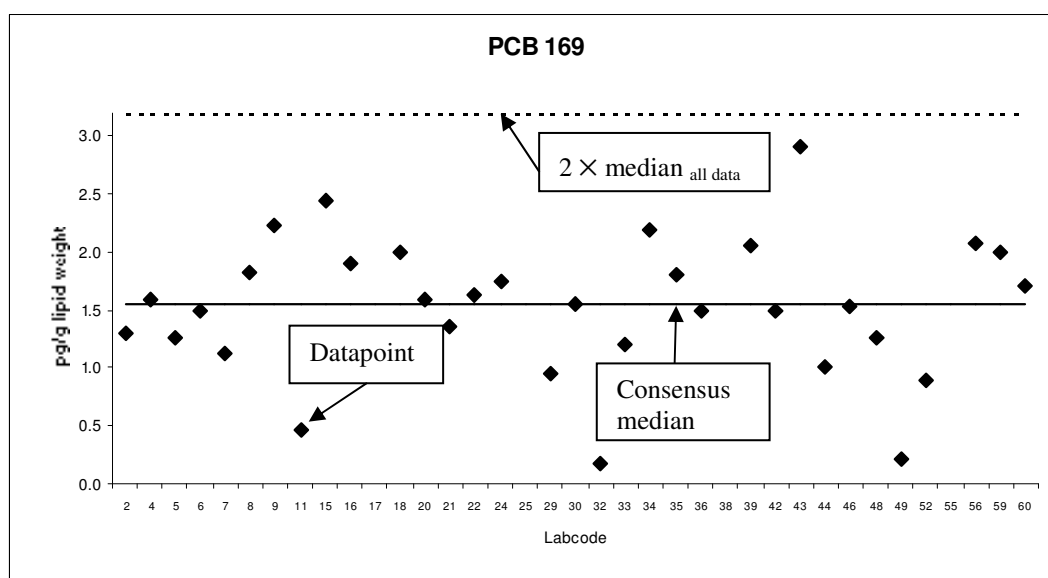
1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

### Statistic calculations for indicator PCBs, PBDEs and HBCD

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).
2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set. The NDs were also removed.
3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

The diagram shows the reported data up to approximately the limit for outliers ( $2 \times$  the first median).



### Z-Scores of individual congeners

Z-scores of each congener were calculated for each laboratory according to the following equation:

$$z = (x - X) / \sigma$$

where  $x$  = reported value;  $X$  = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm 20\%$  from the consensus value.

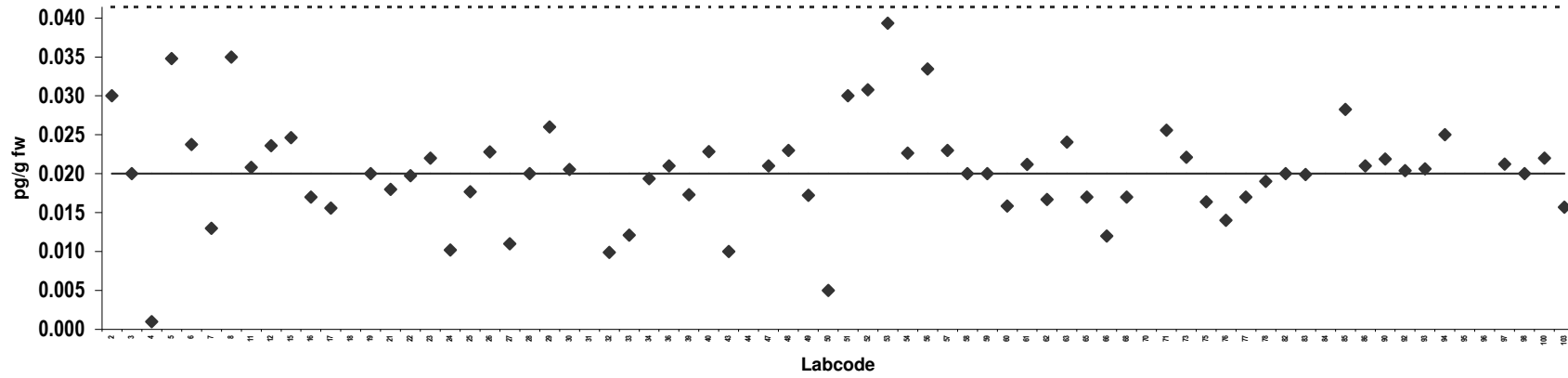
**Egg**  
Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030		60	0.016	
3	0.020		61	0.021	
4	0.0010	ND	62	0.017	
5	0.035		63	0.024	
6	0.024		65	0.017	
7	0.013		66	0.012	
8	0.035		68	0.017	
11	0.021		70	0.050	Outlier
12	0.024		71	0.026	
15	0.025		73	0.022	
16	0.017		75	0.016	
17	0.016		76	0.014	
18	0.42	Outlier	77	0.017	
19	0.020	ND	78	0.019	
21	0.018		82	0.020	
22	0.020		83	0.020	
23	0.022		84	0.12	Outlier,ND
24	0.010		85	0.028	
25	0.018		86	0.021	
26	0.023		90	0.022	
27	0.011		92	0.020	
28	0.020		93	0.021	
29	0.026		94	0.025	
30	0.021		95	0.21	Outlier,ND
31	0.21	Outlier	96	0.043	Outlier
32	0.0099	ND	97	0.021	
33	0.012		98	0.020	
34	0.019		100	0.022	
36	0.021		103	0.016	
39	0.017				
40	0.023				
43	0.010	ND			
44	0.11	Outlier,ND			
47	0.021				
48	0.023				
49	0.017				
50	0.0050	ND			
51	0.030				
52	0.031				
53	0.039				
54	0.023				
56	0.033				
57	0.023				
58	0.020				
59	0.020				

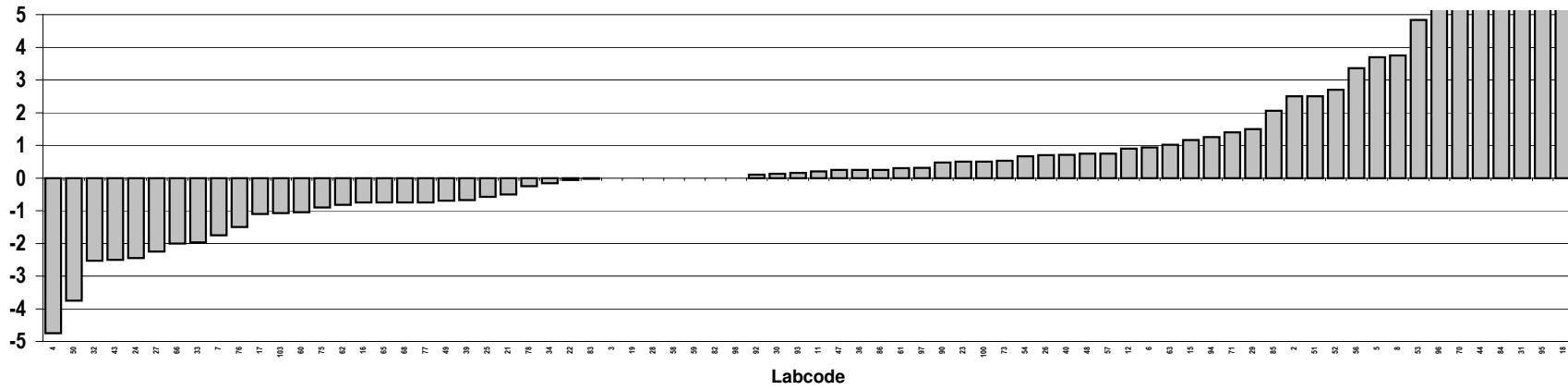
**Consensus statistics**

Consensus median, pg/g	0.020
Median all values pg/g	0.021
Consensus mean, pg/g	0.020
Standard deviation, pg/g	0.0066
Relative standard deviation, %	33
No. of values reported	74
No. of values removed	7
No. of reported non-detects	8

### 2,3,7,8 TCDD



### Z-score: 2,3,7,8 TCDD



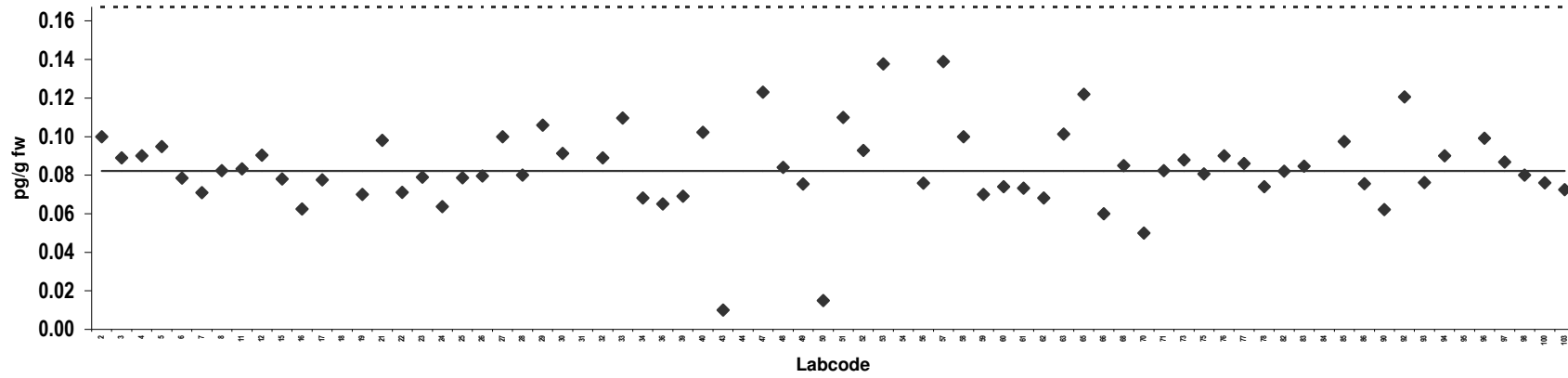
**Egg**  
Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.10		60	0.074	
3	0.089		61	0.073	
4	0.090		62	0.068	
5	0.095		63	0.10	
6	0.079		65	0.12	
7	0.071		66	0.060	
8	0.082		68	0.085	
11	0.083		70	0.050	ND
12	0.090		71	0.082	
15	0.078		73	0.088	
16	0.063		75	0.081	
17	0.078		76	0.090	
18	1.4	Outlier	77	0.086	
19	0.070		78	0.074	
21	0.098		82	0.082	
22	0.071		83	0.085	
23	0.079		84	0.17	Outlier
24	0.064		85	0.097	
25	0.079		86	0.076	
26	0.080		90	0.062	
27	0.10		92	0.12	
28	0.080		93	0.076	
29	0.11		94	0.090	
30	0.091		95	0.48	Outlier,ND
31	1.0	Outlier	96	0.099	
32	0.089		97	0.087	
33	0.11		98	0.080	
34	0.068		100	0.076	
36	0.065		103	0.073	
39	0.069				
40	0.10				
43	0.010	ND			
44	0.20	Outlier,ND			
47	0.12				
48	0.084				
49	0.075				
50	0.015	ND			
51	0.11				
52	0.093				
53	0.14				
54	0.17	Outlier			
56	0.076				
57	0.14				
58	0.10				
59	0.070				

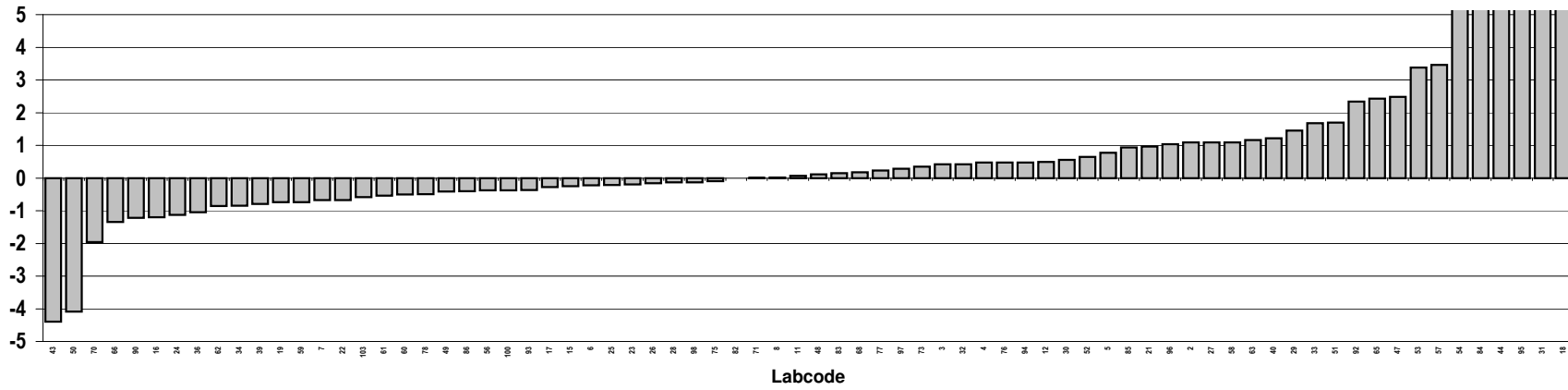
**Consensus statistics**

Consensus median, pg/g	0.082
Median all values pg/g	0.084
Consensus mean, pg/g	0.084
Standard deviation, pg/g	0.021
Relative standard deviation, %	26
No. of values reported	74
No. of values removed	6
No. of reported non-detects	5

### 1,2,3,7,8 PeCDD



### Z-score: 1,2,3,7,8 PeCDD



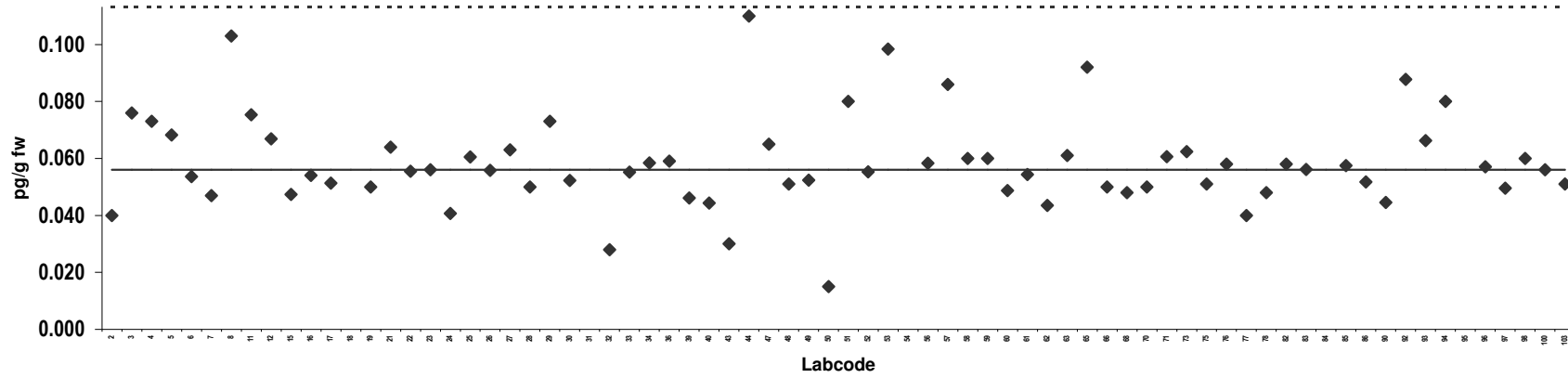
**Egg**  
Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.040		60	0.049	
3	0.076		61	0.054	
4	0.073		62	0.044	
5	0.068		63	0.061	
6	0.054		65	0.092	
7	0.047		66	0.050	
8	0.10		68	0.048	
11	0.075		70	0.050	ND
12	0.067		71	0.061	
15	0.047		73	0.062	
16	0.054		75	0.051	
17	0.051		76	0.058	
18	0.16	Outlier,ND	77	0.040	
19	0.050		78	0.048	
21	0.064		82	0.058	
22	0.055		83	0.056	
23	0.056		84	0.15	Outlier,ND
24	0.041		85	0.057	
25	0.061		86	0.052	
26	0.056		90	0.045	
27	0.063		92	0.088	
28	0.050		93	0.066	
29	0.073		94	0.080	
30	0.052		95	0.18	Outlier,ND
31	0.49	Outlier	96	0.057	
32	0.028	ND	97	0.050	
33	0.055		98	0.060	
34	0.058		100	0.056	
36	0.059		103	0.051	
39	0.046				
40	0.044				
43	0.030	ND			
44	0.11	ND			
47	0.065				
48	0.051				
49	0.052				
50	0.015	ND			
51	0.080				
52	0.055				
53	0.098				
54	0.16	Outlier			
56	0.058				
57	0.086				
58	0.060				
59	0.060				

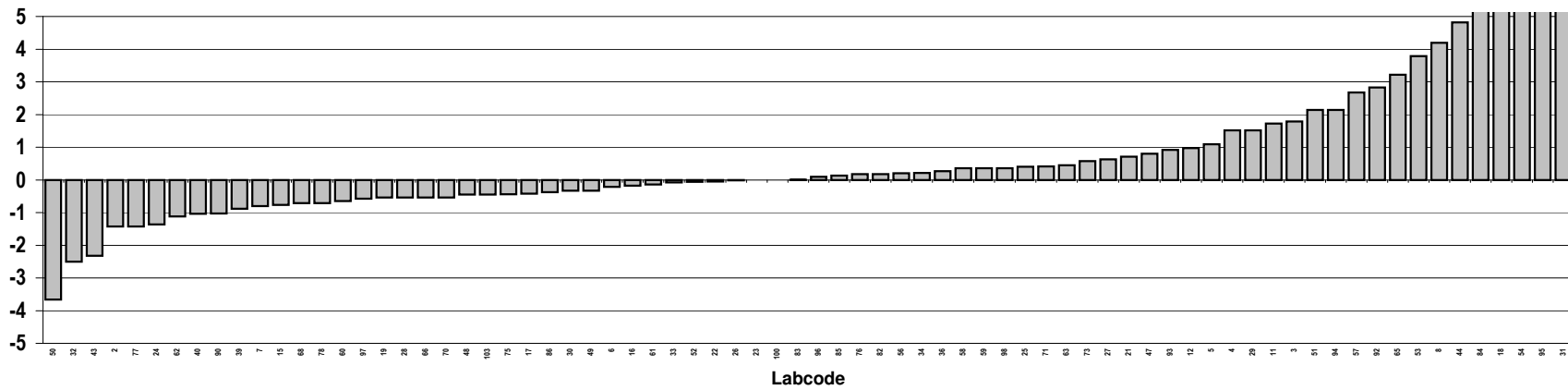
**Consensus statistics**

Consensus median, pg/g	0.056
Median all values pg/g	0.057
Consensus mean, pg/g	0.058
Standard deviation, pg/g	0.016
Relative standard deviation, %	28
No. of values reported	74
No. of values removed	5
No. of reported non-detects	8

1,2,3,4,7,8 HxCDD



Z-score: 1,2,3,4,7,8 HxCDD



**Egg**  
Congener: 1,2,3,6,7,8 HxCDD

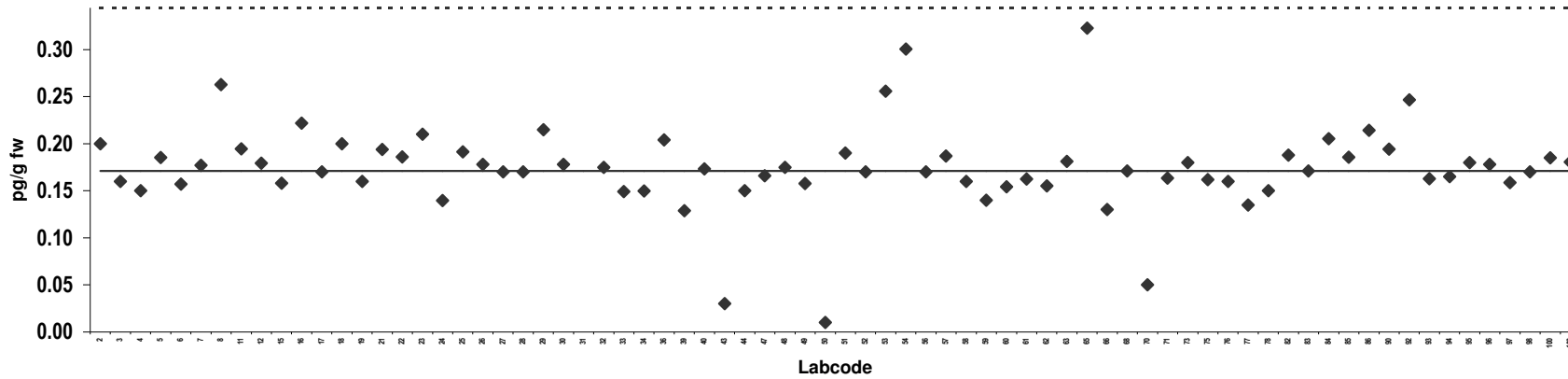
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.20		60	0.15	
3	0.16		61	0.16	
4	0.15		62	0.16	
5	0.19		63	0.18	
6	0.16		65	0.32	
7	0.18		66	0.13	
8	0.26		68	0.17	
11	0.19		70	0.050	ND
12	0.18		71	0.16	
15	0.16		73	0.18	
16	0.22		75	0.16	
17	0.17		76	0.16	
18	0.20	ND	77	0.14	
19	0.16		78	0.15	
21	0.19		82	0.19	
22	0.19		83	0.17	
23	0.21		84	0.21	
24	0.14		85	0.19	
25	0.19		86	0.21	
26	0.18		90	0.19	
27	0.17		92	0.25	
28	0.17		93	0.16	
29	0.22		94	0.17	
30	0.18		95	0.18	ND
31	2.3	Outlier	96	0.18	
32	0.18		97	0.16	
33	0.15		98	0.17	
34	0.15		100	0.19	
36	0.20		103	0.18	
39	0.13				
40	0.17				
43	0.030	ND			
44	0.15	ND			
47	0.17				
48	0.18				
49	0.16				
50	0.010	ND			
51	0.19				
52	0.17				
53	0.26				
54	0.30				
56	0.17				
57	0.19				
58	0.16				
59	0.14				

**Consensus statistics**

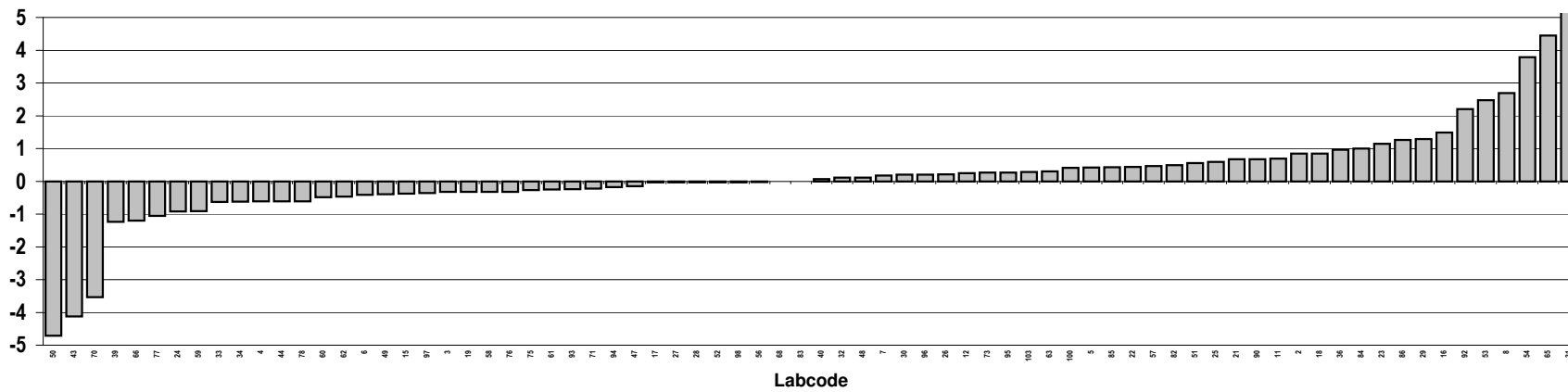
Consensus median, pg/g	0.17
Median all values pg/g	0.17
Consensus mean, pg/g	0.17
Standard deviation, pg/g	0.045
Relative standard deviation, %	26
No. of values reported	74
No. of values removed	1
No. of reported non-detects	6



1,2,3,6,7,8 HxCDD



Z-score: 1,2,3,6,7,8 HxCDD



**Egg**  
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.070		60	0.055	
3	0.061		61	0.064	
4	0.0028	ND	62	0.041	
5	0.082		63	0.078	
6	0.063		65	0.086	
7	0.069		66	0.030	
8	0.13		68	0.074	
11	0.064		70	0.050	ND
12	0.079		71	0.067	
15	0.060		73	0.074	
16	0.065		75	0.060	
17	0.067		76	0.068	
18	0.059	ND	77	0.063	
19	0.070		78	0.063	
21	0.084		82	0.069	
22	0.069		83	0.071	
23	0.073		84	0.16	Outlier,ND
24	0.15	Outlier	85	0.075	
25	0.061		86	0.088	
26	0.10		90	0.089	
27	0.060		92	0.12	
28	0.070		93	0.068	
29	0.077		94	0.075	
30	0.067		95	0.17	Outlier,ND
31	0.41	Outlier	96	0.087	
32	0.093		97	0.033	
33	0.071		98	0.060	
34	0.057		100	0.050	
36	0.061		103	0.058	
39	0.052				
40	0.071				
43	0.020	ND			
44	0.15	Outlier,ND			
47	0.058				
48	0.067				
49	0.062				
50	0.010	ND			
51	0.10				
52	0.048				
53	0.16	Outlier			
54	0.19	Outlier			
56	0.070				
57	0.065				
58	0.060				
59	0.060				

**Consensus statistics**

Consensus median, pg/g	0.067
Median all values pg/g	0.068
Consensus mean, pg/g	0.066
Standard deviation, pg/g	0.020
Relative standard deviation, %	31
No. of values reported	74
No. of values removed	7
No. of reported non-detects	8



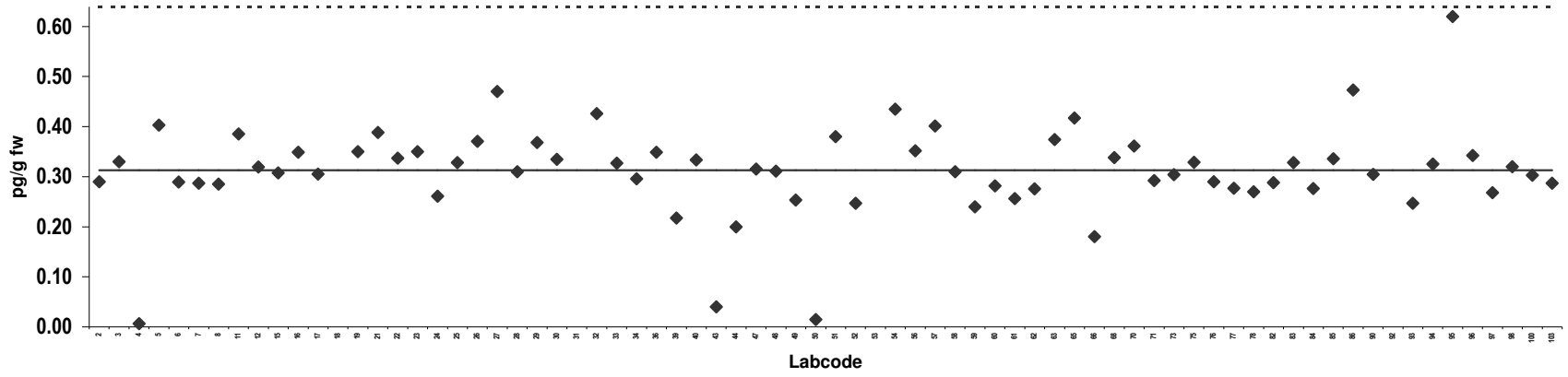
**Egg**  
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.29		60	0.28	
3	0.33		61	0.26	
4	0.0063	ND	62	0.28	
5	0.40		63	0.37	
6	0.29		65	0.42	
7	0.29		66	0.18	
8	0.29		68	0.34	
11	0.39		70	0.36	
12	0.32		71	0.29	
15	0.31		73	0.30	
16	0.35		75	0.33	
17	0.31		76	0.29	
18	1.9	Outlier	77	0.28	
19	0.35		78	0.27	
21	0.39		82	0.29	
22	0.34		83	0.33	
23	0.35		84	0.28	ND
24	0.26		85	0.34	
25	0.33		86	0.47	
26	0.37		90	0.30	
27	0.47		92	0.66	Outlier
28	0.31		93	0.25	
29	0.37		94	0.33	
30	0.33		95	0.62	
31	3.5	Outlier	96	0.34	
32	0.43		97	0.27	
33	0.33		98	0.32	
34	0.30		100	0.30	
36	0.35		103	0.29	
39	0.22				
40	0.33				
43	0.040	ND			
44	0.20	ND			
47	0.32				
48	0.31				
49	0.25				
50	0.015	ND			
51	0.38				
52	0.25				
53	0.69	Outlier			
54	0.43				
56	0.35				
57	0.40				
58	0.31				
59	0.24				

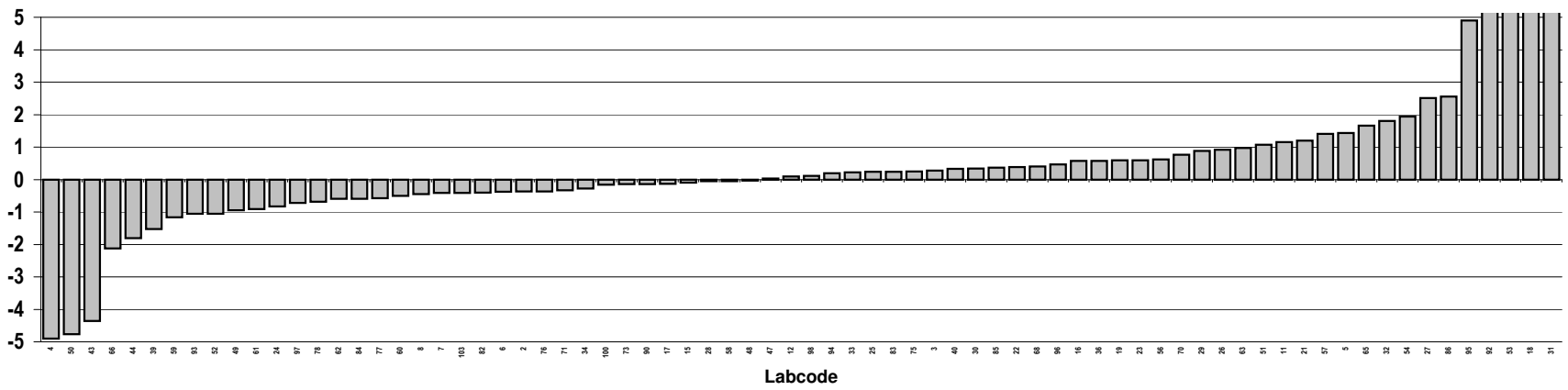
**Consensus statistics**

Consensus median, pg/g	0.31
Median all values pg/g	0.32
Consensus mean, pg/g	0.31
Standard deviation, pg/g	0.091
Relative standard deviation, %	29
No. of values reported	74
No. of values removed	4
No. of reported non-detects	5

### 1,2,3,4,6,7,8 HpCDD



### Z-score: 1,2,3,4,6,7,8 HpCDD

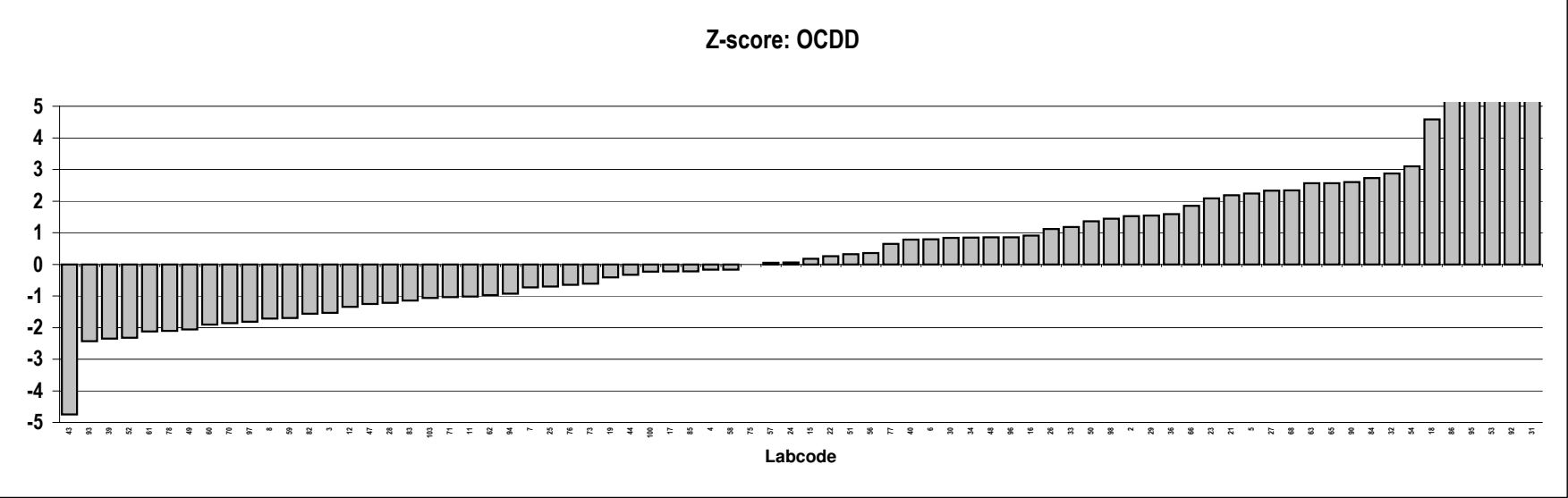
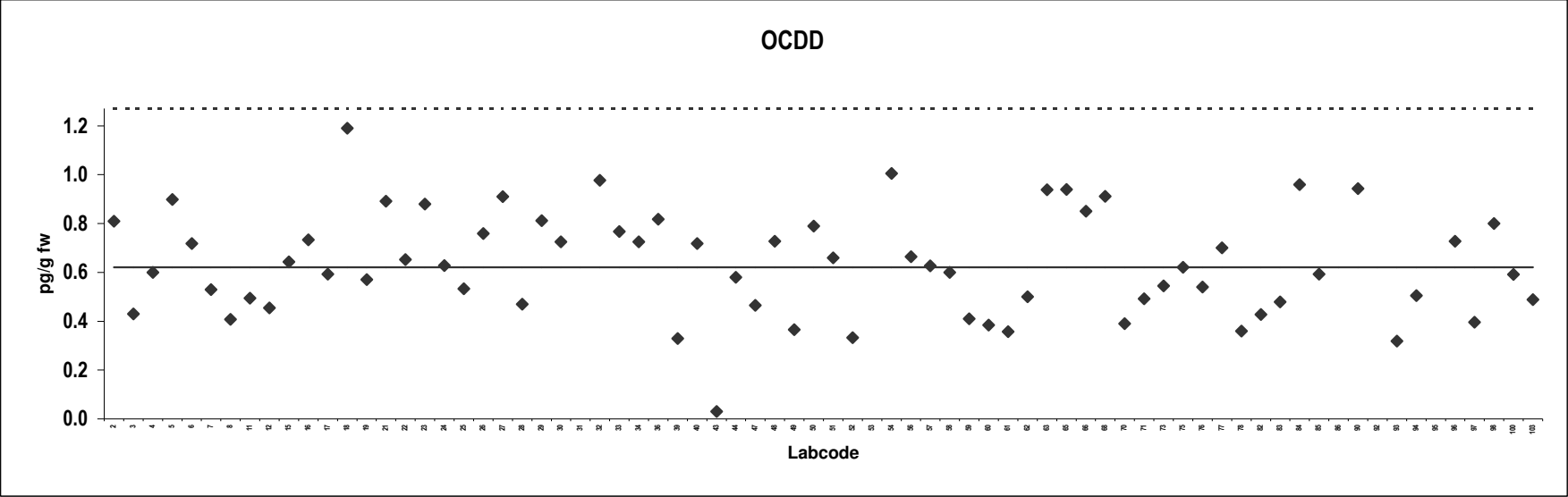


**Egg**  
Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.81		60	0.38	
3	0.43		61	0.36	
4	0.60		62	0.50	ND
5	0.90		63	0.94	
6	0.72		65	0.94	
7	0.53		66	0.85	
8	0.41		68	0.91	
11	0.49		70	0.39	
12	0.45		71	0.49	
15	0.64		73	0.55	
16	0.73		75	0.62	
17	0.59		76	0.54	
18	1.2		77	0.70	
19	0.57		78	0.36	
21	0.89		82	0.43	
22	0.65		83	0.48	
23	0.88		84	0.96	
24	0.63		85	0.59	
25	0.53		86	1.4	Outlier
26	0.76		90	0.94	
27	0.91		92	4.4	Outlier
28	0.47		93	0.32	
29	0.81		94	0.51	
30	0.72		95	1.5	Outlier
31	6.7	Outlier	96	0.73	
32	0.98		97	0.40	
33	0.77		98	0.80	
34	0.73		100	0.59	
36	0.82		103	0.49	
39	0.33				
40	0.72				
43	0.031				
44	0.58				
47	0.47				
48	0.73				
49	0.37				
50	0.79				
51	0.66				
52	0.33				
53	1.7	Outlier			
54	1.0				
56	0.66				
57	0.63				
58	0.60	ND			
59	0.41				

**Consensus statistics**

Consensus median, pg/g	0.62
Median all values pg/g	0.64
Consensus mean, pg/g	0.63
Standard deviation, pg/g	0.21
Relative standard deviation, %	34
No. of values reported	74
No. of values removed	5
No. of reported non-detects	2



**Egg**  
Congener: 2,3,7,8 TCDF

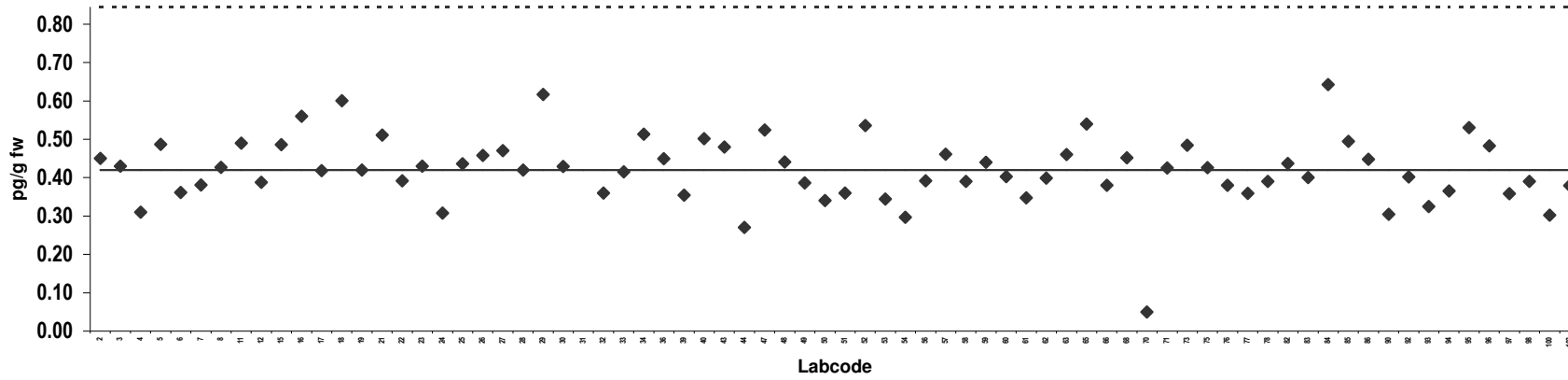
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.45		60	0.40	
3	0.43		61	0.35	
4	0.31		62	0.40	
5	0.49		63	0.46	
6	0.36		65	0.54	
7	0.38		66	0.38	
8	0.43		68	0.45	
11	0.49		70	0.050	ND
12	0.39		71	0.42	
15	0.49		73	0.48	
16	0.56		75	0.43	
17	0.42		76	0.38	
18	0.60		77	0.36	
19	0.42		78	0.39	
21	0.51		82	0.44	
22	0.39		83	0.40	
23	0.43		84	0.64	
24	0.31		85	0.49	
25	0.44		86	0.45	
26	0.46		90	0.30	
27	0.47		92	0.40	
28	0.42		93	0.32	
29	0.62		94	0.37	
30	0.43		95	0.53	
31	5.2	Outlier	96	0.48	
32	0.36		97	0.36	
33	0.41		98	0.39	
34	0.51		100	0.30	
36	0.45		103	0.38	
39	0.35				
40	0.50				
43	0.48				
44	0.27				
47	0.52				
48	0.44				
49	0.39				
50	0.34				
51	0.36				
52	0.54				
53	0.34				
54	0.30				
56	0.39				
57	0.46				
58	0.39				
59	0.44				

**Consensus statistics**

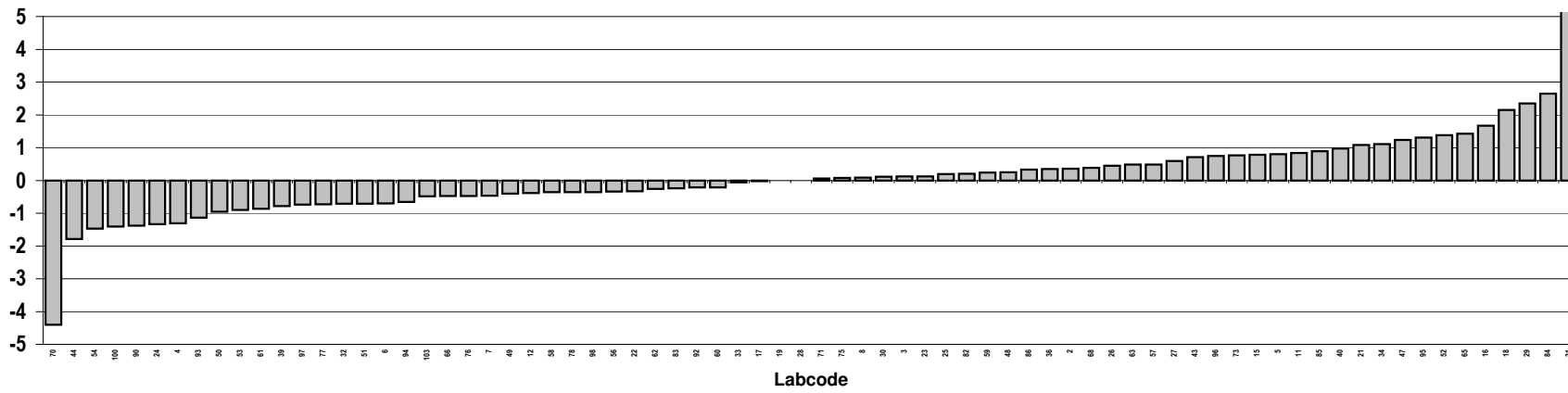
Consensus median, pg/g	0.42
Median all values pg/g	0.42
Consensus mean, pg/g	0.42
Standard deviation, pg/g	0.088
Relative standard deviation, %	21
No. of values reported	74
No. of values removed	1
No. of reported non-detects	1



### 2,3,7,8 TCDF



### Z-score: 2,3,7,8 TCDF



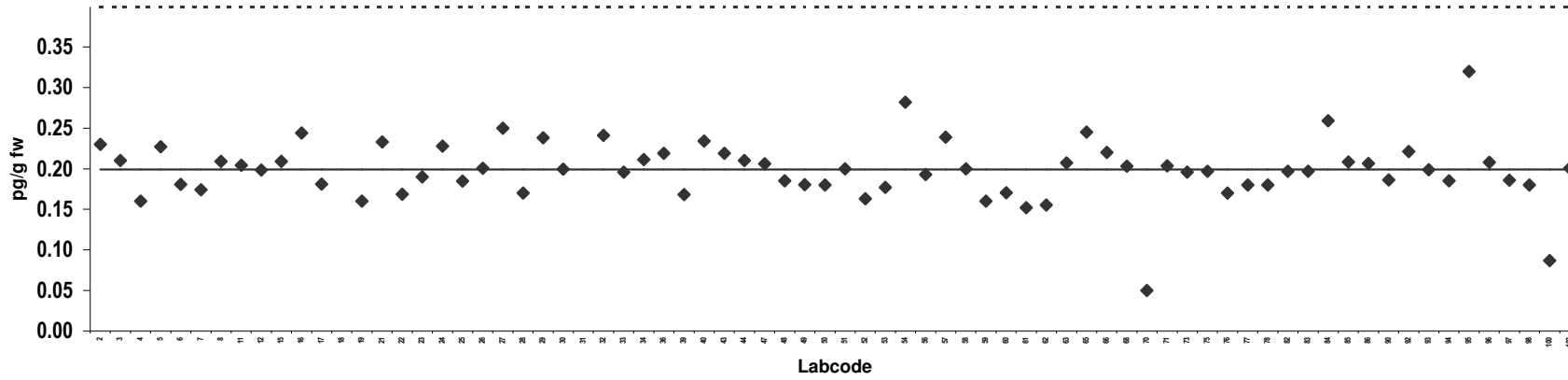
**Egg**  
Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.23		60	0.17	
3	0.21		61	0.15	
4	0.16		62	0.16	
5	0.23		63	0.21	
6	0.18		65	0.25	
7	0.17		66	0.22	
8	0.21		68	0.20	
11	0.20		70	0.050	ND
12	0.20		71	0.20	
15	0.21		73	0.20	
16	0.24		75	0.20	
17	0.18		76	0.17	
18	0.85	Outlier	77	0.18	
19	0.16		78	0.18	
21	0.23		82	0.20	
22	0.17		83	0.20	
23	0.19		84	0.26	
24	0.23		85	0.21	
25	0.18		86	0.21	
26	0.20		90	0.19	
27	0.25		92	0.22	
28	0.17		93	0.20	
29	0.24		94	0.19	
30	0.20		95	0.32	ND
31	2.3	Outlier	96	0.21	
32	0.24		97	0.19	
33	0.20		98	0.18	
34	0.21		100	0.087	
36	0.22		103	0.20	
39	0.17				
40	0.23				
43	0.22				
44	0.21				
47	0.21				
48	0.19				
49	0.18				
50	0.18				
51	0.20				
52	0.16				
53	0.18				
54	0.28				
56	0.19				
57	0.24				
58	0.20				
59	0.16				

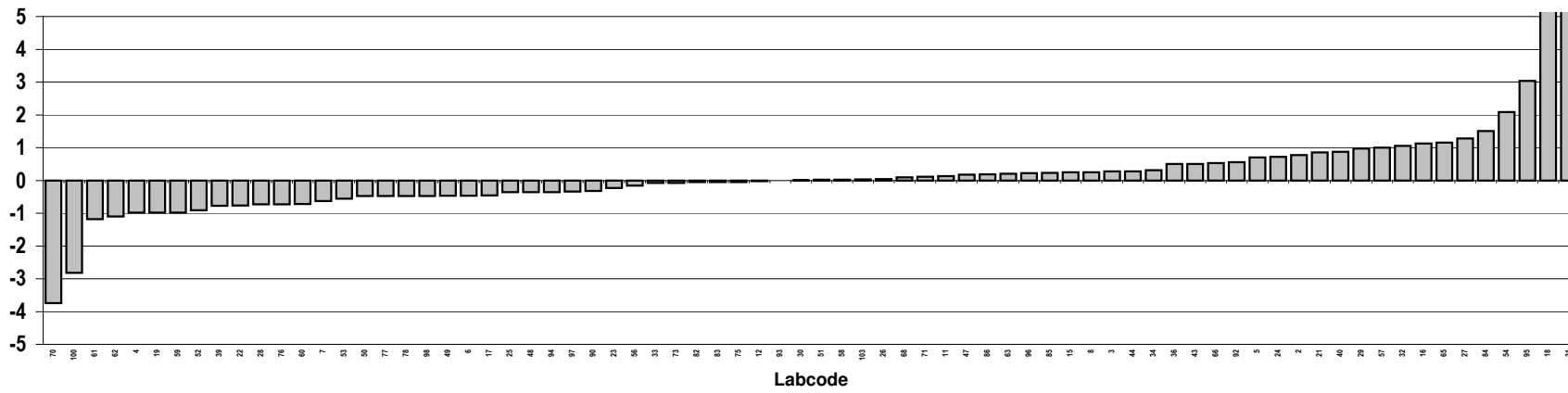
**Consensus statistics**

Consensus median, pg/g	0.20
Median all values pg/g	0.20
Consensus mean, pg/g	0.20
Standard deviation, pg/g	0.037
Relative standard deviation, %	19
No. of values reported	74
No. of values removed	2
No. of reported non-detects	2

1,2,3,7,8 PeCDF



Z-score: 1,2,3,7,8 PeCDF



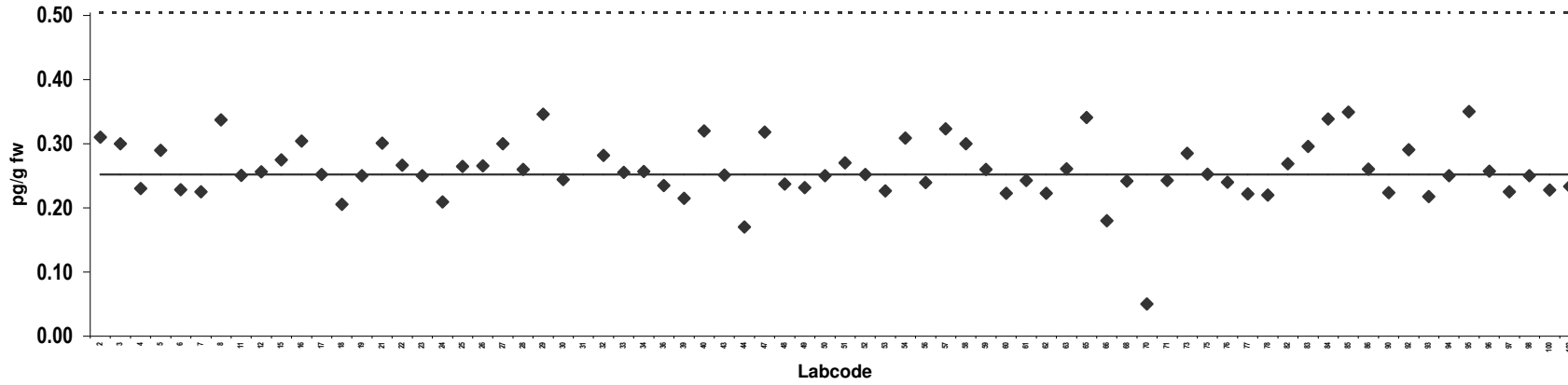
**Egg**  
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.31		60	0.22	
3	0.30		61	0.24	
4	0.23		62	0.22	
5	0.29		63	0.26	
6	0.23		65	0.34	
7	0.23		66	0.18	
8	0.34		68	0.24	
11	0.25		70	0.050	ND
12	0.26		71	0.24	
15	0.27		73	0.29	
16	0.30		75	0.25	
17	0.25		76	0.24	
18	0.21		77	0.22	
19	0.25		78	0.22	
21	0.30		82	0.27	
22	0.27		83	0.30	
23	0.25		84	0.34	
24	0.21		85	0.35	
25	0.26		86	0.26	
26	0.27		90	0.22	
27	0.30		92	0.29	
28	0.26		93	0.22	
29	0.35		94	0.25	
30	0.24		95	0.35	ND
31	3.2	Outlier	96	0.26	
32	0.28		97	0.23	
33	0.26		98	0.25	
34	0.26		100	0.23	
36	0.24		103	0.23	
39	0.22				
40	0.32				
43	0.25				
44	0.17				
47	0.32				
48	0.24				
49	0.23				
50	0.25				
51	0.27				
52	0.25				
53	0.23				
54	0.31				
56	0.24				
57	0.32				
58	0.30				
59	0.26				

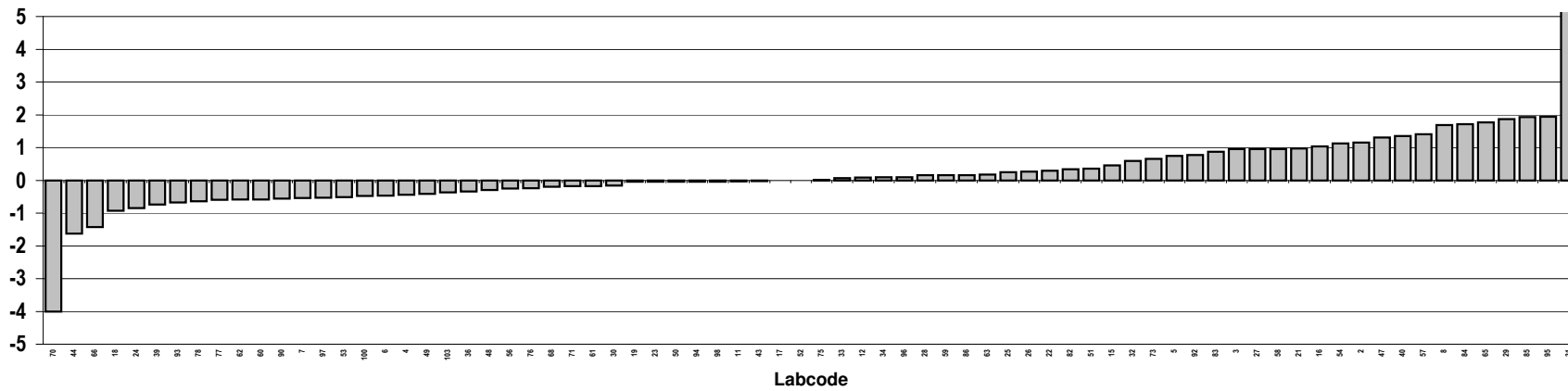
**Consensus statistics**

Consensus median, pg/g	0.25
Median all values pg/g	0.25
Consensus mean, pg/g	0.26
Standard deviation, pg/g	0.047
Relative standard deviation, %	18
No. of values reported	74
No. of values removed	1
No. of reported non-detects	2

### 2,3,4,7,8 PeCDF



### Z-score: 2,3,4,7,8 PeCDF



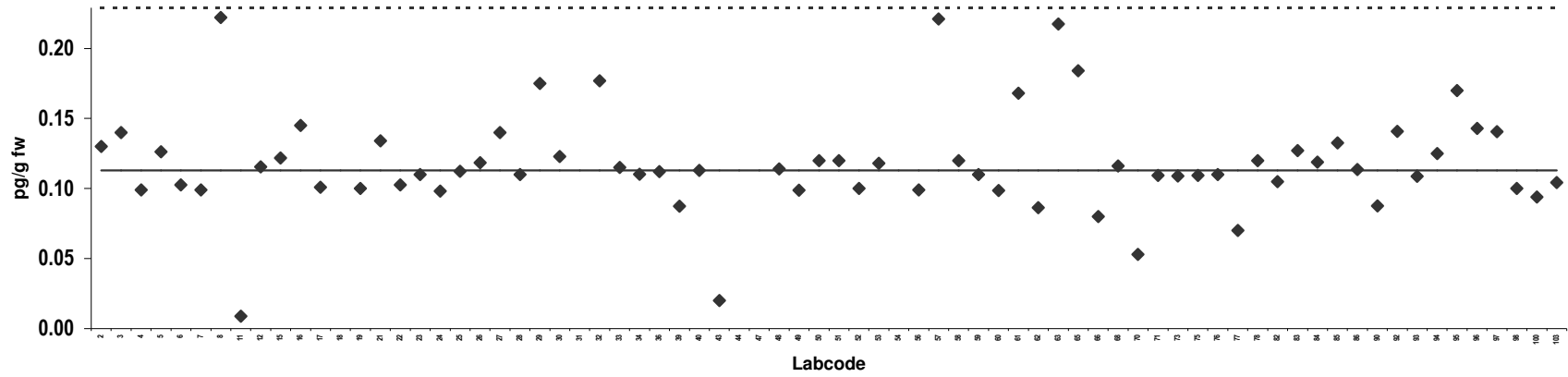
**Egg**  
Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.13		60	0.099	
3	0.14		61	0.17	
4	0.099		62	0.086	
5	0.13		63	0.22	
6	0.10		65	0.18	
7	0.099		66	0.080	
8	0.22		68	0.12	
11	0.0090	ND	70	0.053	
12	0.12		71	0.11	
15	0.12		73	0.11	
16	0.15		75	0.11	
17	0.10		76	0.11	
18	0.40	Outlier	77	0.070	
19	0.10		78	0.12	
21	0.13		82	0.11	
22	0.10		83	0.13	
23	0.11		84	0.12	ND
24	0.098		85	0.13	
25	0.11		86	0.11	
26	0.12		90	0.088	
27	0.14		92	0.14	
28	0.11		93	0.11	
29	0.18		94	0.13	
30	0.12		95	0.17	ND
31	1.5	Outlier	96	0.14	
32	0.18		97	0.14	
33	0.12		98	0.10	
34	0.11		100	0.094	
36	0.11		103	0.10	
39	0.087				
40	0.11				
43	0.020	ND			
44	0.30	Outlier,ND			
47	0.28	Outlier			
48	0.11				
49	0.099				
50	0.12				
51	0.12				
52	0.10				
53	0.12				
54	0.25	Outlier			
56	0.099				
57	0.22				
58	0.12				
59	0.11				

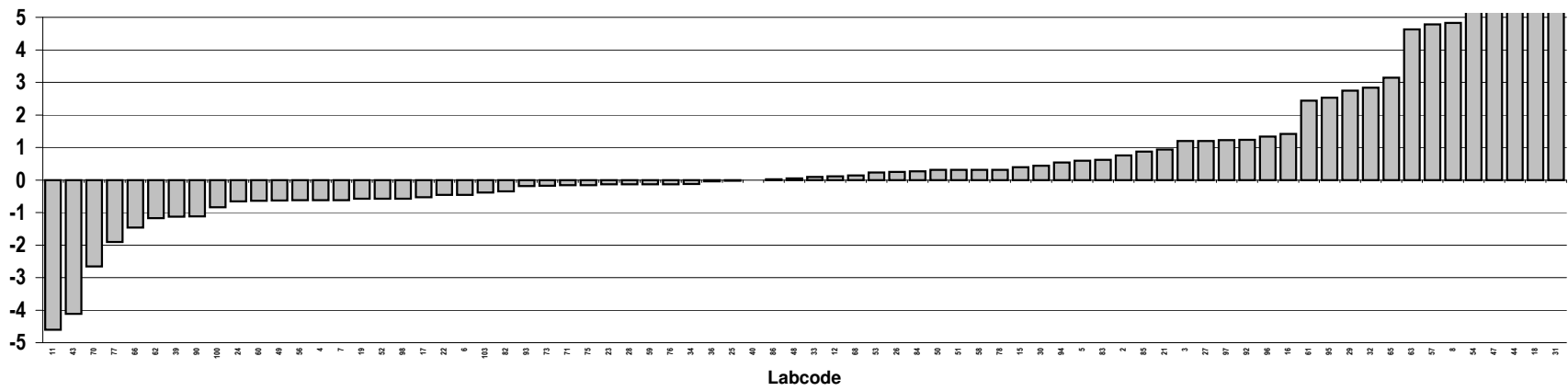
**Consensus statistics**

Consensus median, pg/g	0.11
Median all values pg/g	0.11
Consensus mean, pg/g	0.12
Standard deviation, pg/g	0.036
Relative standard deviation, %	31
No. of values reported	74
No. of values removed	5
No. of reported non-detects	5

1,2,3,4,7,8 HxCDF



Z-score: 1,2,3,4,7,8 HxCDF



**Egg**  
Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.10		60	0.080	
3	0.094		61	0.083	
4	0.090		62	0.076	
5	0.12		63	0.13	
6	0.083		65	0.18	
7	0.074		66	0.090	
8	0.21	Outlier	68	0.088	
11	0.15		70	0.082	
12	0.10		71	0.097	
15	0.10		73	0.099	
16	0.12		75	0.097	
17	0.10		76	0.091	
18	0.94	Outlier	77	0.012	ND
19	0.080		78	0.079	
21	0.10		82	0.093	
22	0.078		83	0.10	
23	0.093		84	0.12	
24	0.083		85	0.094	
25	0.090		86	0.097	
26	0.10		90	0.079	
27	0.12		92	0.14	
28	0.10		93	0.083	
29	0.13		94	0.085	
30	0.093		95	0.098	ND
31	1.1	Outlier	96	0.097	
32	0.050		97	0.091	
33	0.10		98	0.090	
34	0.089		100	0.10	
36	0.11		103	0.086	
39	0.075				
40	0.091				
43	0.010	ND			
44	0.30	Outlier,ND			
47	0.11				
48	0.094				
49	0.080				
50	0.010	ND			
51	0.10				
52	0.086				
53	0.098				
54	0.26	Outlier			
56	0.079				
57	0.13				
58	0.10				
59	0.10				

**Consensus statistics**

Consensus median, pg/g	0.094
Median all values pg/g	0.096
Consensus mean, pg/g	0.093
Standard deviation, pg/g	0.026
Relative standard deviation, %	28
No. of values reported	74
No. of values removed	5
No. of reported non-detects	5





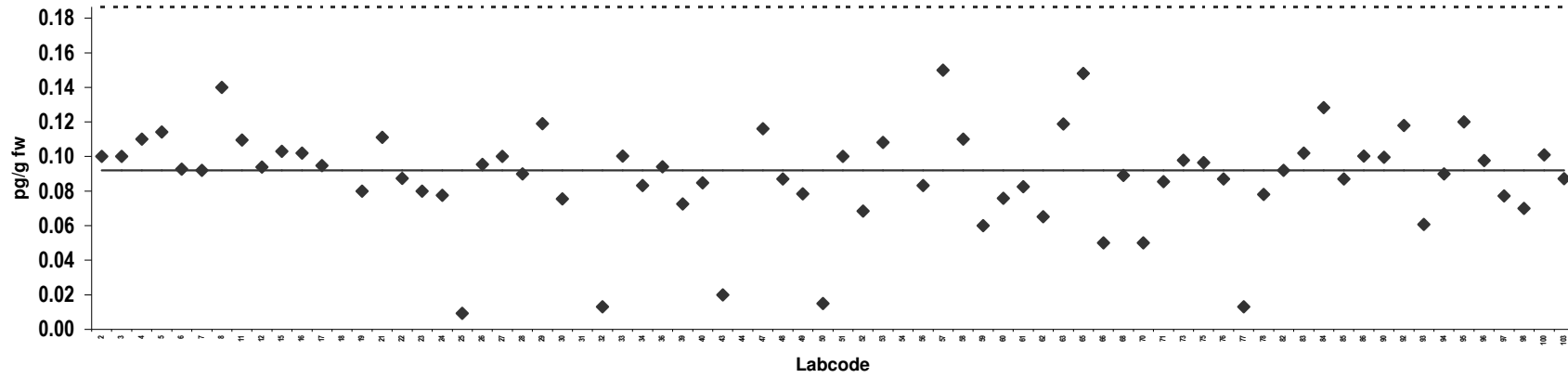
**Egg**  
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.10		60	0.076	
3	0.10		61	0.083	
4	0.11		62	0.065	
5	0.11		63	0.12	
6	0.093		65	0.15	
7	0.092		66	0.050	
8	0.14		68	0.089	
11	0.11		70	0.050	ND
12	0.094		71	0.086	
15	0.10		73	0.098	
16	0.10		75	0.097	
17	0.095		76	0.087	
18	1.5	Outlier	77	0.013	ND
19	0.080		78	0.078	
21	0.11		82	0.092	
22	0.087		83	0.10	
23	0.080		84	0.13	ND
24	0.078		85	0.087	
25	0.0092		86	0.10	
26	0.096		90	0.100	
27	0.10		92	0.12	
28	0.090		93	0.061	
29	0.12		94	0.090	
30	0.075		95	0.12	ND
31	0.94	Outlier	96	0.098	
32	0.013	ND	97	0.077	
33	0.10		98	0.070	
34	0.083		100	0.10	
36	0.094		103	0.087	
39	0.072				
40	0.085				
43	0.020	ND			
44	0.30	Outlier,ND			
47	0.12				
48	0.087				
49	0.078				
50	0.015	ND			
51	0.10				
52	0.068				
53	0.11				
54	0.26	Outlier			
56	0.083				
57	0.15				
58	0.11				
59	0.060				

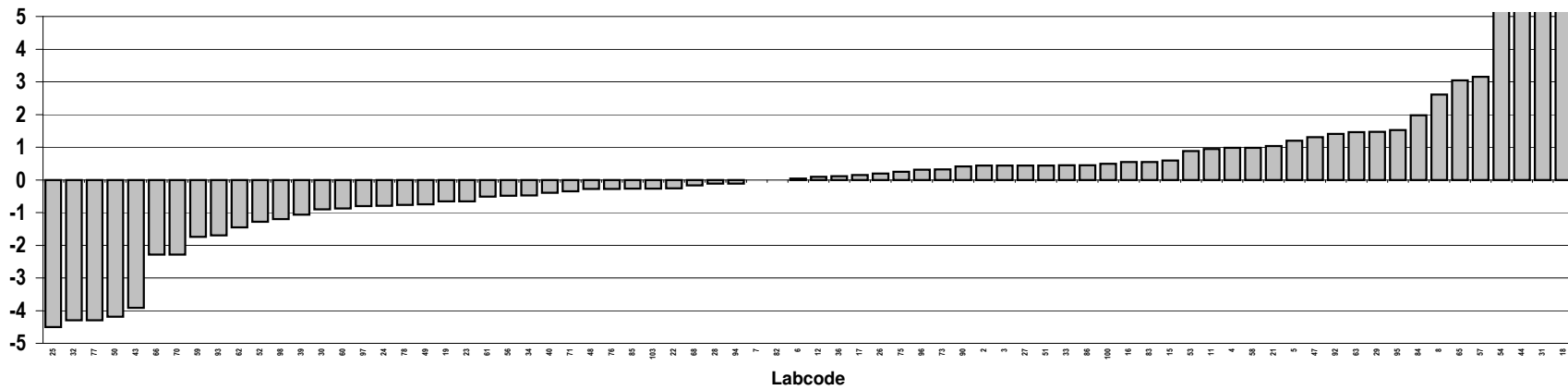
**Consensus statistics**

Consensus median, pg/g	0.092
Median all values pg/g	0.093
Consensus mean, pg/g	0.088
Standard deviation, pg/g	0.028
Relative standard deviation, %	32
No. of values reported	74
No. of values removed	4
No. of reported non-detects	8

2,3,4,6,7,8 HxCDF



Z-score: 2,3,4,6,7,8 HxCDF



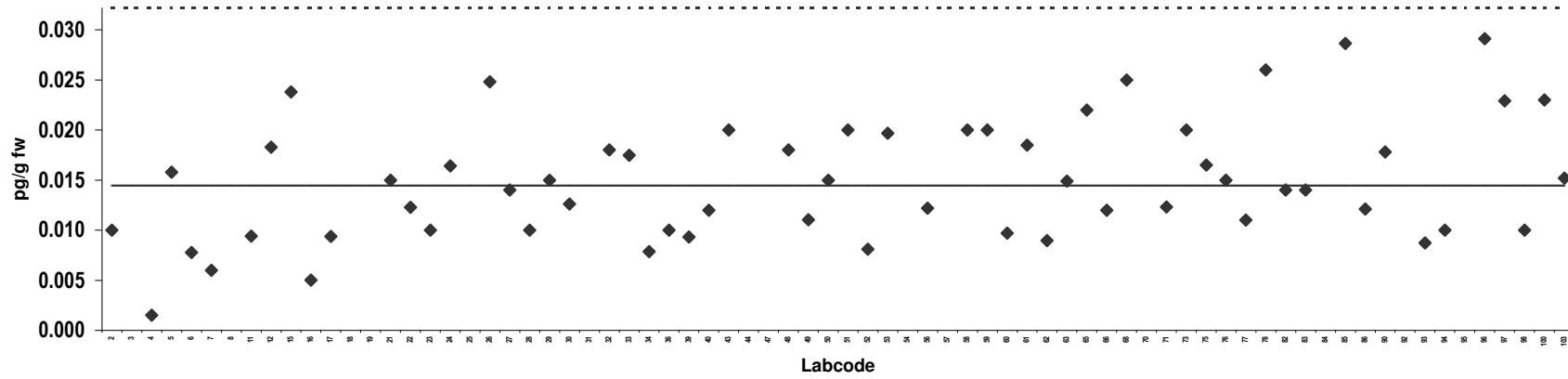
**Egg**  
Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010		60	0.0097	
3	0.040	Outlier	61	0.019	
4	0.0015	ND	62	0.0090	
5	0.016		63	0.015	ND
6	0.0078		65	0.022	
7	0.0060		66	0.012	
8	0.078	Outlier	68	0.025	ND
11	0.0094	ND	70	0.050	Outlier,ND
12	0.018		71	0.012	
15	0.024		73	0.020	ND
16	0.0050	ND	75	0.017	
17	0.0094		76	0.015	
18	1.6	Outlier	77	0.011	ND
19	0.050	Outlier,ND	78	0.026	ND
21	0.015		82	0.014	
22	0.012		83	0.014	
23	0.010		84	0.19	Outlier,ND
24	0.016		85	0.029	ND
25	0.079	Outlier	86	0.012	
26	0.025		90	0.018	ND
27	0.014		92	0.041	Outlier
28	0.010	ND	93	0.0087	
29	0.015		94	0.010	ND
30	0.013		95	0.12	Outlier,ND
31	0.38	Outlier	96	0.029	ND
32	0.018	ND	97	0.023	ND
33	0.017		98	0.010	ND
34	0.0079		100	0.023	
36	0.010		103	0.015	
39	0.0093				
40	0.012	ND			
43	0.020	ND			
44	0.30	Outlier,ND			
47	0.034	Outlier			
48	0.018	ND			
49	0.011				
50	0.015	ND			
51	0.020				
52	0.0081				
53	0.020				
54	0.19	Outlier			
56	0.012				
57	0.053	Outlier			
58	0.020	ND			
59	0.020	ND			

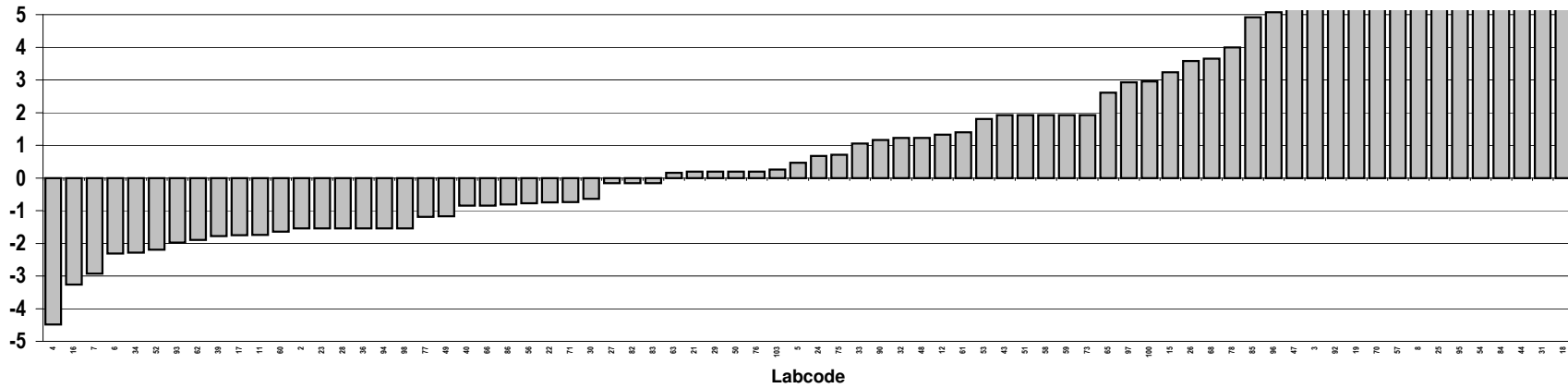
**Consensus statistics**

Consensus median, pg/g	0.014
Median all values pg/g	0.016
Consensus mean, pg/g	0.015
Standard deviation, pg/g	0.0060
Relative standard deviation, %	40
No. of values reported	74
No. of values removed	14
No. of reported non-detects	27

1,2,3,7,8,9 HxCDF



Z-score: 1,2,3,7,8,9 HxCDF

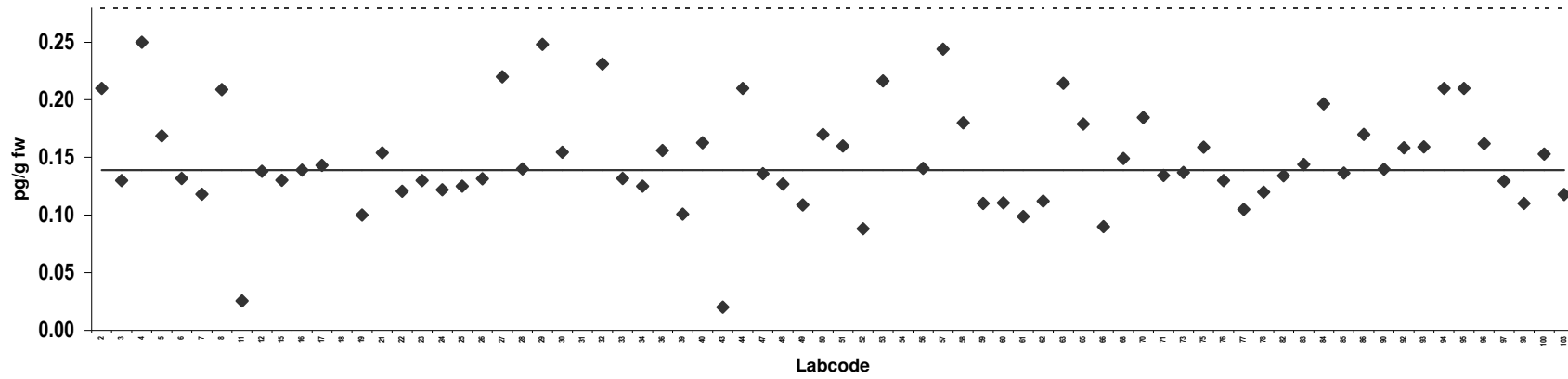


**Egg**  
Congener: 1,2,3,4,6,7,8 HpCDF

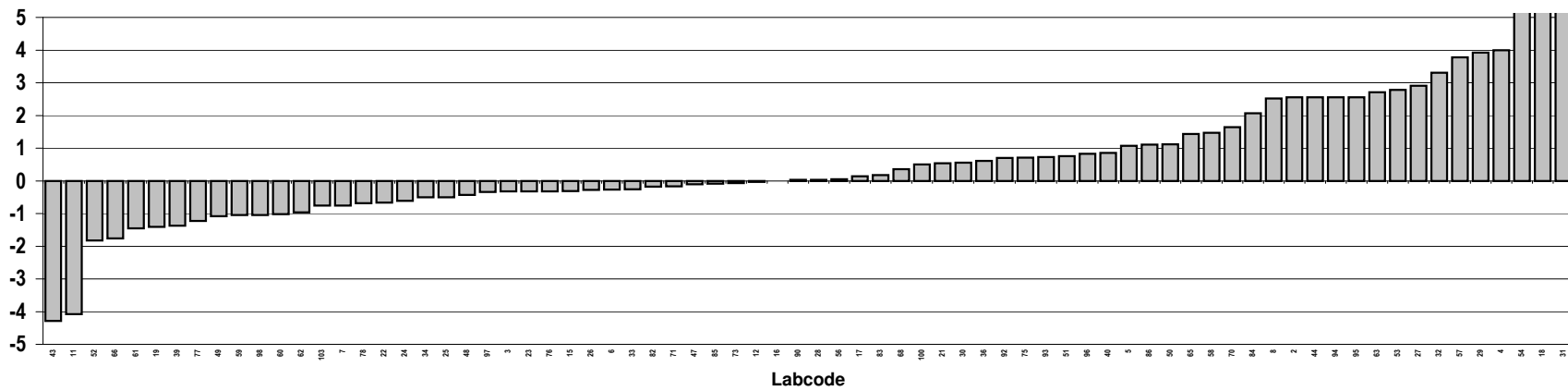
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.21		60	0.11	
3	0.13		61	0.099	
4	0.25		62	0.11	
5	0.17		63	0.21	
6	0.13		65	0.18	
7	0.12		66	0.090	
8	0.21		68	0.15	
11	0.026	ND	70	0.18	
12	0.14		71	0.13	
15	0.13		73	0.14	
16	0.14		75	0.16	
17	0.14		76	0.13	
18	1.6	Outlier	77	0.11	
19	0.10		78	0.12	
21	0.15		82	0.13	
22	0.12		83	0.14	
23	0.13		84	0.20	
24	0.12		85	0.14	
25	0.13		86	0.17	
26	0.13		90	0.14	
27	0.22		92	0.16	
28	0.14		93	0.16	
29	0.25		94	0.21	
30	0.15		95	0.21	ND
31	1.6	Outlier	96	0.16	
32	0.23		97	0.13	
33	0.13		98	0.11	
34	0.12		100	0.15	
36	0.16		103	0.12	
39	0.10				
40	0.16				
43	0.020	ND			
44	0.21				
47	0.14				
48	0.13				
49	0.11				
50	0.17				
51	0.16				
52	0.088				
53	0.22				
54	0.32	Outlier			
56	0.14				
57	0.24				
58	0.18				
59	0.11				

Consensus statistics	
Consensus median, pg/g	0.14
Median all values pg/g	0.14
Consensus mean, pg/g	0.15
Standard deviation, pg/g	0.045
Relative standard deviation, %	30
No. of values reported	74
No. of values removed	3
No. of reported non-detects	3

1,2,3,4,6,7,8 HpCDF



Z-score: 1,2,3,4,6,7,8 HpCDF



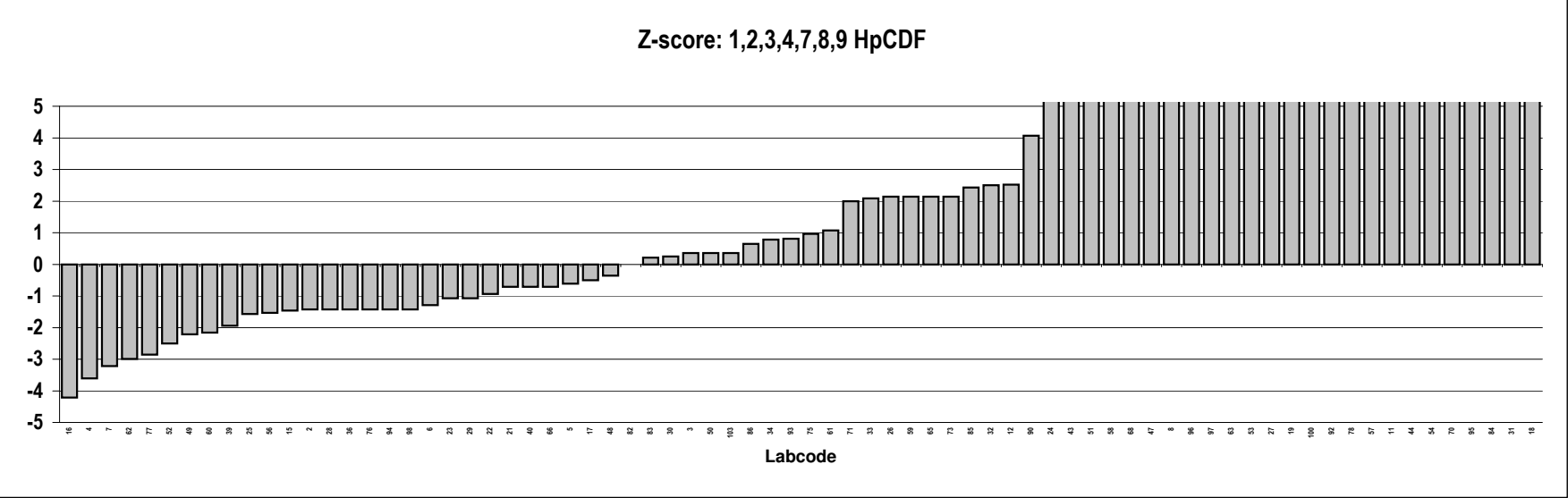
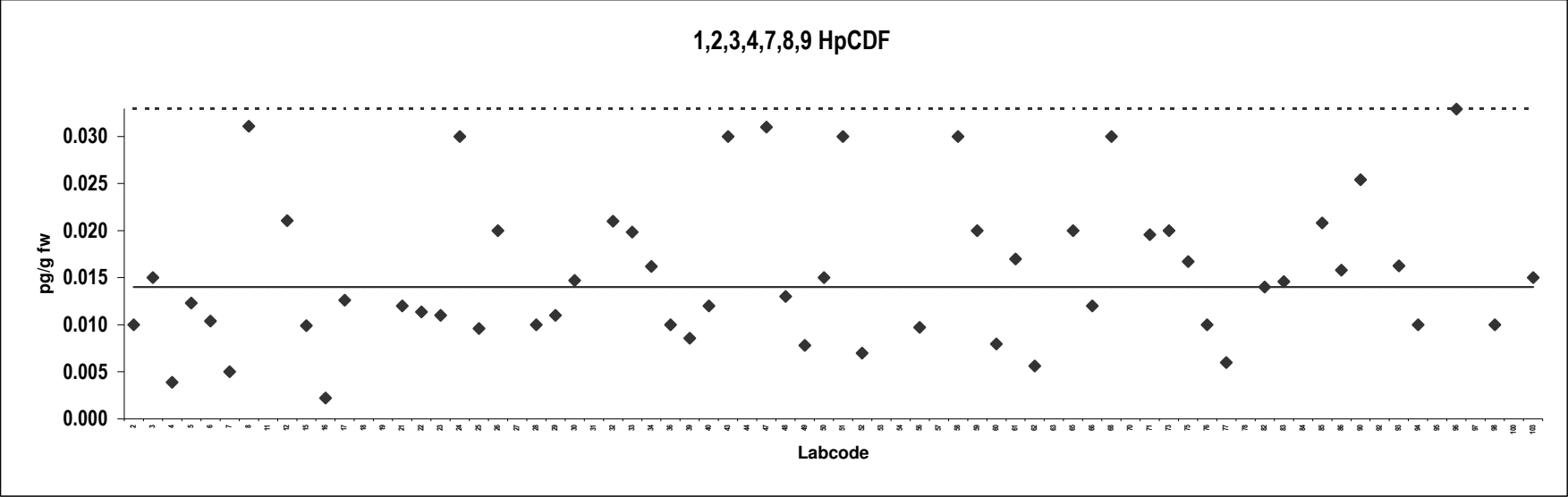
**Egg**  
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010		60	0.0080	
3	0.015	ND	61	0.017	ND
4	0.0039	ND	62	0.0056	
5	0.012		63	0.036	Outlier
6	0.010		65	0.020	
7	0.0050	ND	66	0.012	
8	0.031		68	0.030	ND
11	0.10	Outlier	70	0.20	Outlier,ND
12	0.021		71	0.020	
15	0.0099		73	0.020	ND
16	0.0022	ND	75	0.017	
17	0.013		76	0.010	ND
18	1.2	Outlier	77	0.0060	
19	0.050	Outlier,ND	78	0.071	Outlier,ND
21	0.012		82	0.014	
22	0.011		83	0.015	
23	0.011		84	0.26	Outlier,ND
24	0.030		85	0.021	
25	0.0096		86	0.016	
26	0.020		90	0.025	
27	0.040	Outlier	92	0.070	Outlier
28	0.010	ND	93	0.016	
29	0.011		94	0.010	ND
30	0.015		95	0.26	Outlier,ND
31	0.31	Outlier	96	0.033	ND
32	0.021	ND	97	0.035	Outlier,ND
33	0.020		98	0.010	ND
34	0.016		100	0.050	Outlier,ND
36	0.010		103	0.015	ND
39	0.0086				
40	0.012	ND			
43	0.030	ND			
44	0.15	Outlier,ND			
47	0.031				
48	0.013	ND			
49	0.0078				
50	0.015	ND			
51	0.030				
52	0.0070	ND			
53	0.039	Outlier			
54	0.19	Outlier			
56	0.0097				
57	0.078	Outlier			
58	0.030				
59	0.020	ND			

**Consensus statistics**

Consensus median, pg/g	0.014
Median all values pg/g	0.016
Consensus mean, pg/g	0.016
Standard deviation, pg/g	0.0078
Relative standard deviation, %	50
No. of values reported	74
No. of values removed	17
No. of reported non-detects	28



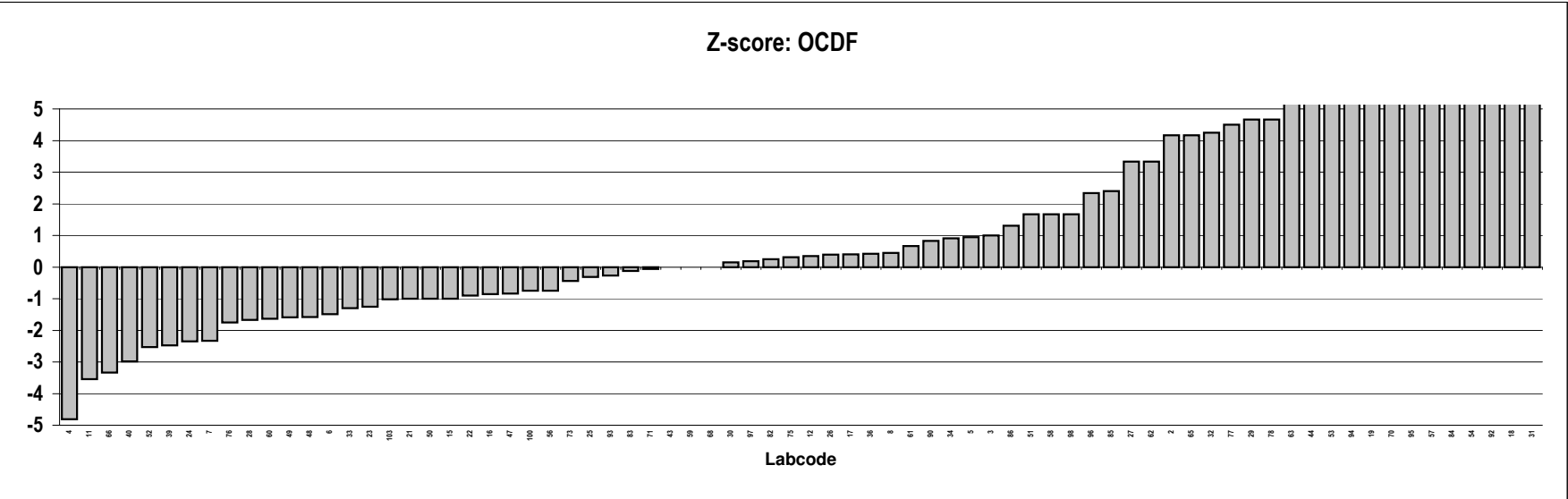
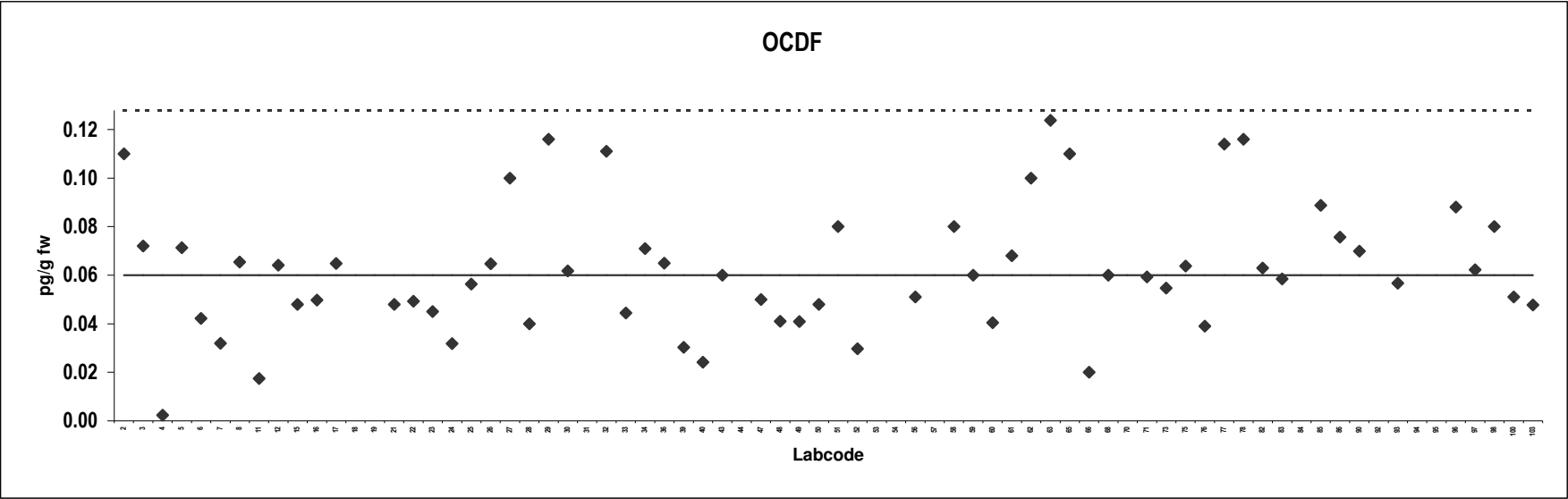


**Egg**  
Congener: OCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.11		60	0.040	
3	0.072		61	0.068	ND
4	0.0023	ND	62	0.10	ND
5	0.071		63	0.12	
6	0.042		65	0.11	
7	0.032		66	0.020	
8	0.065		68	0.060	
11	0.017	ND	70	0.20	Outlier,ND
12	0.064		71	0.059	
15	0.048		73	0.055	
16	0.050		75	0.064	
17	0.065		76	0.039	
18	2.9	Outlier	77	0.11	
19	0.20	Outlier,ND	78	0.12	ND
21	0.048		82	0.063	
22	0.049		83	0.059	
23	0.045		84	0.36	Outlier,ND
24	0.032		85	0.089	
25	0.056		86	0.076	
26	0.065		90	0.070	
27	0.10		92	0.55	Outlier
28	0.040		93	0.057	
29	0.12		94	0.17	Outlier
30	0.062		95	0.25	Outlier,ND
31	4.1	Outlier	96	0.088	
32	0.11		97	0.062	
33	0.044		98	0.080	ND
34	0.071		100	0.051	
36	0.065		103	0.048	
39	0.030				
40	0.024				
43	0.060	ND			
44	0.14	Outlier			
47	0.050				
48	0.041				
49	0.041				
50	0.048	ND			
51	0.080				
52	0.030				
53	0.17	Outlier			
54	0.42	Outlier			
56	0.051				
57	0.35	Outlier			
58	0.080	ND			
59	0.060				

**Consensus statistics**

Consensus median, pg/g	0.060
Median all values pg/g	0.064
Consensus mean, pg/g	0.062
Standard deviation, pg/g	0.026
Relative standard deviation, %	43
No. of values reported	74
No. of values removed	12
No. of reported non-detects	13



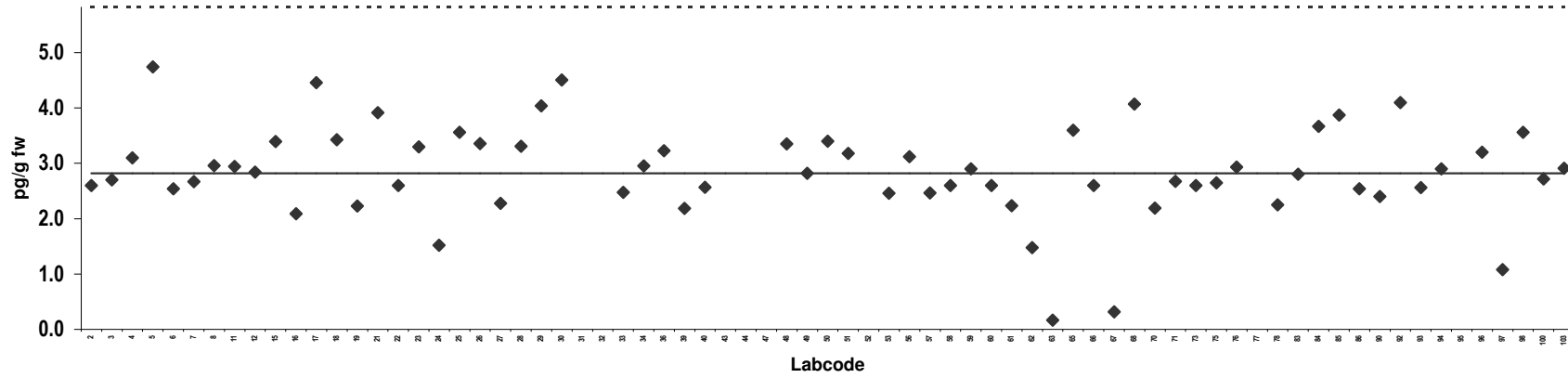
**Egg**  
Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	2.6		61	2.2	
3	2.7		62	1.5	
4	3.1		63	0.16	ND
5	4.7		65	3.6	
6	2.5		66	2.6	
7	2.7		67	0.32	
8	3.0		68	4.1	
11	2.9		70	2.2	
12	2.8		71	2.7	
15	3.4		73	2.6	
16	2.1		75	2.6	
17	4.5		76	2.9	
18	3.4		77	3.3	Outlier
19	2.2		78	2.3	
21	3.9		83	2.8	
22	2.6		84	3.7	
23	3.3		85	3.9	
24	1.5		86	2.5	
25	3.6		90	2.4	
26	3.4		92	4.1	
27	2.3		93	2.6	
28	3.3		94	2.9	
29	4.0		95	9.7	Outlier,ND
30	4.5		96	3.2	
31	25	Outlier	97	1.1	ND
32	16	Outlier	98	3.6	
33	2.5		100	2.7	
34	3.0		103	2.9	
36	3.2				
39	2.2				
40	2.6				
43	21	Outlier			
44	7.0	Outlier,ND			
47	14	Outlier			
48	3.4				
49	2.8				
50	3.4				
51	3.2				
52	8.1	Outlier			
53	2.5				
56	3.1				
57	2.5				
58	2.6				
59	2.9				
60	2.6				

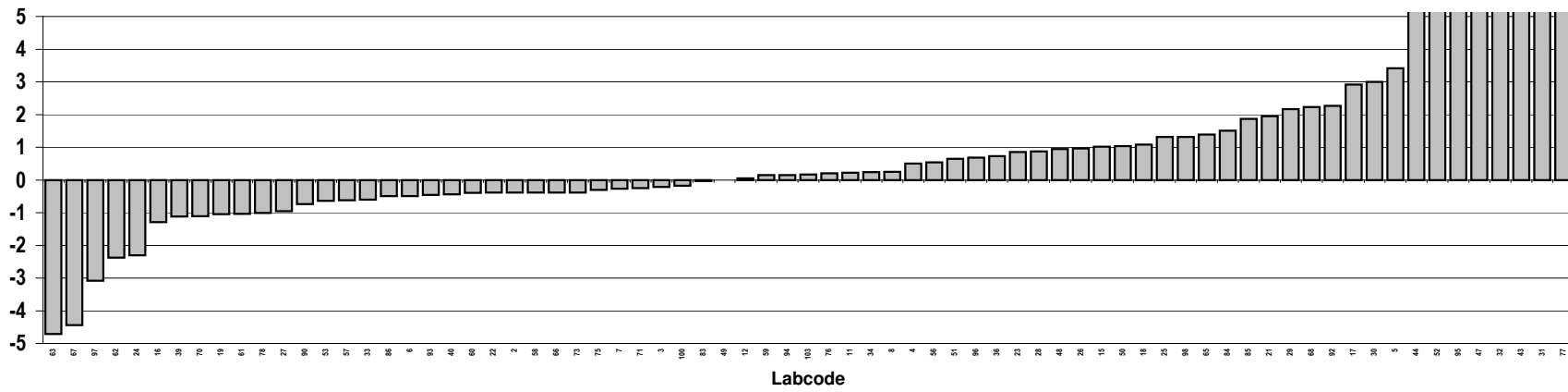
**Consensus statistics**

Consensus median, pg/g	2.8
Median all values pg/g	2.9
Consensus mean, pg/g	2.9
Standard deviation, pg/g	0.84
Relative standard deviation, %	29
No. of values reported	73
No. of values removed	8
No. of reported non-detects	4

### PCB 77



### Z-score: PCB 77

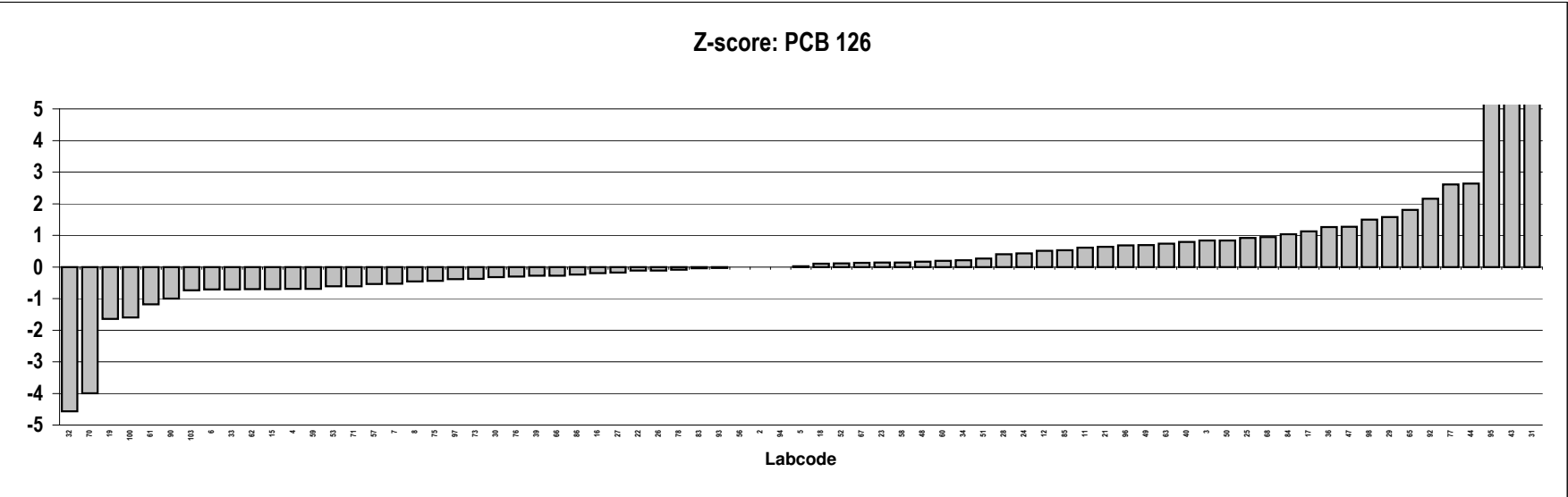
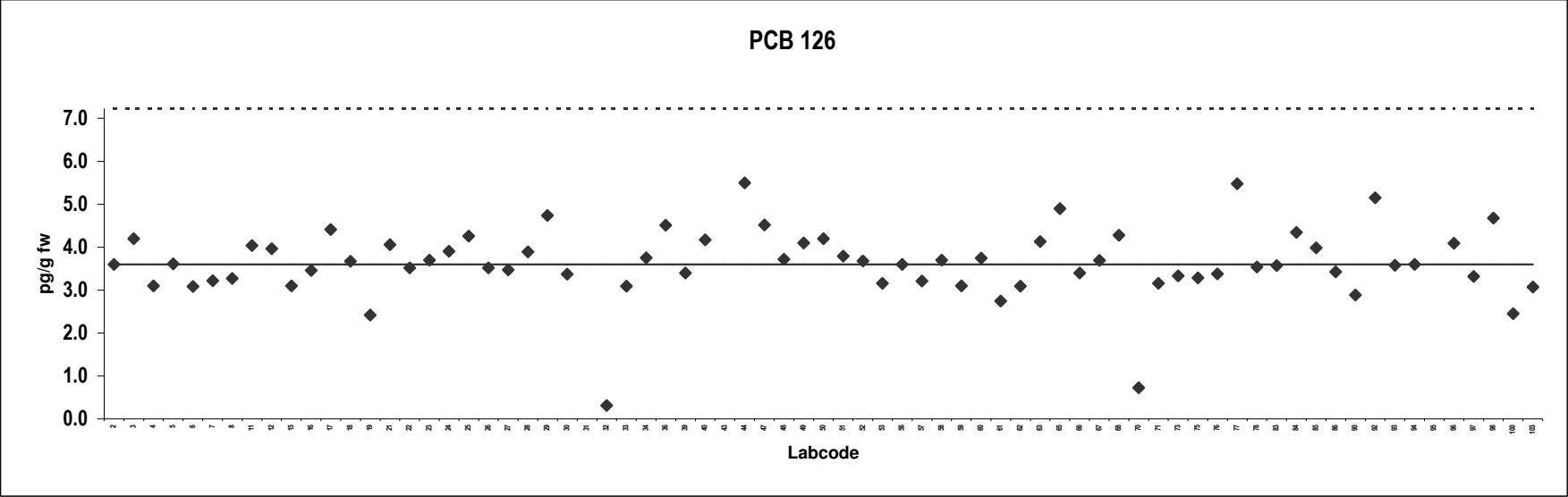


**Egg**  
Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	3.6		61	2.7	
3	4.2		62	3.1	
4	3.1		63	4.1	
5	3.6		65	4.9	
6	3.1		66	3.4	
7	3.2		67	3.7	
8	3.3		68	4.3	
11	4.0		70	0.72	
12	4.0		71	3.2	
15	3.1		73	3.3	
16	3.5		75	3.3	
17	4.4		76	3.4	
18	3.7		77	5.5	
19	2.4		78	3.5	
21	4.1		83	3.6	
22	3.5		84	4.3	
23	3.7		85	4.0	
24	3.9		86	3.4	
25	4.3		90	2.9	
26	3.5		92	5.2	
27	3.5		93	3.6	
28	3.9		94	3.6	
29	4.7		95	9.7	Outlier,ND
30	3.4		96	4.1	
31	31	Outlier	97	3.3	
32	0.31	ND	98	4.7	
33	3.1		100	2.5	
34	3.8		103	3.1	
36	4.5				
39	3.4				
40	4.2				
43	16	Outlier			
44	5.5	ND			
47	4.5				
48	3.7				
49	4.1				
50	4.2				
51	3.8				
52	3.7				
53	3.2				
56	3.6				
57	3.2				
58	3.7				
59	3.1				
60	3.7				

**Consensus statistics**

Consensus median, pg/g	3.6
Median all values pg/g	3.6
Consensus mean, pg/g	3.6
Standard deviation, pg/g	0.82
Relative standard deviation, %	23
No. of values reported	73
No. of values removed	3
No. of reported non-detects	3



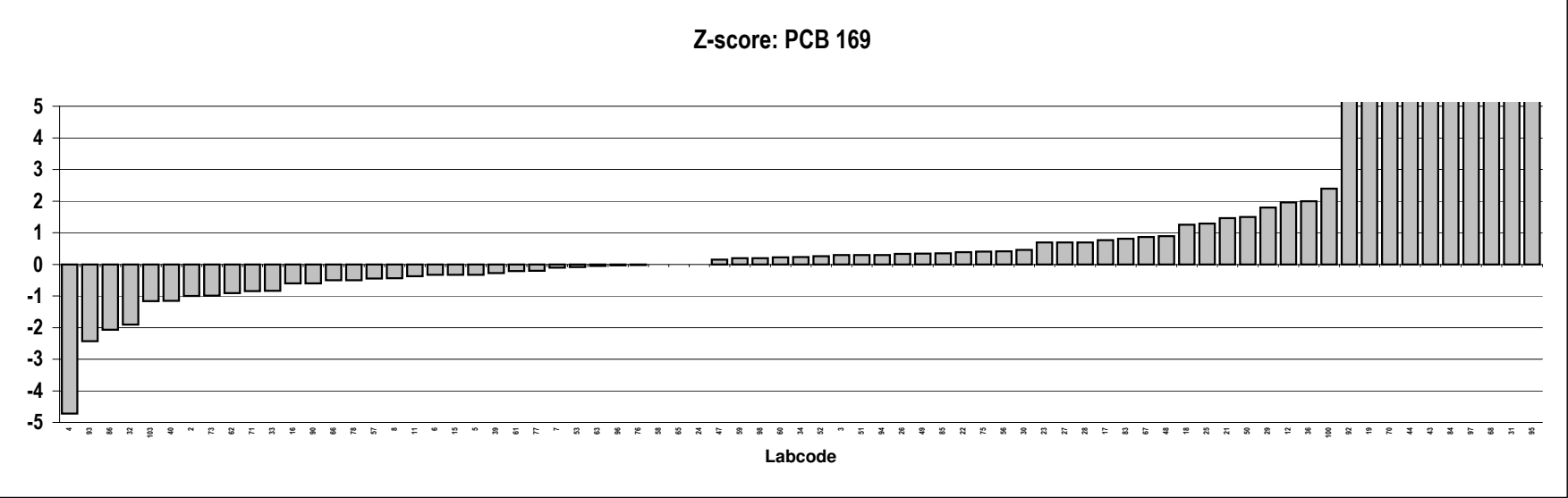
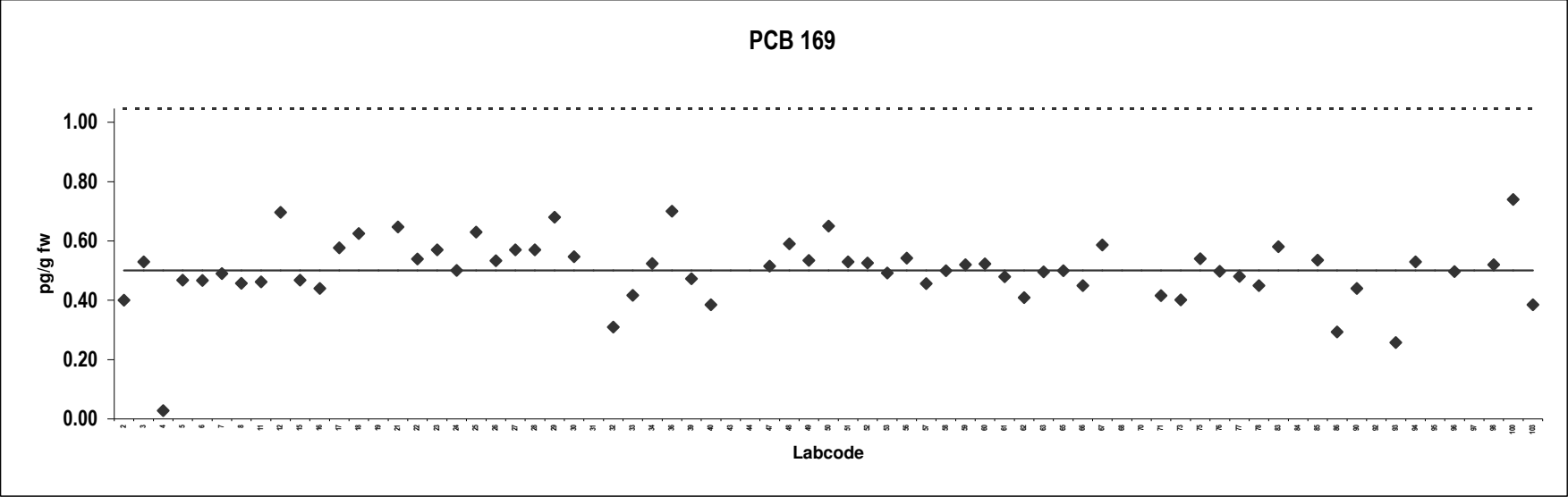
**Egg**  
**Congener: PCB 169**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.40		61	0.48	
3	0.53		62	0.41	
4	0.028	ND	63	0.50	
5	0.47		65	0.50	ND
6	0.47		66	0.45	
7	0.49		67	0.59	
8	0.46		68	4.0	Outlier,ND
11	0.46		70	2.0	Outlier,ND
12	0.70		71	0.42	
15	0.47		73	0.40	
16	0.44		75	0.54	
17	0.58		76	0.50	
18	0.63		77	0.48	
19	2.0	Outlier,ND	78	0.45	
21	0.65		83	0.58	
22	0.54		84	3.0	Outlier
23	0.57		85	0.54	
24	0.50		86	0.29	
25	0.63		90	0.44	
26	0.53		92	1.5	Outlier
27	0.57		93	0.26	
28	0.57		94	0.53	
29	0.68		95	9.7	Outlier,ND
30	0.55		96	0.50	
31	5.2	Outlier	97	3.3	Outlier,ND
32	0.31	ND	98	0.52	
33	0.42		100	0.74	
34	0.52		103	0.38	
36	0.70				
39	0.47				
40	0.38				
43	2.3	Outlier			
44	2.3	Outlier,ND			
47	0.52				
48	0.59				
49	0.53				
50	0.65				
51	0.53				
52	0.53				
53	0.49				
56	0.54				
57	0.46				
58	0.50				
59	0.52				
60	0.52				

**Consensus statistics**

Consensus median, pg/g	0.50
Median all values pg/g	0.52
Consensus mean, pg/g	0.50
Standard deviation, pg/g	0.11
Relative standard deviation, %	22
No. of values reported	73
No. of values removed	10
No. of reported non-detects	9



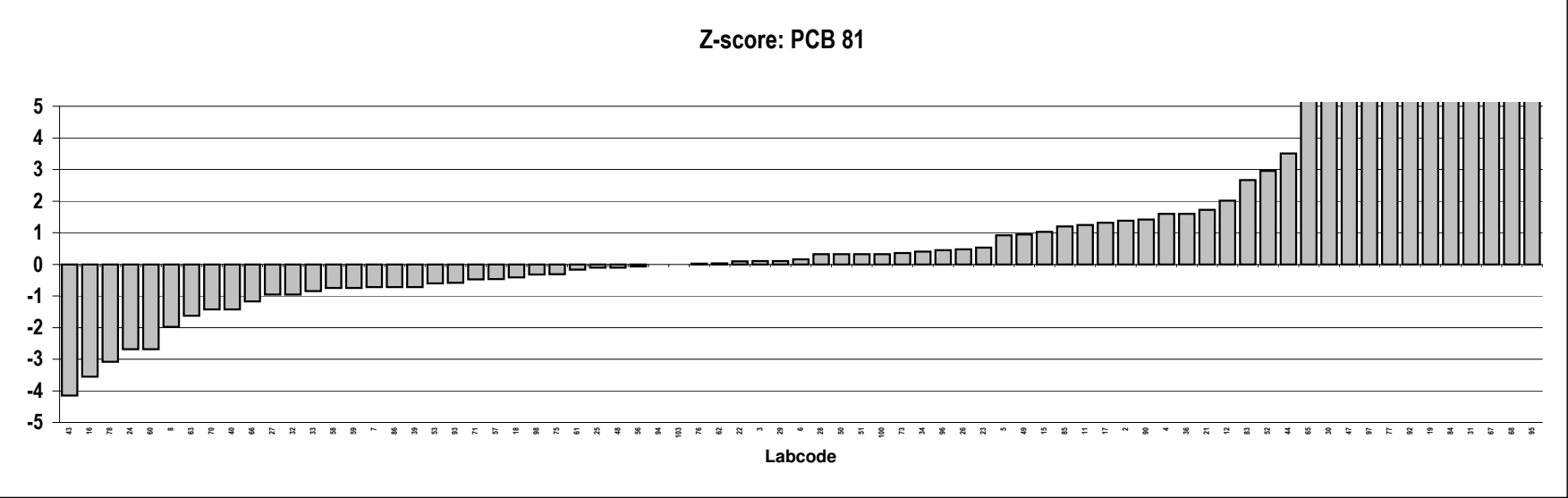
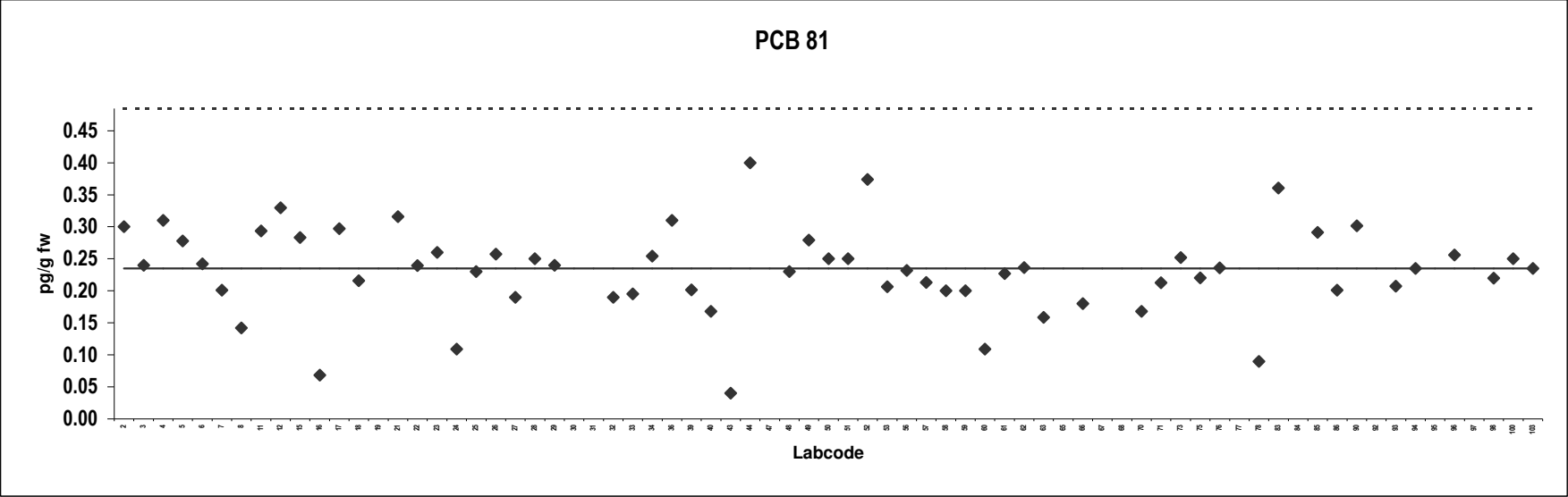


**Egg**  
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.30		61	0.23	
3	0.24		62	0.24	
4	0.31		63	0.16	ND
5	0.28		65	0.50	Outlier,ND
6	0.24		66	0.18	
7	0.20		67	3.5	Outlier
8	0.14		68	4.0	Outlier,ND
11	0.29		70	0.17	
12	0.33		71	0.21	
15	0.28		73	0.25	
16	0.068		75	0.22	
17	0.30		76	0.24	
18	0.22		77	1.2	Outlier
19	2.0	Outlier,ND	78	0.090	
21	0.32		83	0.36	
22	0.24		84	2.1	Outlier,ND
23	0.26		85	0.29	
24	0.11		86	0.20	
25	0.23		90	0.30	
26	0.26		92	1.2	Outlier
27	0.19		93	0.21	
28	0.25		94	0.24	
29	0.24		95	9.7	Outlier,ND
30	0.58	Outlier	96	0.26	
31	2.1	Outlier	97	1.0	Outlier,ND
32	0.19		98	0.22	
33	0.20		100	0.25	
34	0.25		103	0.24	
36	0.31				
39	0.20				
40	0.17				
43	0.040	ND			
44	0.40	ND			
47	0.67	Outlier			
48	0.23				
49	0.28				
50	0.25				
51	0.25				
52	0.37				
53	0.21				
56	0.23				
57	0.21				
58	0.20				
59	0.20				
60	0.11				

**Consensus statistics**

Consensus median, pg/g	0.24
Median all values pg/g	0.24
Consensus mean, pg/g	0.23
Standard deviation, pg/g	0.068
Relative standard deviation, %	29
No. of values reported	73
No. of values removed	12
No. of reported non-detects	9



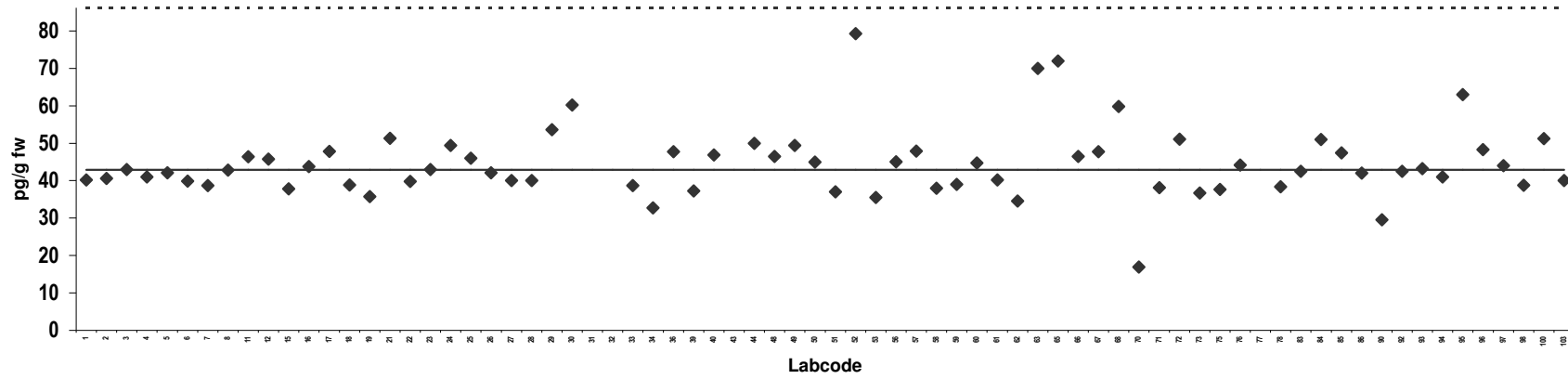
**Egg**  
Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	40		61	40	
2	41		62	35	
3	43		63	70	
4	41		65	72	
5	42		66	47	
6	40		67	48	
7	39		68	60	
8	43		70	17	
11	46		71	38	
12	46		72	51	
15	38		73	37	
16	44		75	38	
17	48		76	44	
18	39		77	237	Outlier
19	36		78	38	
21	51		83	43	
22	40		84	51	
23	43		85	47	
24	49		86	42	
25	46		90	30	
26	42		92	42	
27	40		93	43	
28	40		94	41	
29	54		95	63	
30	60		96	48	
31	370	Outlier	97	44	
32	97	Outlier	98	39	
33	39		100	51	
34	33		103	40	
36	48				
39	37				
40	47				
43	230	Outlier			
44	50				
48	46				
49	49				
50	45				
51	37				
52	79				
53	36				
56	45				
57	48				
58	38				
59	39				
60	45				

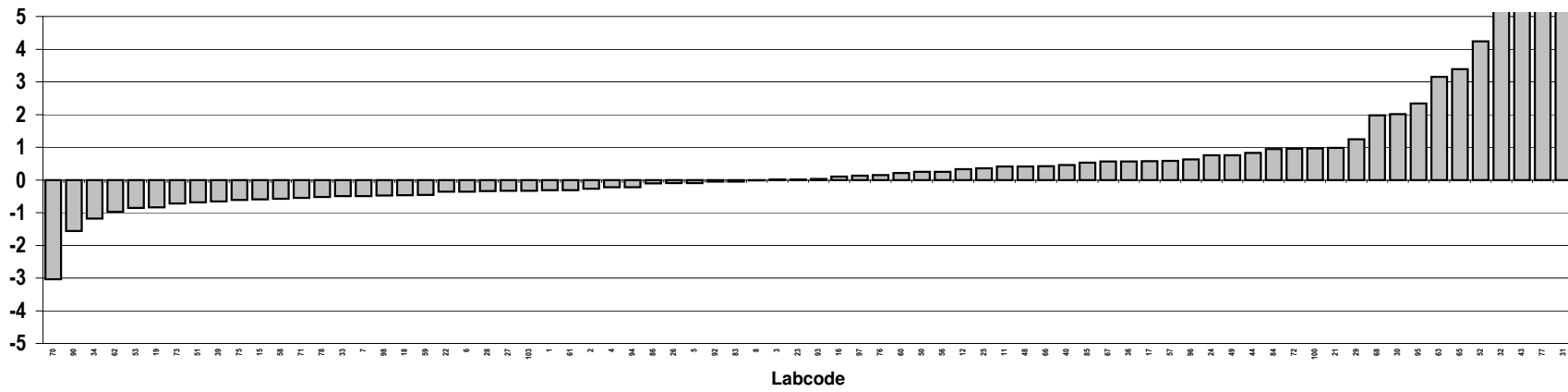
**Consensus statistics**

Consensus median, pg/g	43
Median all values pg/g	43
Consensus mean, pg/g	44
Standard deviation, pg/g	9.3
Relative standard deviation, %	21
No. of values reported	74
No. of values removed	4
No. of reported non-detects	0

### PCB 105



### Z-score: PCB 105

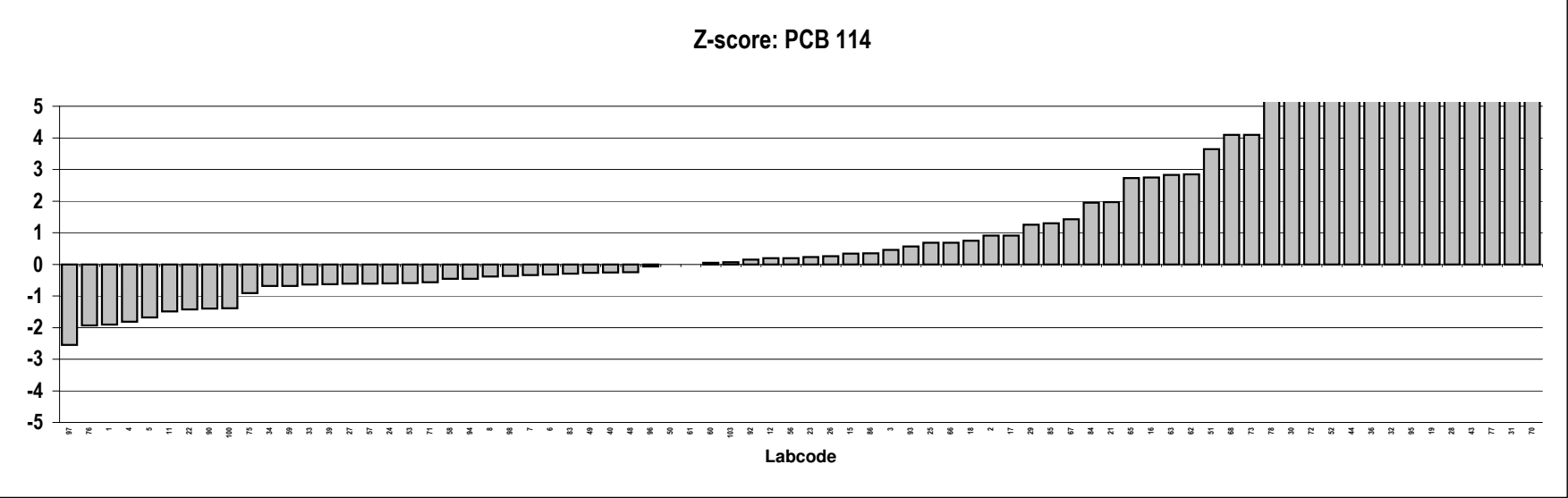
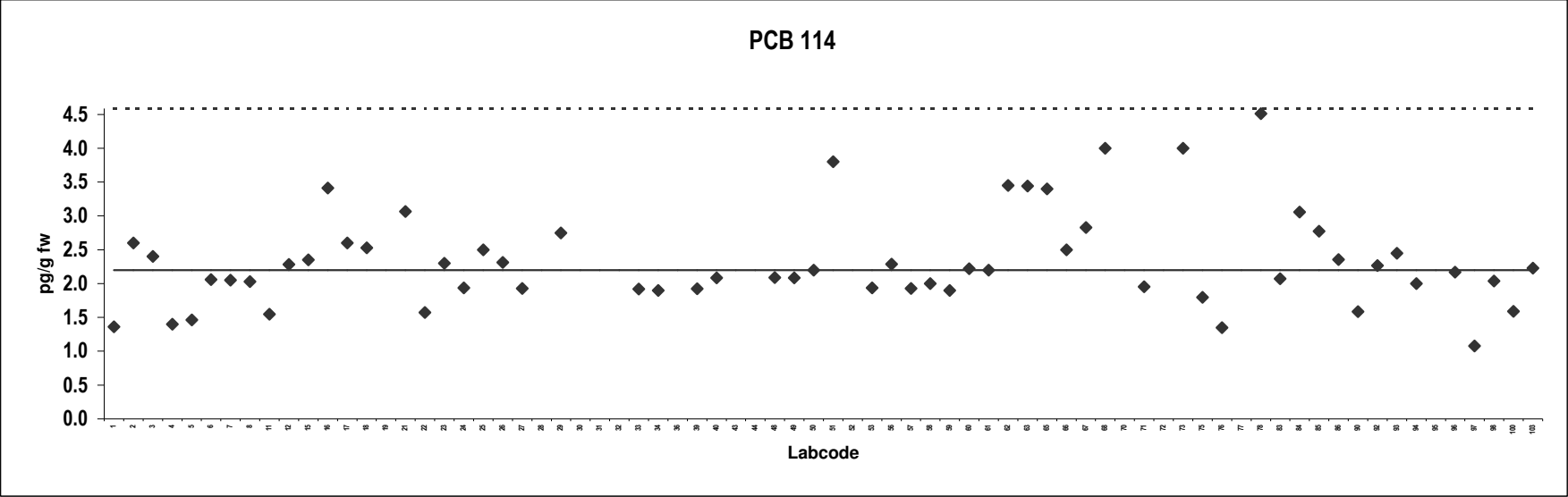


**Egg**  
**Congener: PCB 114**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.4	ND	61	2.2	
2	2.6		62	3.5	
3	2.4		63	3.4	
4	1.4		65	3.4	
5	1.5	ND	66	2.5	
6	2.1		67	2.8	
7	2.0		68	4.0	ND
8	2.0		70	2.3	Outlier
11	1.5		71	2.0	
12	2.3		72	4.9	Outlier,ND
15	2.3		73	4.0	ND
16	3.4		75	1.8	
17	2.6		76	1.4	
18	2.5		77	2.0	Outlier
19	10	Outlier,ND	78	4.5	ND
21	3.1		83	2.1	
22	1.6		84	3.1	
23	2.3		85	2.8	
24	1.9		86	2.4	
25	2.5		90	1.6	
26	2.3		92	2.3	
27	1.9		93	2.4	
28	10	Outlier,ND	94	2.0	
29	2.8		95	9.7	Outlier,ND
30	4.7	Outlier	96	2.2	
31	21	Outlier	97	1.1	
32	7.8	Outlier	98	2.0	
33	1.9		100	1.6	
34	1.9	ND	103	2.2	
36	6.5	Outlier			
39	1.9				
40	2.1				
43	15	Outlier			
44	5.9	Outlier			
48	2.1				
49	2.1				
50	2.2				
51	3.8				
52	5.6	Outlier			
53	1.9				
56	2.3				
57	1.9				
58	2.0				
59	1.9				
60	2.2				

**Consensus statistics**

Consensus median, pg/g	2.2
Median all values pg/g	2.3
Consensus mean, pg/g	2.3
Standard deviation, pg/g	0.70
Relative standard deviation, %	30
No. of values reported	74
No. of values removed	13
No. of reported non-detects	10



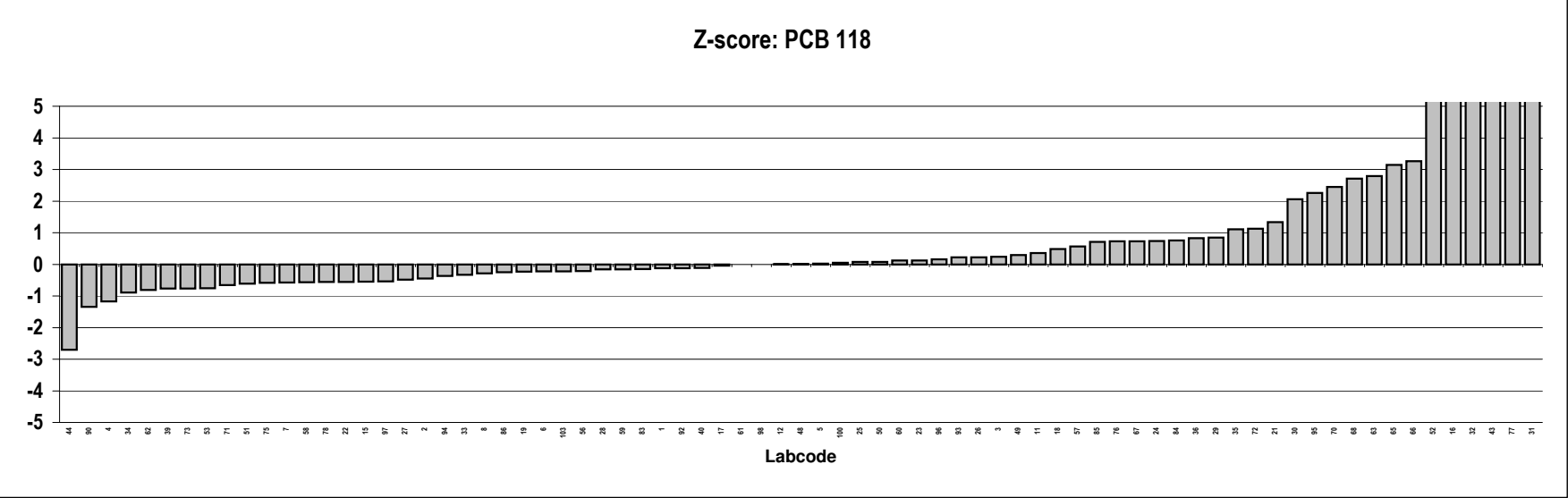
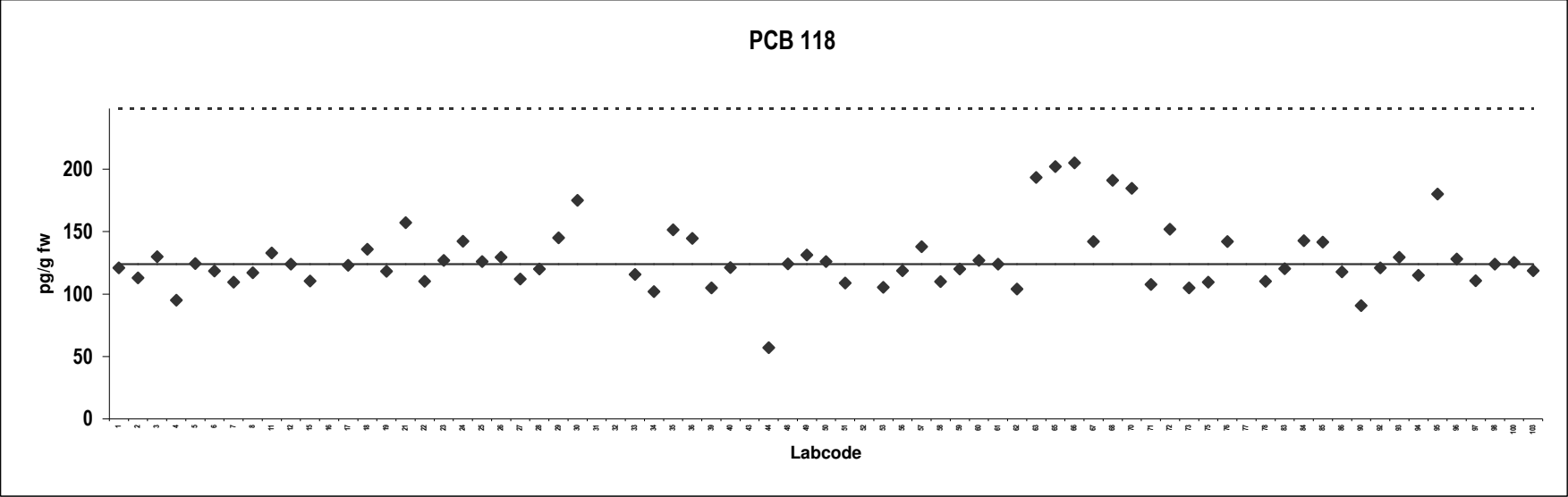
**Egg**  
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	121		60	127	
2	113		61	124	
3	130		62	104	
4	95		63	193	
5	125		65	202	
6	119		66	205	
7	110		67	142	
8	117		68	191	
11	133		70	185	
12	124		71	108	
15	110		72	152	
16	299	Outlier	73	105	
17	123		75	110	
18	136		76	142	
19	118		77	804	Outlier
21	157		78	110	
22	110		83	120	
23	127		84	143	
24	142		85	142	
25	126		86	118	
26	130		90	91	
27	112		92	121	
28	120		93	129	
29	145		94	115	
30	175		95	180	
31	1140	Outlier	96	128	
32	318	Outlier	97	111	
33	116		98	124	
34	102		100	125	
35	151		103	119	
36	145				
39	105				
40	121				
43	676	Outlier			
44	57				
48	124				
49	131				
50	126				
51	109				
52	266	Outlier			
53	105				
56	119				
57	138				
58	110				
59	120				

**Consensus statistics**

Consensus median, pg/g	124
Median all values pg/g	124
Consensus mean, pg/g	128
Standard deviation, pg/g	26
Relative standard deviation, %	20
No. of values reported	75
No. of values removed	6
No. of reported non-detects	0



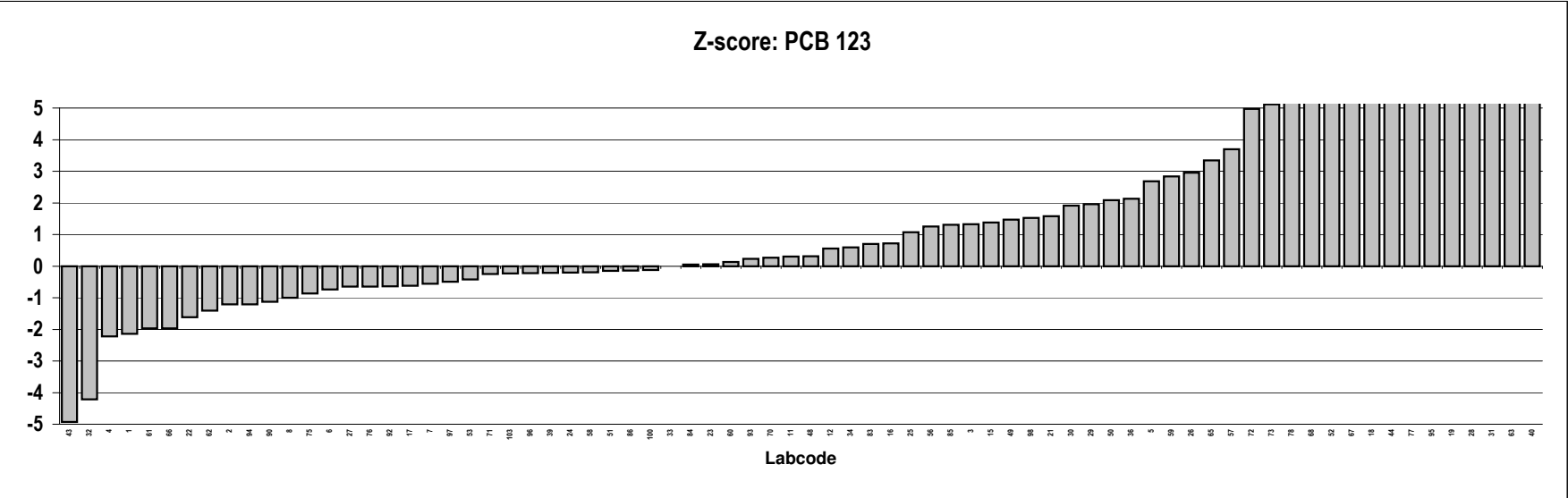
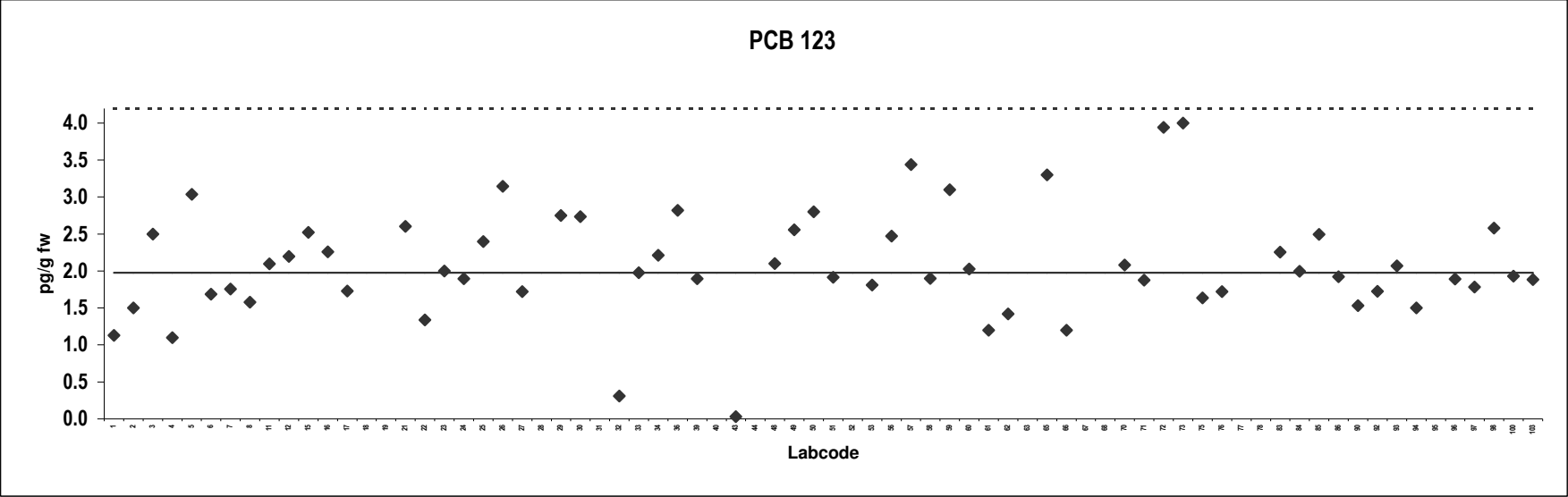


**Egg**  
**Congener: PCB 123**

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.1	ND	61	1.2	
2	1.5		62	1.4	
3	2.5		63	99	Outlier
4	1.1		65	3.3	
5	3.0	ND	66	1.2	
6	1.7		67	7.0	Outlier
7	1.8		68	5.2	Outlier
8	1.6		70	2.1	
11	2.1		71	1.9	
12	2.2		72	3.9	ND
15	2.5		73	4.0	ND
16	2.3		75	1.6	
17	1.7		76	1.7	
18	7.3	Outlier	77	9.0	Outlier
19	10	Outlier,ND	78	4.5	Outlier,ND
21	2.6		83	2.3	
22	1.3		84	2.0	
23	2.0		85	2.5	
24	1.9		86	1.9	
25	2.4		90	1.5	
26	3.1		92	1.7	
27	1.7		93	2.1	
28	10	Outlier,ND	94	1.5	
29	2.8		95	9.7	Outlier,ND
30	2.7		96	1.9	
31	18	Outlier	97	1.8	
32	0.31	ND	98	2.6	
33	2.0		100	1.9	
34	2.2	ND	103	1.9	
36	2.8				
39	1.9				
40	122	Outlier			
43	0.030	ND			
44	8.0	Outlier,ND			
48	2.1				
49	2.6				
50	2.8				
51	1.9				
52	6.5	Outlier			
53	1.8				
56	2.5				
57	3.4				
58	1.9				
59	3.1				
60	2.0				

**Consensus statistics**

Consensus median, pg/g	2.0
Median all values pg/g	2.1
Consensus mean, pg/g	2.1
Standard deviation, pg/g	0.73
Relative standard deviation, %	35
No. of values reported	74
No. of values removed	13
No. of reported non-detects	12

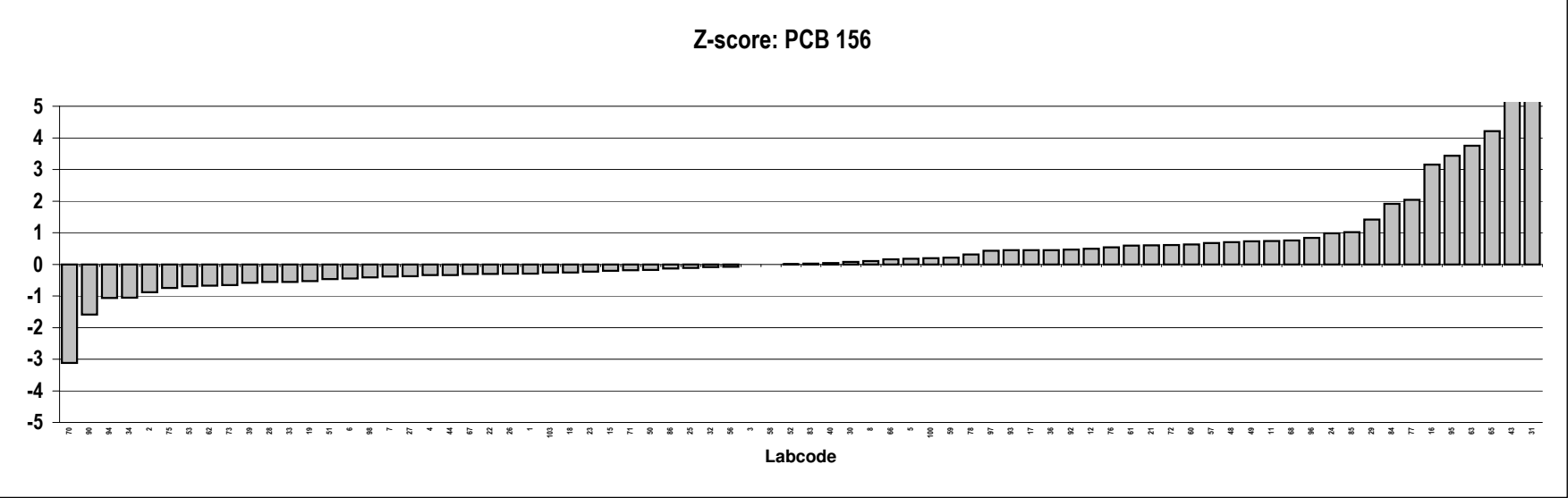
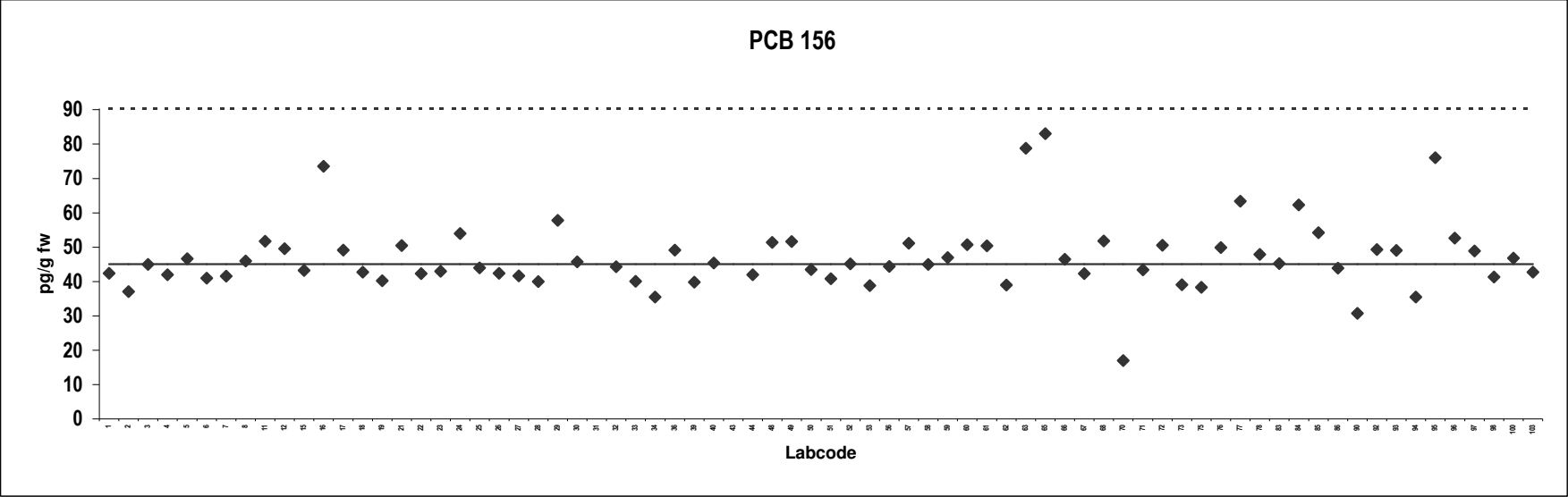


**Egg**  
Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	42		61	50	
2	37		62	39	
3	45		63	79	
4	42		65	83	
5	47		66	47	
6	41		67	42	
7	42		68	52	
8	46		70	17	
11	52		71	43	
12	50		72	51	
15	43		73	39	
16	74		75	38	
17	49		76	50	
18	43		77	63	
19	40		78	48	
21	50		83	45	
22	42		84	62	
23	43		85	54	
24	54		86	44	
25	44		90	31	
26	42		92	49	
27	42		93	49	
28	40		94	36	
29	58		95	76	
30	46		96	53	
31	438	Outlier	97	49	
32	44		98	41	
33	40		100	47	
34	36		103	43	
36	49				
39	40				
40	45				
43	220	Outlier			
44	42				
48	51				
49	52				
50	44				
51	41				
52	45				
53	39				
56	44				
57	51				
58	45				
59	47				
60	51				

**Consensus statistics**

Consensus median, pg/g	45
Median all values pg/g	45
Consensus mean, pg/g	47
Standard deviation, pg/g	10
Relative standard deviation, %	22
No. of values reported	74
No. of values removed	2
No. of reported non-detects	0



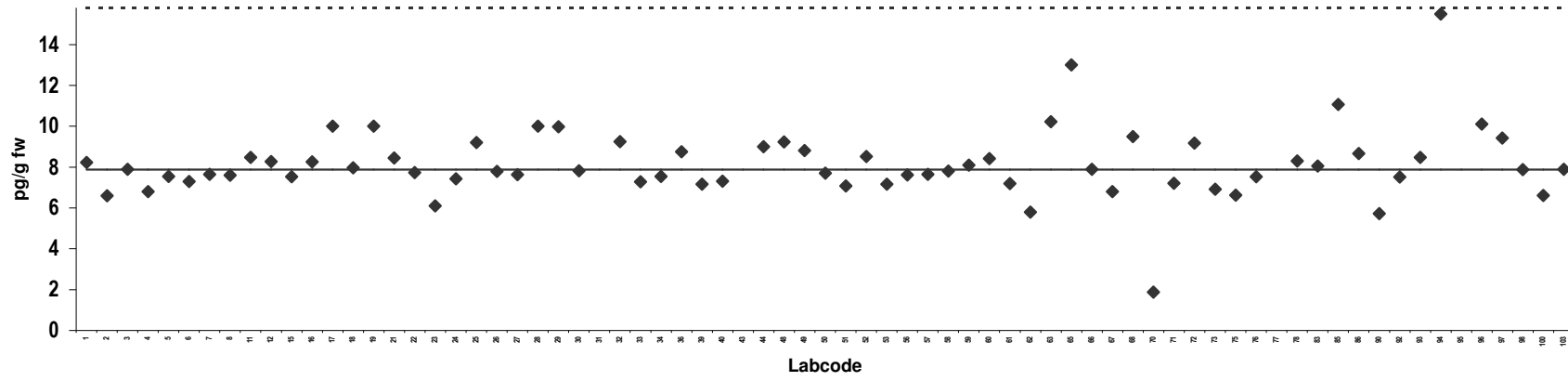
**Egg**  
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	8.2		61	7.2	
2	6.6		62	5.8	
3	7.9		63	10	
4	6.8		65	13	
5	7.5	ND	66	7.9	
6	7.3		67	6.8	
7	7.6		68	9.5	
8	7.6		70	1.9	
11	8.5		71	7.2	
12	8.3		72	9.2	
15	7.5		73	6.9	
16	8.3		75	6.6	
17	10		76	7.5	
18	8.0		77	38	Outlier
19	10	ND	78	8.3	
21	8.5		83	8.1	
22	7.7		85	11	
23	6.1		86	8.7	
24	7.4		90	5.7	
25	9.2		92	7.5	
26	7.8		93	8.5	
27	7.6		94	16	
28	10	ND	95	76	Outlier
29	10.0		96	10	
30	7.8		97	9.4	
31	75	Outlier	98	7.9	
32	9.2		100	6.6	
33	7.3		103	7.9	
34	7.5				
36	8.8				
39	7.2				
40	7.3				
43	33	Outlier			
44	9.0				
48	9.2				
49	8.8				
50	7.7				
51	7.1				
52	8.5				
53	7.2				
56	7.6				
57	7.6				
58	7.8				
59	8.1				
60	8.4				

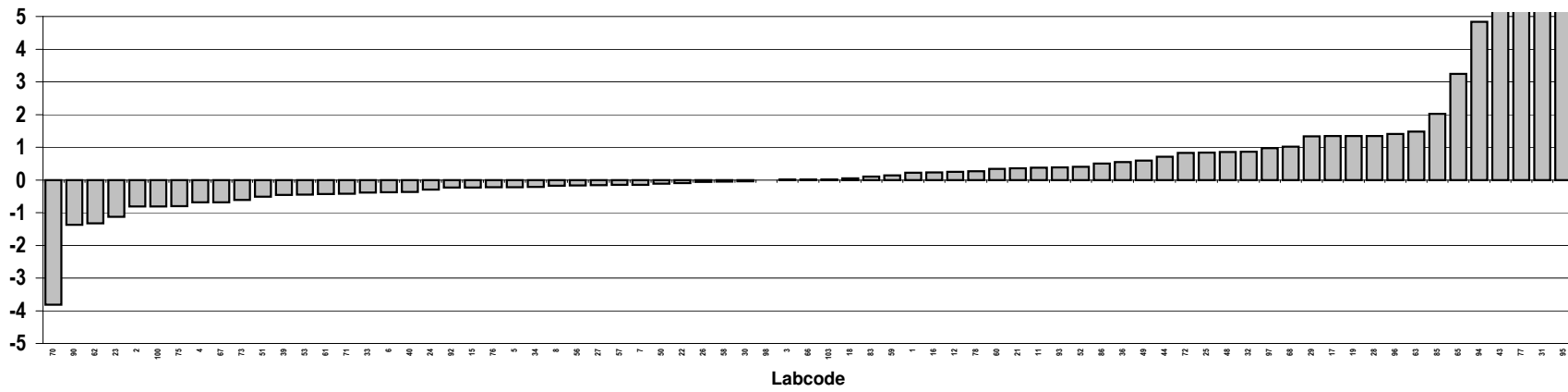
**Consensus statistics**

Consensus median, pg/g	7.9
Median all values pg/g	7.9
Consensus mean, pg/g	8.1
Standard deviation, pg/g	1.7
Relative standard deviation, %	21
No. of values reported	73
No. of values removed	4
No. of reported non-detects	3

### PCB 157



### Z-score: PCB 157



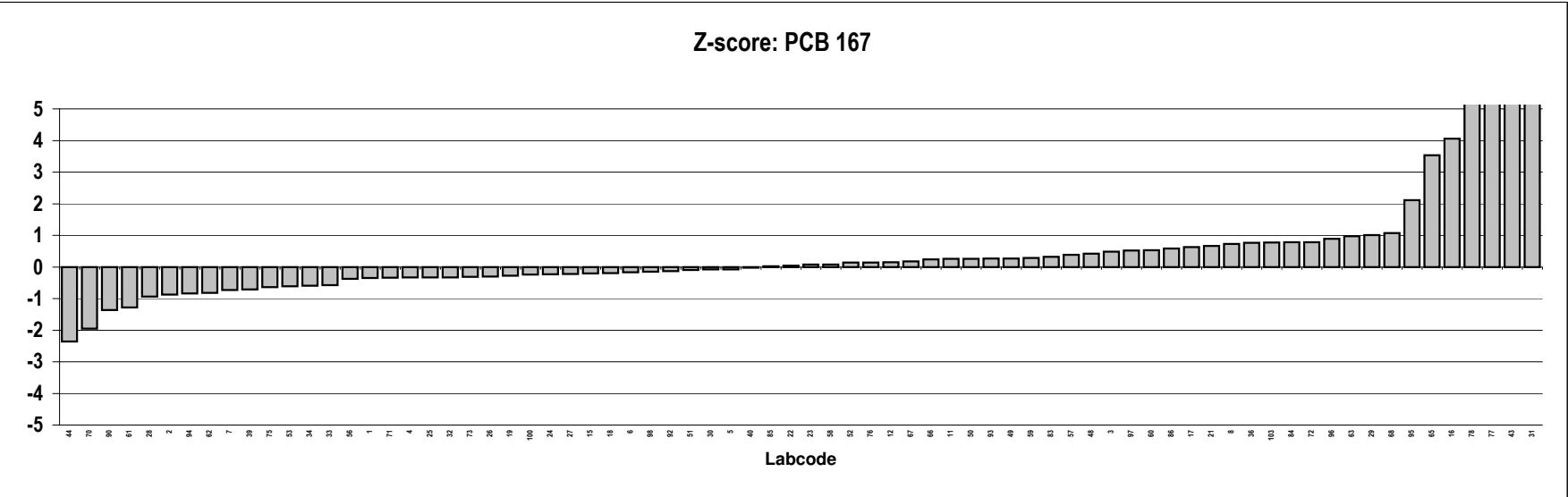
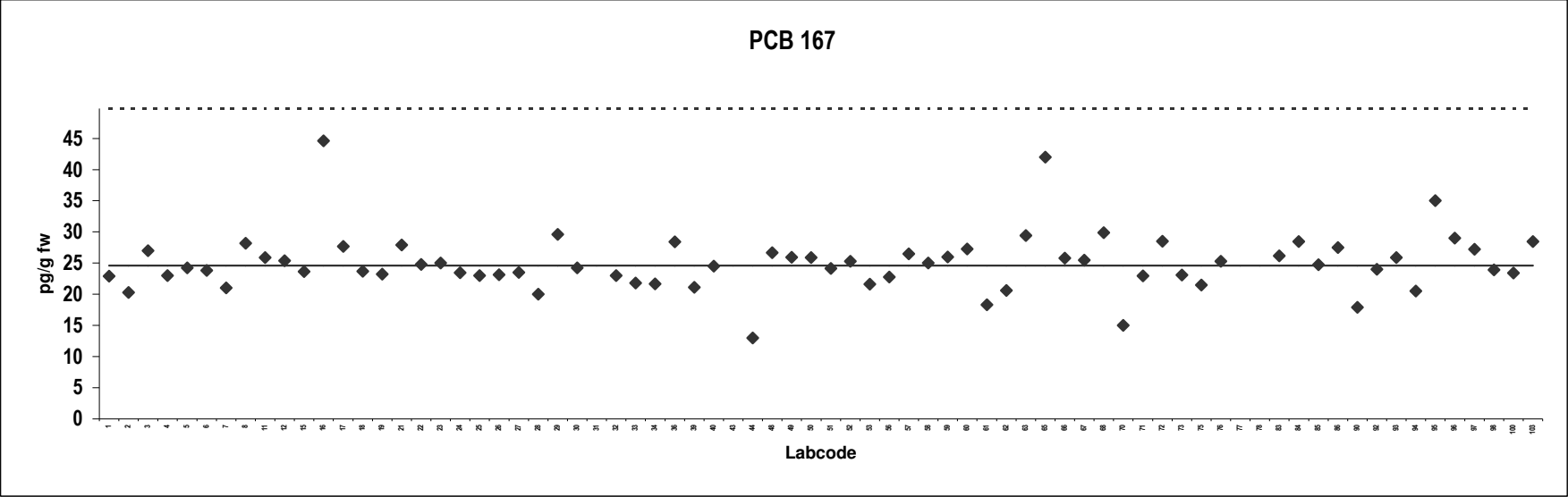
**Egg**  
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	23		61	18	
2	20		62	21	
3	27		63	29	
4	23		65	42	
5	24		66	26	
6	24		67	25	
7	21		68	30	
8	28		70	15	
11	26		71	23	
12	25		72	28	
15	24		73	23	
16	45		75	21	
17	28		76	25	
18	24		77	53	Outlier
19	23		78	52	Outlier
21	28		83	26	
22	25		84	28	
23	25		85	25	
24	23		86	27	
25	23		90	18	
26	23		92	24	
27	24		93	26	
28	20		94	21	
29	30		95	35	
30	24		96	29	
31	248	Outlier	97	27	
32	23		98	24	
33	22		100	23	
34	22		103	28	
36	28				
39	21				
40	25				
43	119	Outlier			
44	13				
48	27				
49	26				
50	26				
51	24				
52	25				
53	22				
56	23				
57	27				
58	25				
59	26				
60	27				

**Consensus statistics**

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	4.7
Relative standard deviation, %	19
No. of values reported	74
No. of values removed	4
No. of reported non-detects	0





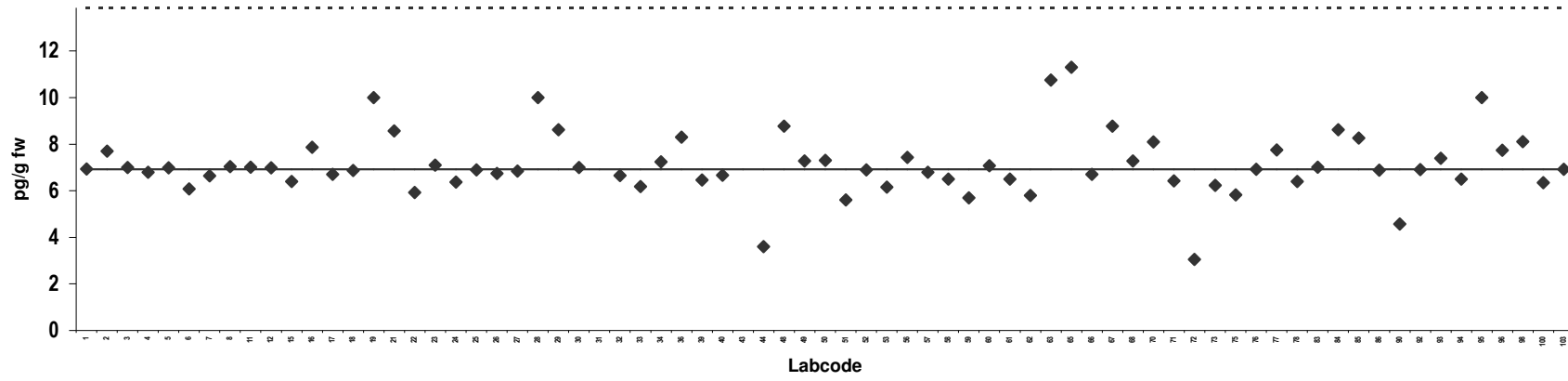
**Egg**  
Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	6.9		61	6.5	
2	7.7		62	5.8	
3	7.0		63	11	
4	6.8		65	11	
5	7.0		66	6.7	
6	6.1		67	8.8	
7	6.6		68	7.3	
8	7.0		70	8.1	
11	7.0		71	6.4	
12	7.0		72	3.1	ND
15	6.4		73	6.2	
16	7.9		75	5.8	
17	6.7		76	6.9	
18	6.9		77	7.8	
19	10	ND	78	6.4	
21	8.6		83	7.0	
22	5.9		84	8.6	
23	7.1		85	8.3	
24	6.4		86	6.9	
25	6.9		90	4.6	
26	6.7		92	6.9	
27	6.8		93	7.4	
28	10	ND	94	6.5	
29	8.6		95	10	
30	7.0		96	7.7	
31	61	Outlier	98	8.1	
32	6.7		100	6.4	
33	6.2		103	6.9	
34	7.2				
36	8.3				
39	6.5				
40	6.7				
43	32	Outlier			
44	3.6	ND			
48	8.8				
49	7.3				
50	7.3				
51	5.6				
52	6.9				
53	6.2				
56	7.4				
57	6.8				
58	6.5				
59	5.7				
60	7.1				

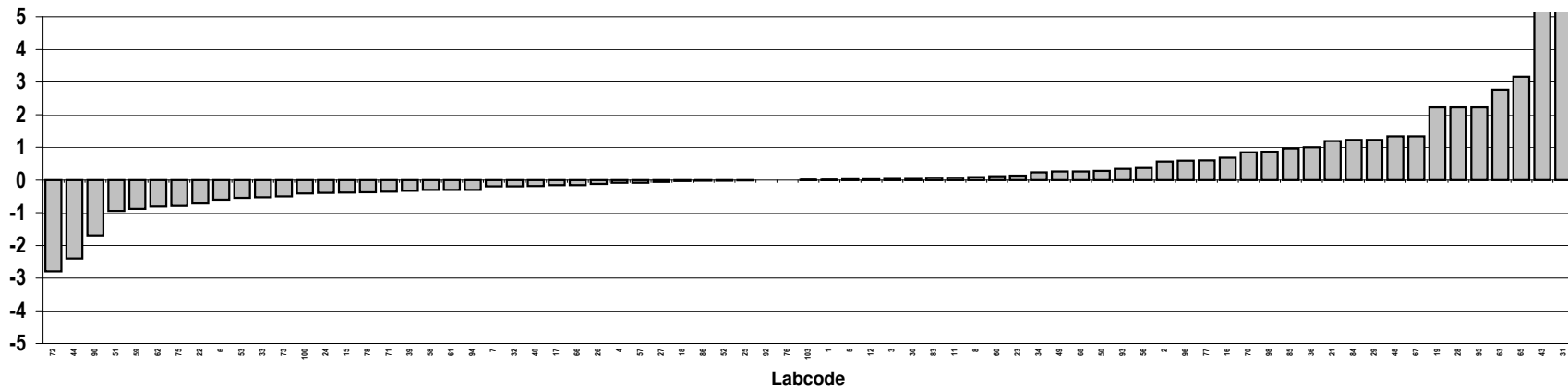
**Consensus statistics**

Consensus median, pg/g	6.9
Median all values pg/g	6.9
Consensus mean, pg/g	7.1
Standard deviation, pg/g	1.4
Relative standard deviation, %	19
No. of values reported	73
No. of values removed	2
No. of reported non-detects	4

### PCB 189



### Z-score: PCB 189



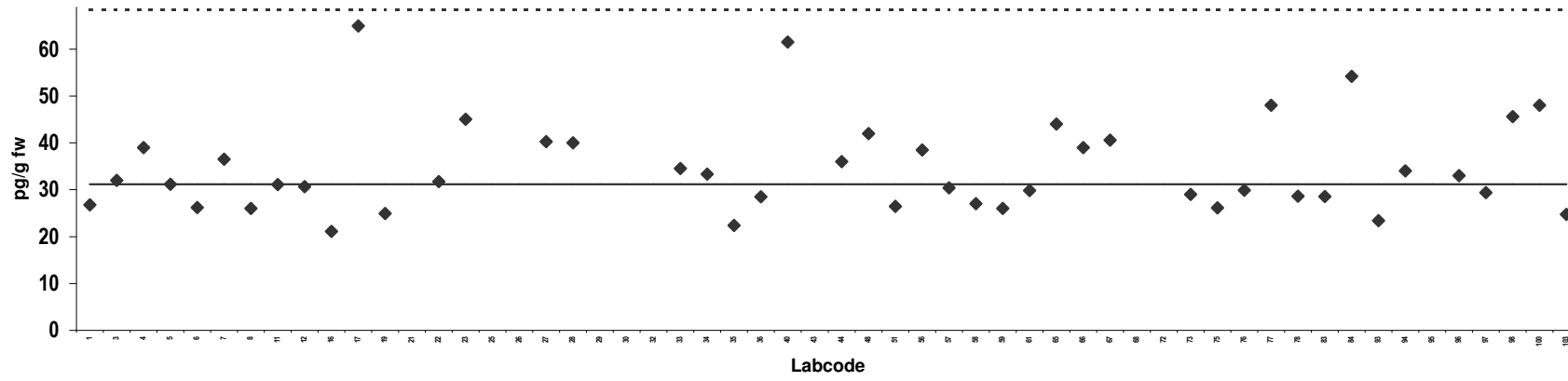
**Egg**  
Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	27		78	29	
3	32		83	29	
4	39		84	54	
5	31		93	23	
6	26		94	34	
7	36		95	97	Outlier,ND
8	26		96	33	
11	31		97	29	
12	31		98	46	
16	21		100	48	
17	65		103	25	
19	25				
21	76	Outlier			
22	32				
23	45				
25	83	Outlier			
26	264	Outlier			
27	40				
28	40				
29	199	Outlier			
30	103	Outlier			
32	201	Outlier			
33	35				
34	33				
35	22				
36	29				
40	61				
43	891	Outlier			
44	36				
48	42				
51	26				
56	38				
57	30				
58	27				
59	26				
61	30				
65	44				
66	39				
67	41				
68	182	Outlier			
72	166	Outlier			
73	29				
75	26				
76	30				
77	48	ND			

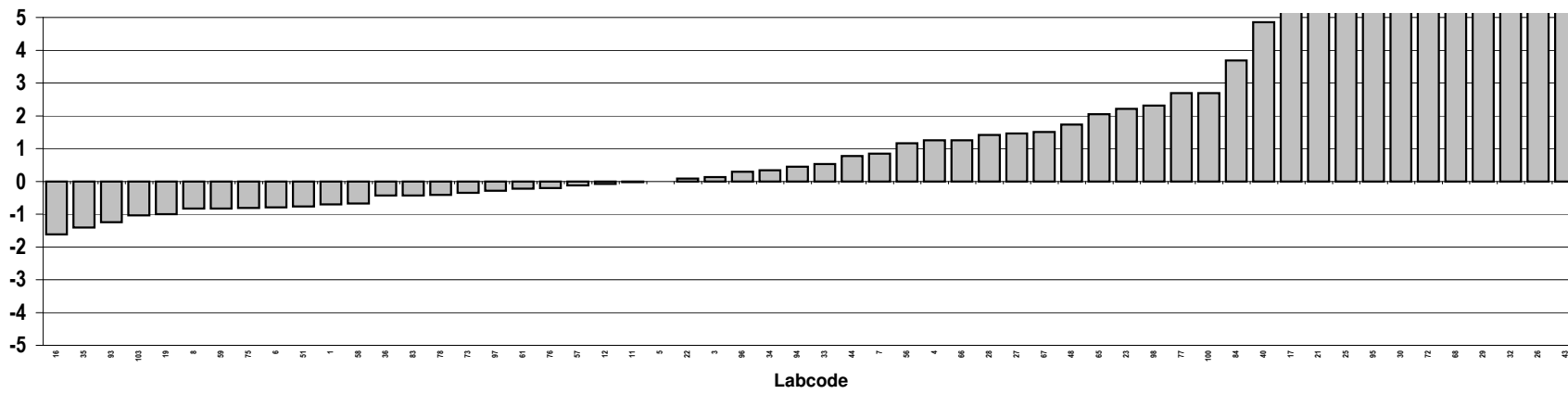
**Consensus statistics**

Consensus median, pg/g	31
Median all values pg/g	34
Consensus mean, pg/g	35
Standard deviation, pg/g	9.8
Relative standard deviation, %	28
No. of values reported	56
No. of values removed	10
No. of reported non-detects	2

### CB 28



### Z-score: CB 28

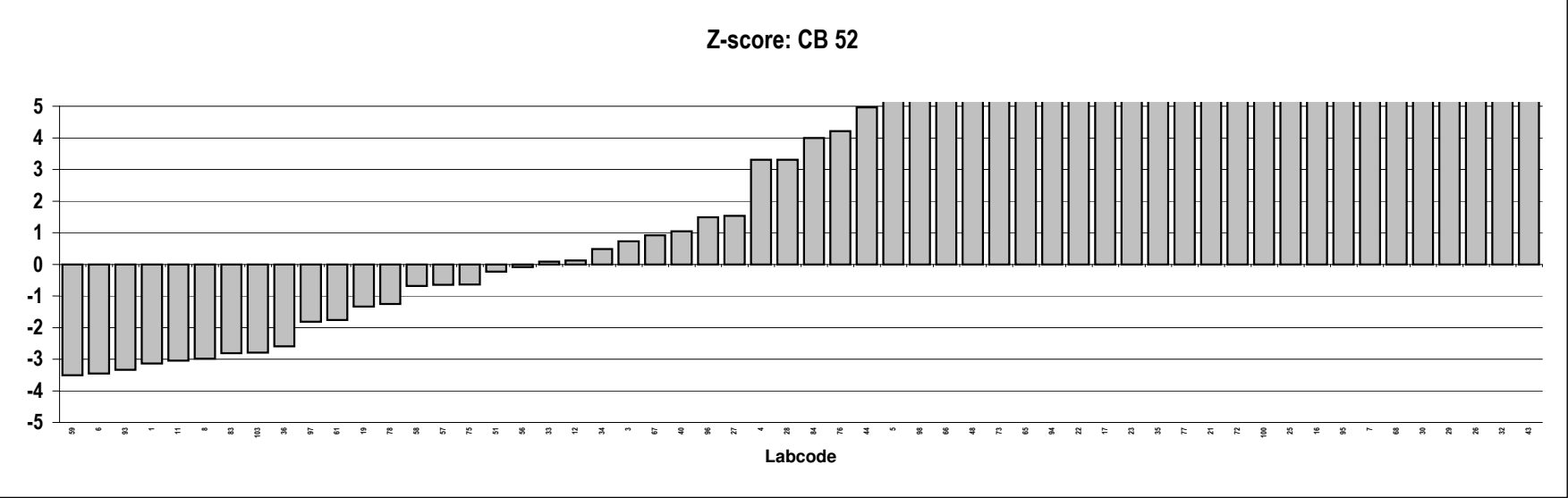
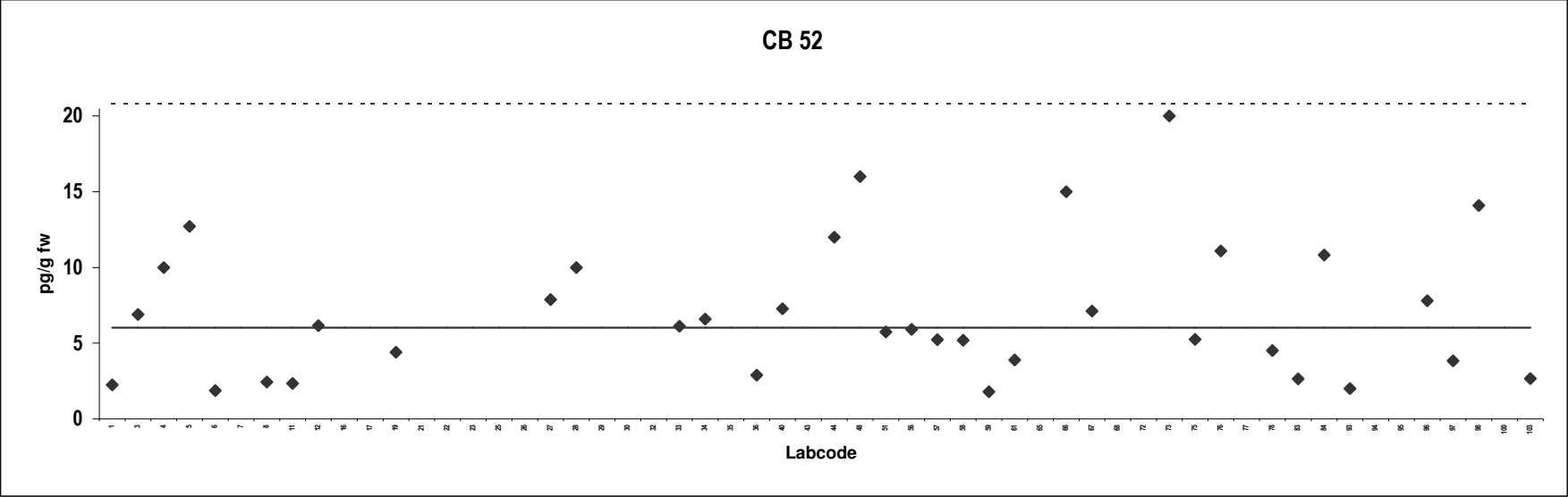


**Egg**  
Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.3		78	4.5	ND
3	6.9		83	2.6	
4	10		84	11	
5	13	ND	93	2.0	ND
6	1.9		94	22	Outlier
7	105	Outlier	95	97	Outlier,ND
8	2.4		96	7.8	
11	2.4		97	3.8	
12	6.2		98	14	
16	92	Outlier	100	90	Outlier
17	30	Outlier	103	2.7	
19	4.4				
21	51	Outlier			
22	23	Outlier			
23	38	Outlier			
25	90	Outlier			
26	194	Outlier			
27	7.9				
28	10				
29	153	Outlier			
30	146	Outlier			
32	451	Outlier			
33	6.1				
34	6.6				
35	40	Outlier			
36	2.9				
40	7.3				
43	730	Outlier			
44	12				
48	16				
51	5.7				
56	5.9				
57	5.2				
58	5.2				
59	1.8				
61	3.9				
65	21	Outlier			
66	15				
67	7.1				
68	141	Outlier			
72	75	Outlier			
73	20	ND			
75	5.3				
76	11				
77	48	Outlier,ND			

**Consensus statistics**

Consensus median, pg/g	6.0
Median all values pg/g	10
Consensus mean, pg/g	7.0
Standard deviation, pg/g	4.5
Relative standard deviation, %	65
No. of values reported	56
No. of values removed	20
No. of reported non-detects	6



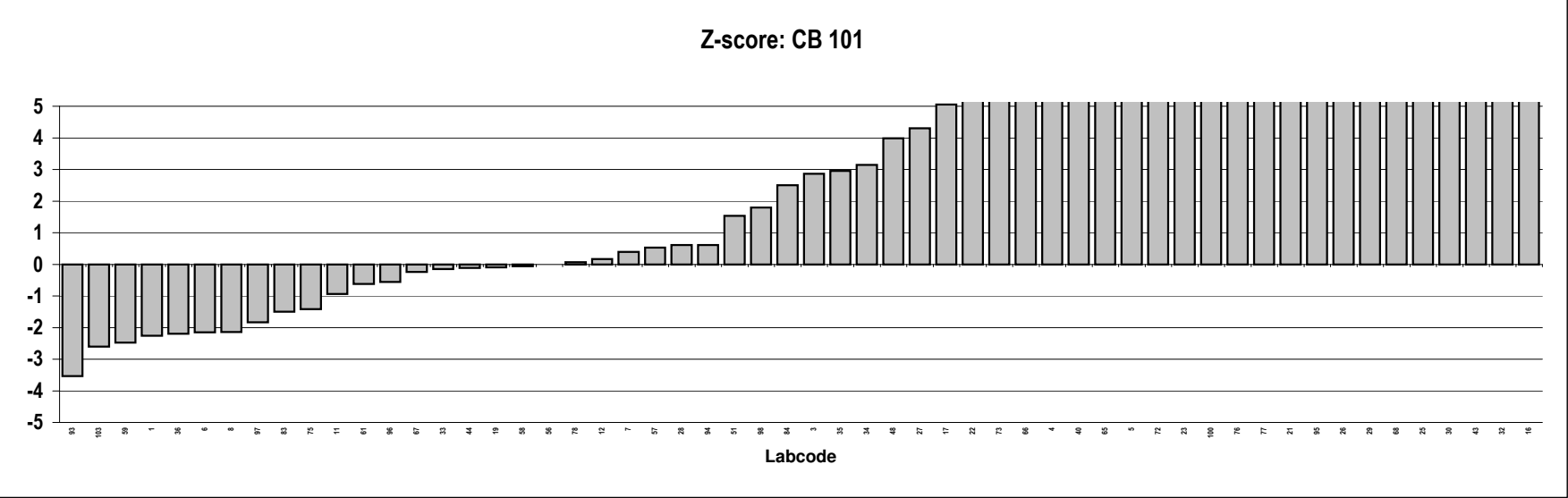
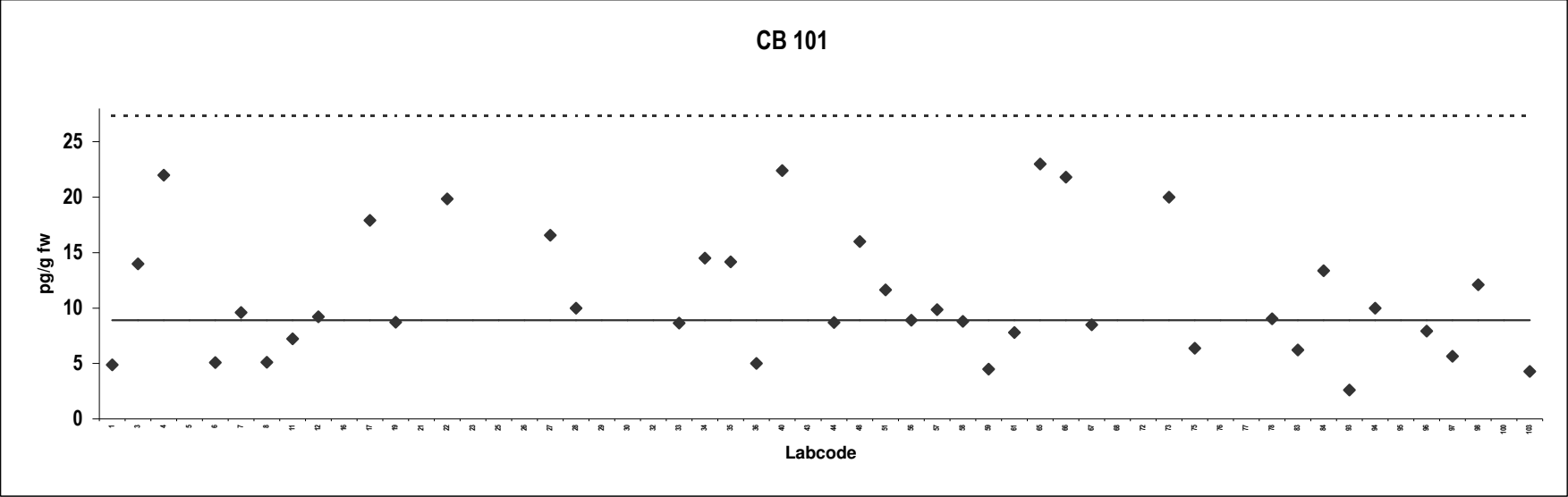
**Egg**  
Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.9		78	9.0	ND
3	14		83	6.2	
4	22		84	13	
5	29	Outlier	93	2.6	
6	5.1		94	10	
7	9.6		95	97	Outlier,ND
8	5.1		96	7.9	
11	7.2		97	5.6	
12	9.2		98	12	
16	1005	Outlier	100	37	Outlier
17	18		103	4.3	
19	8.7				
21	49	Outlier			
22	20				
23	33	Outlier			
25	124	Outlier			
26	101	Outlier			
27	17				
28	10	ND			
29	112	Outlier			
30	179	Outlier			
32	362	Outlier			
33	8.6				
34	15				
35	14				
36	5.0				
40	22				
43	301	Outlier			
44	8.7				
48	16				
51	12				
56	8.9				
57	9.9				
58	8.8				
59	4.5				
61	7.8				
65	23				
66	22				
67	8.5				
68	117	Outlier			
72	30	Outlier			
73	20	ND			
75	6.4				
76	43	Outlier			
77	48	Outlier,ND			

**Consensus statistics**

Consensus median, pg/g	8.9
Median all values pg/g	14
Consensus mean, pg/g	11
Standard deviation, pg/g	5.7
Relative standard deviation, %	52
No. of values reported	56
No. of values removed	16
No. of reported non-detects	5





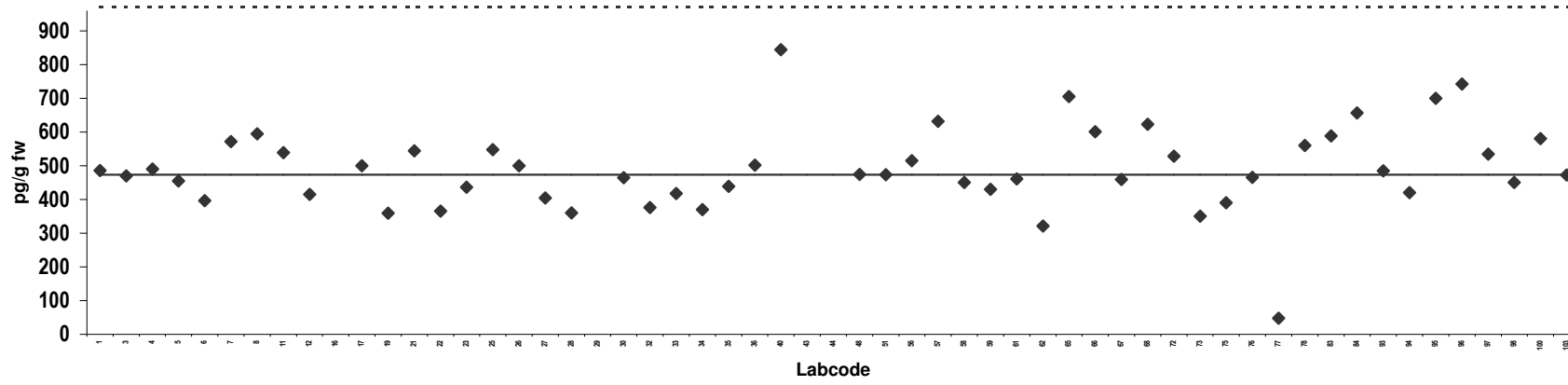
**Egg**  
Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	486		77	48	ND
3	470		78	560	
4	490		83	589	
5	454		84	656	
6	396		93	485	
7	572		94	420	
8	595		95	700	
11	539		96	742	
12	415		97	535	
16	1122	Outlier	98	450	
17	500		100	580	
19	359		103	472	
21	545				
22	365				
23	436				
25	548				
26	500				
27	405				
28	360				
29	1170	Outlier			
30	464				
32	376				
33	418				
34	370				
35	439				
36	502				
40	844				
43	2303	Outlier			
44	1600	Outlier			
48	474				
51	474				
56	515				
57	632				
58	450				
59	430				
61	461				
62	322				
65	705				
66	601				
67	459				
68	623				
72	528				
73	350				
75	390				
76	465				

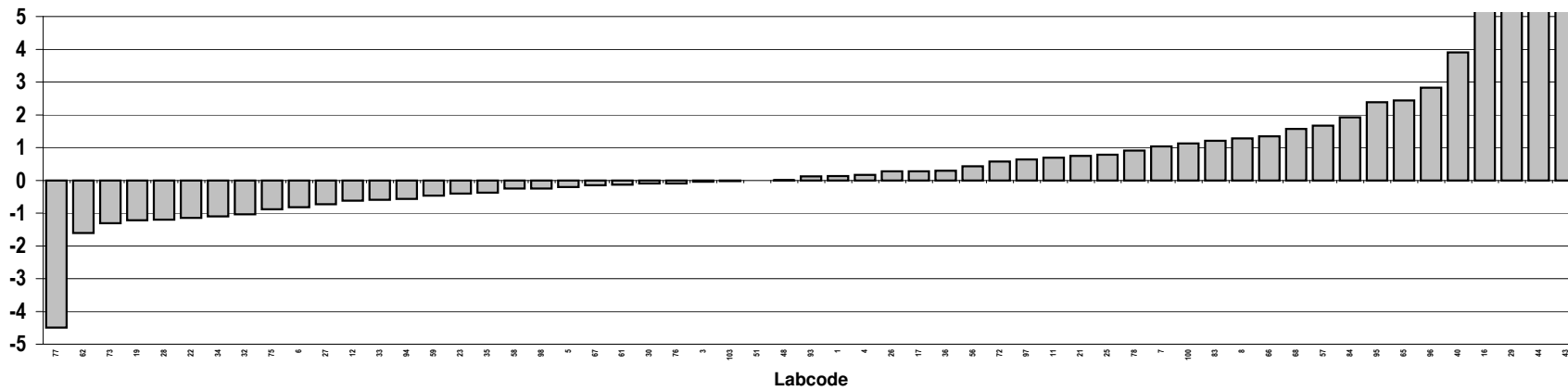
**Consensus statistics**

Consensus median, pg/g	474
Median all values pg/g	485
Consensus mean, pg/g	490
Standard deviation, pg/g	123
Relative standard deviation, %	25
No. of values reported	57
No. of values removed	4
No. of reported non-detects	1

### CB 138



### Z-score: CB 138



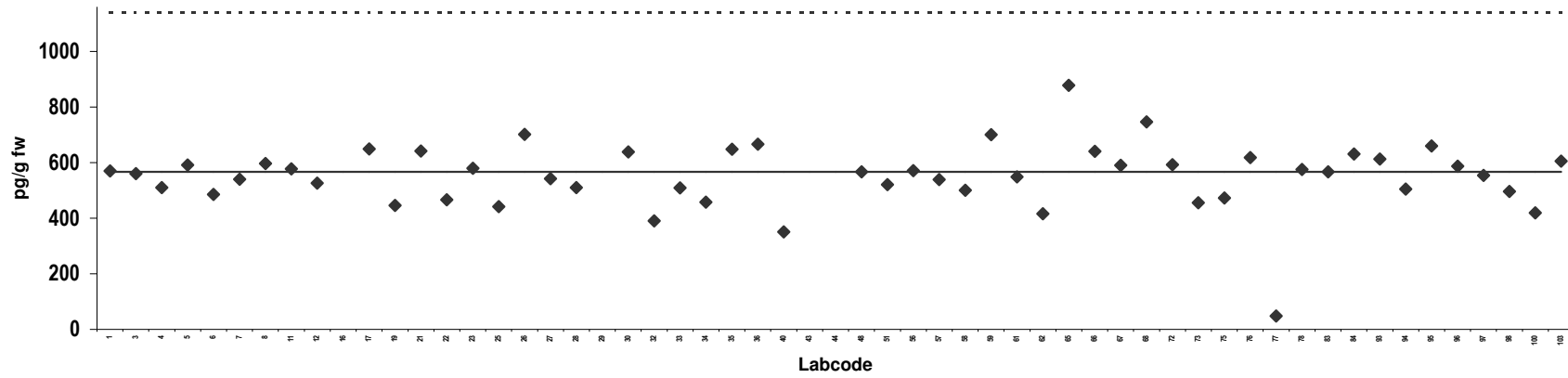
**Egg**  
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	570		77	48	ND
3	560		78	575	
4	510		83	567	
5	592		84	631	
6	486		93	613	
7	540		94	505	
8	597		95	660	
11	577		96	587	
12	526		97	554	
16	1857	Outlier	98	496	
17	649		100	419	
19	446		103	605	
21	641				
22	467				
23	579				
25	442				
26	701				
27	542				
28	510				
29	1380	Outlier			
30	639				
32	391				
33	509				
34	458				
35	648				
36	666				
40	351				
43	2797	Outlier			
44	1600	Outlier			
48	567				
51	521				
56	571				
57	539				
58	500				
59	700				
61	548				
62	415				
65	878				
66	640				
67	590				
68	746				
72	592				
73	455				
75	473				
76	618				

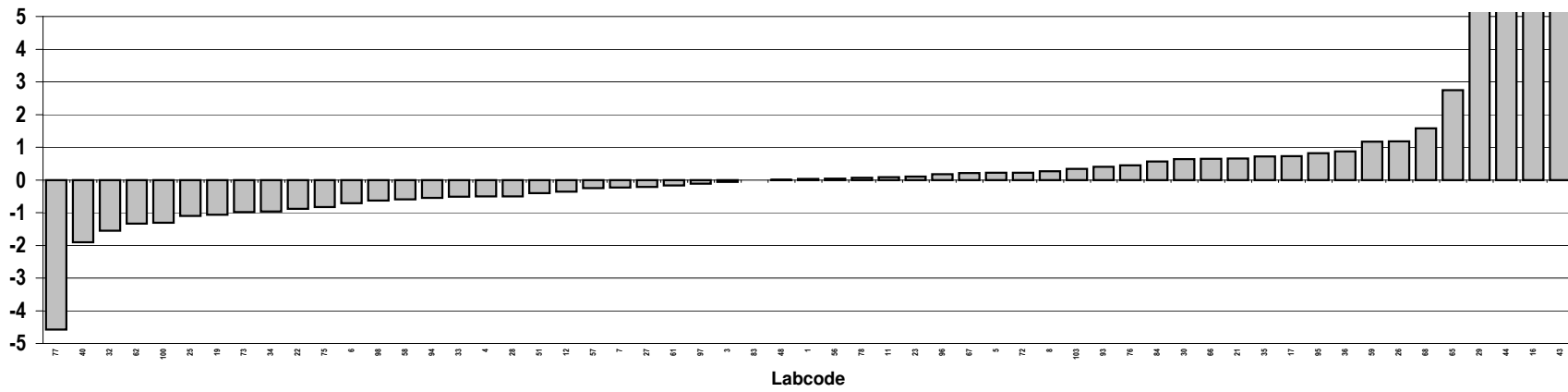
**Consensus statistics**

Consensus median, pg/g	567
Median all values pg/g	570
Consensus mean, pg/g	551
Standard deviation, pg/g	117
Relative standard deviation, %	21
No. of values reported	57
No. of values removed	4
No. of reported non-detects	1

### CB 153



### Z-score: CB 153

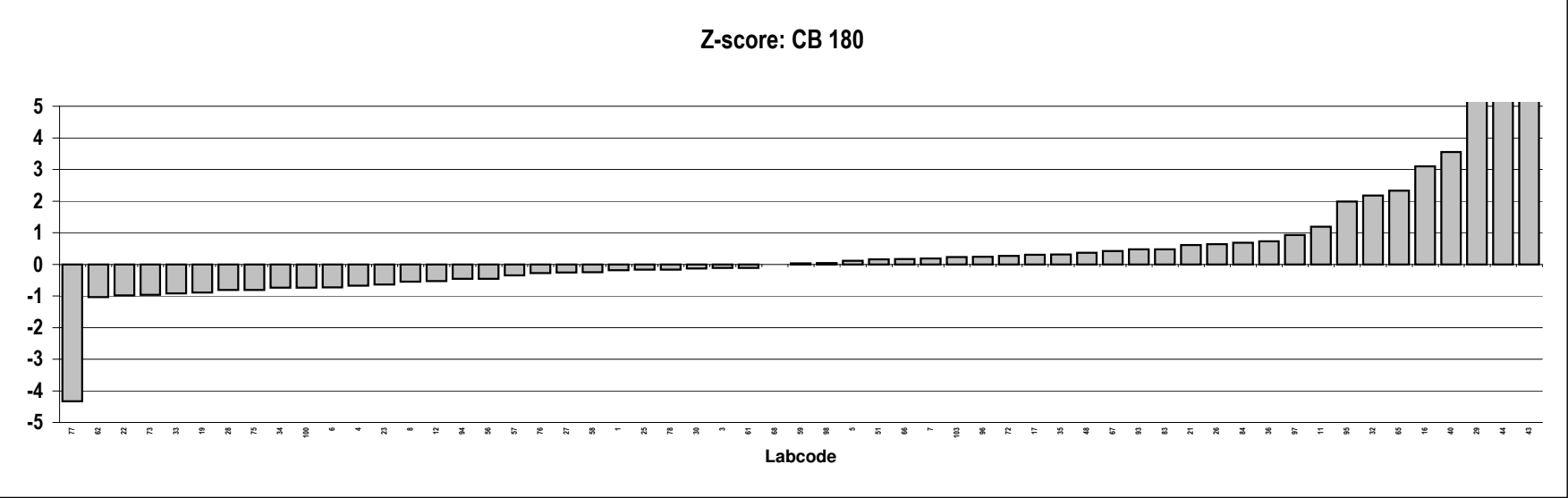
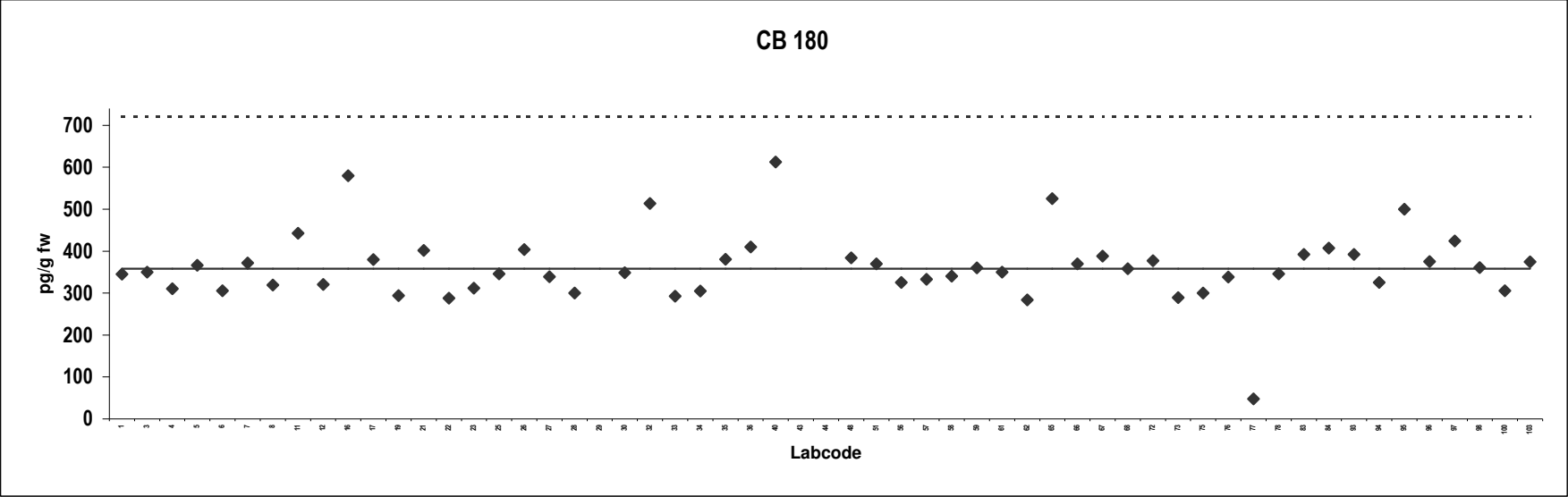


**Egg**  
Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	345		77	48	ND
3	350		78	346	
4	310		83	392	
5	366		84	407	
6	306		93	392	
7	372		94	325	
8	319		95	500	
11	443		96	375	
12	320		97	424	
16	580		98	361	
17	380		100	305	
19	294		103	374	
21	402				
22	288				
23	312				
25	346				
26	404				
27	339				
28	300				
29	867	Outlier			
30	348				
32	514				
33	293				
34	305				
35	380				
36	410				
40	613				
43	1537	Outlier			
44	1100	Outlier			
48	384				
51	370				
56	325				
57	333				
58	340				
59	360				
61	350				
62	284				
65	525				
66	370				
67	388				
68	358				
72	377				
73	289				
75	300				
76	338				

**Consensus statistics**

Consensus median, pg/g	358
Median all values pg/g	360
Consensus mean, pg/g	363
Standard deviation, pg/g	82
Relative standard deviation, %	23
No. of values reported	57
No. of values removed	3
No. of reported non-detects	1



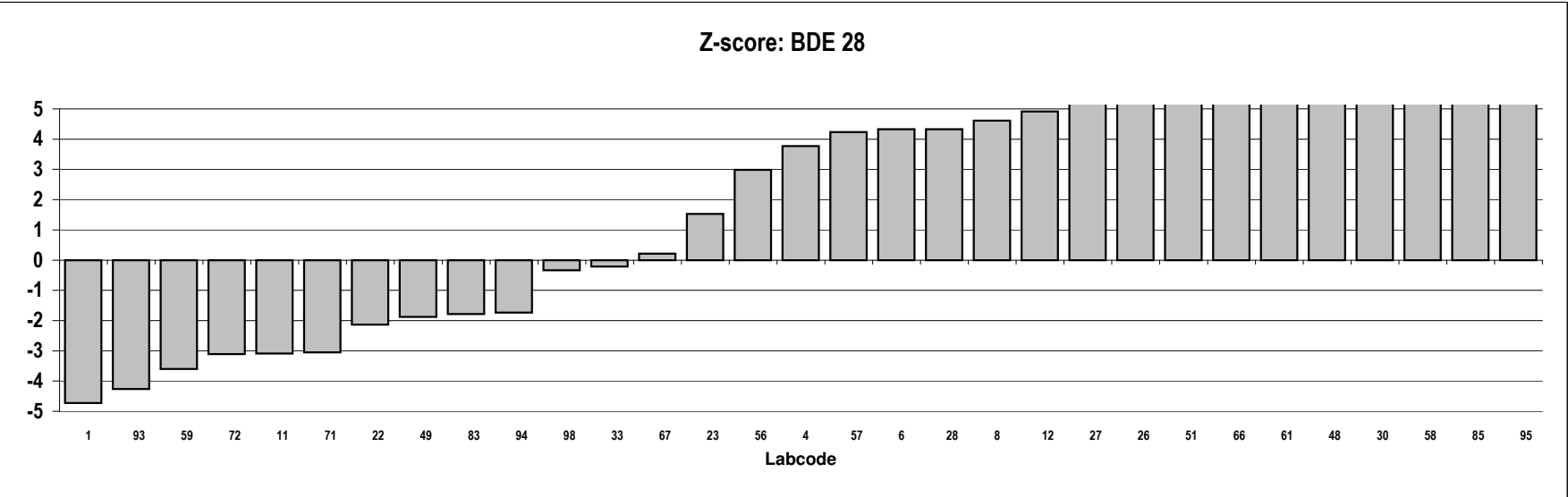
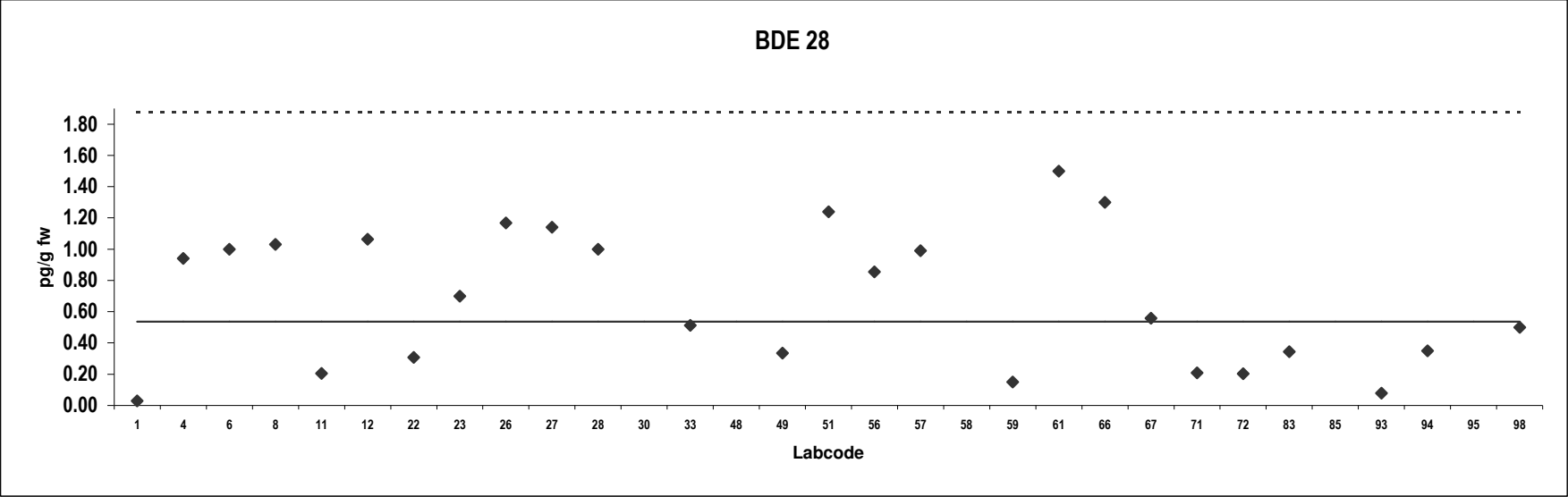
**Egg**  
Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.030				
4	0.94				
6	1.0	ND			
8	1.0				
11	0.21				
12	1.1	ND			
22	0.31				
23	0.70				
26	1.2				
27	1.1				
28	1.0	ND			
30	4.5	Outlier			
33	0.51				
48	2.0	Outlier,ND			
49	0.34				
51	1.2	ND			
56	0.86				
57	0.99				
58	5.0	Outlier,ND			
59	0.15				
61	1.5	ND			
66	1.3				
67	0.56				
71	0.21				
72	0.20	ND			
83	0.35				
85	6.0	Outlier,ND			
93	0.079	ND			
94	0.35				
95	10	Outlier,ND			
98	0.50	ND			

**Consensus statistics**

Consensus median, pg/g	0.54
Median all values pg/g	0.94
Consensus mean, pg/g	0.68
Standard deviation, pg/g	0.44
Relative standard deviation, %	64
No. of values reported	31
No. of values removed	5
No. of reported non-detects	12



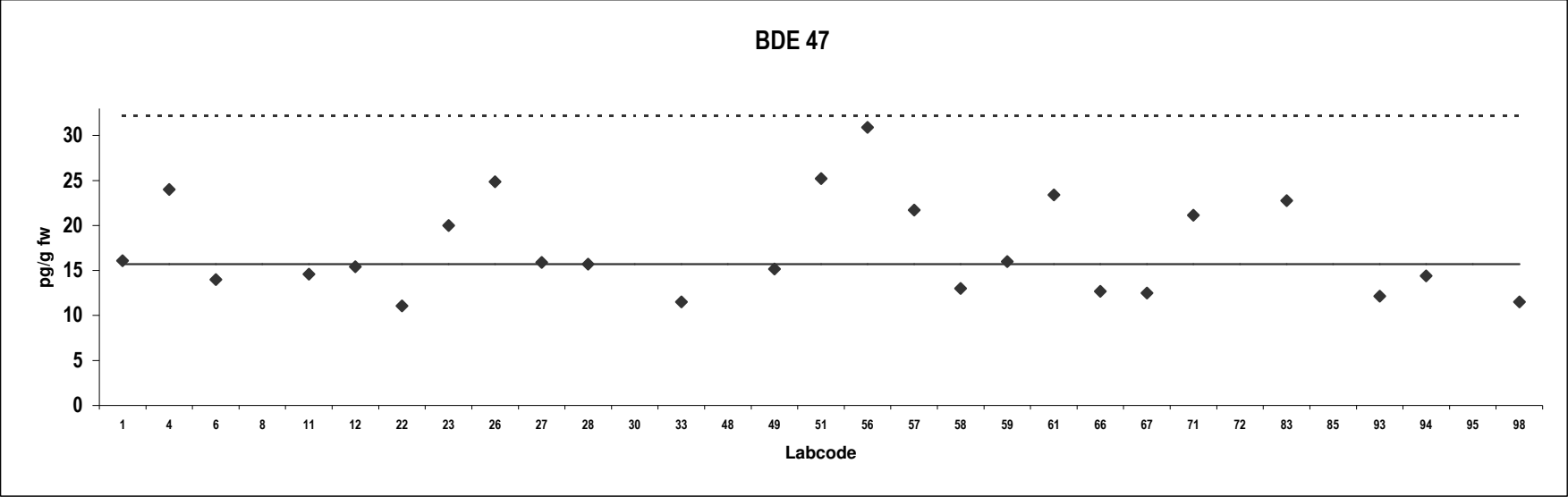


**Egg**  
Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	16				
4	24				
6	14				
8	38	Outlier			
11	15				
12	15				
22	11				
23	20				
26	25				
27	16				
28	16				
30	65	Outlier			
33	12				
48	63	Outlier			
49	15				
51	25				
56	31				
57	22				
58	13				
59	16				
61	23				
66	13				
67	12				
71	21				
72	38	Outlier			
83	23				
85	83	Outlier			
93	12				
94	14				
95	500	Outlier,ND			
98	12				

**Consensus statistics**

Consensus median, pg/g	16
Median all values pg/g	16
Consensus mean, pg/g	17
Standard deviation, pg/g	5.4
Relative standard deviation, %	31
No. of values reported	31
No. of values removed	6
No. of reported non-detects	1

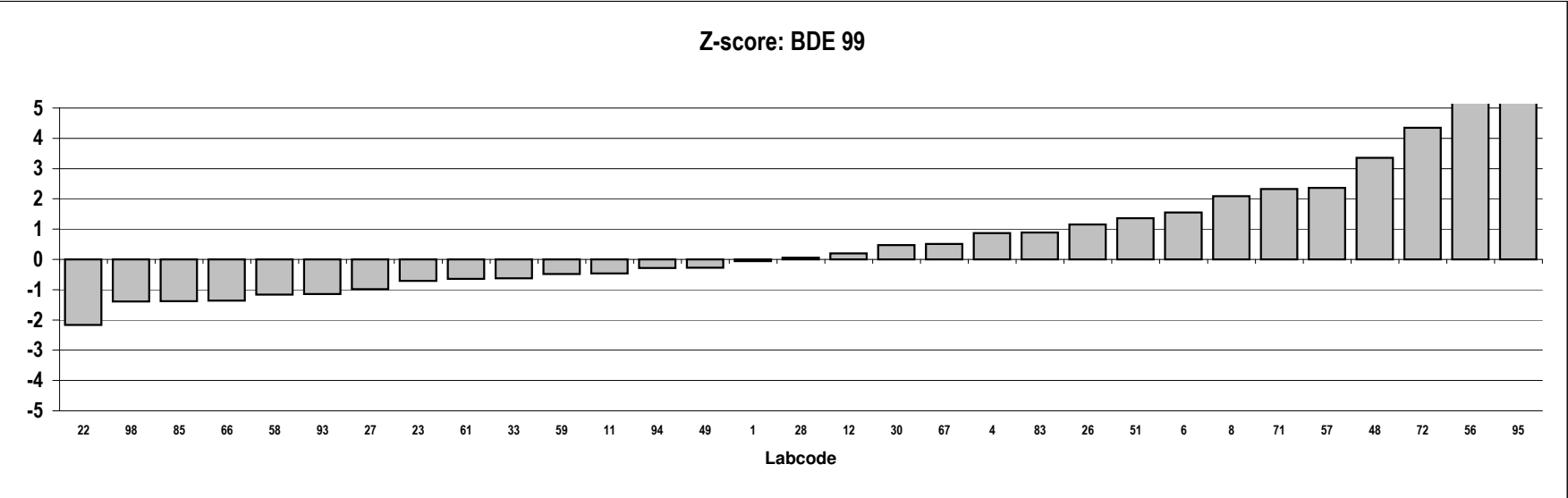
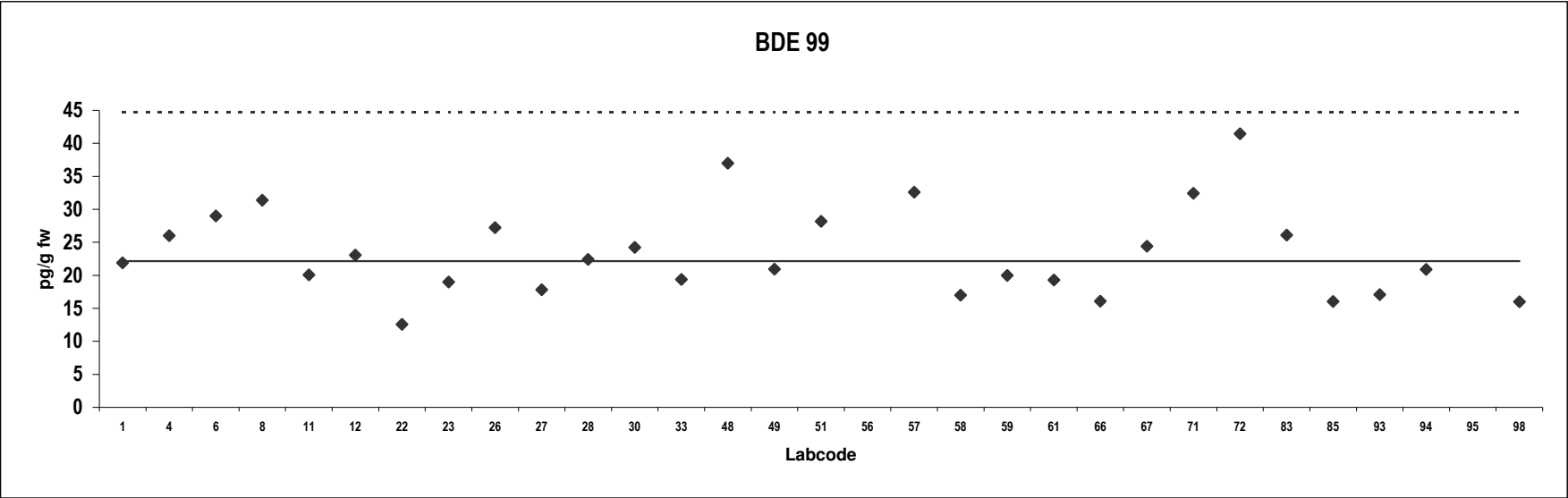


**Egg**  
Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	22				
4	26				
6	29				
8	31				
11	20				
12	23				
22	13				
23	19				
26	27				
27	18				
28	22				
30	24				
33	19				
48	37				
49	21				
51	28				
56	74	Outlier			
57	33				
58	17				
59	20				
61	19				
66	16				
67	24				
71	32				
72	41				
83	26				
85	16	ND			
93	17				
94	21				
95	500	Outlier,ND			
98	16				

**Consensus statistics**

Consensus median, pg/g	22
Median all values pg/g	22
Consensus mean, pg/g	23
Standard deviation, pg/g	6.8
Relative standard deviation, %	29
No. of values reported	31
No. of values removed	2
No. of reported non-detects	2

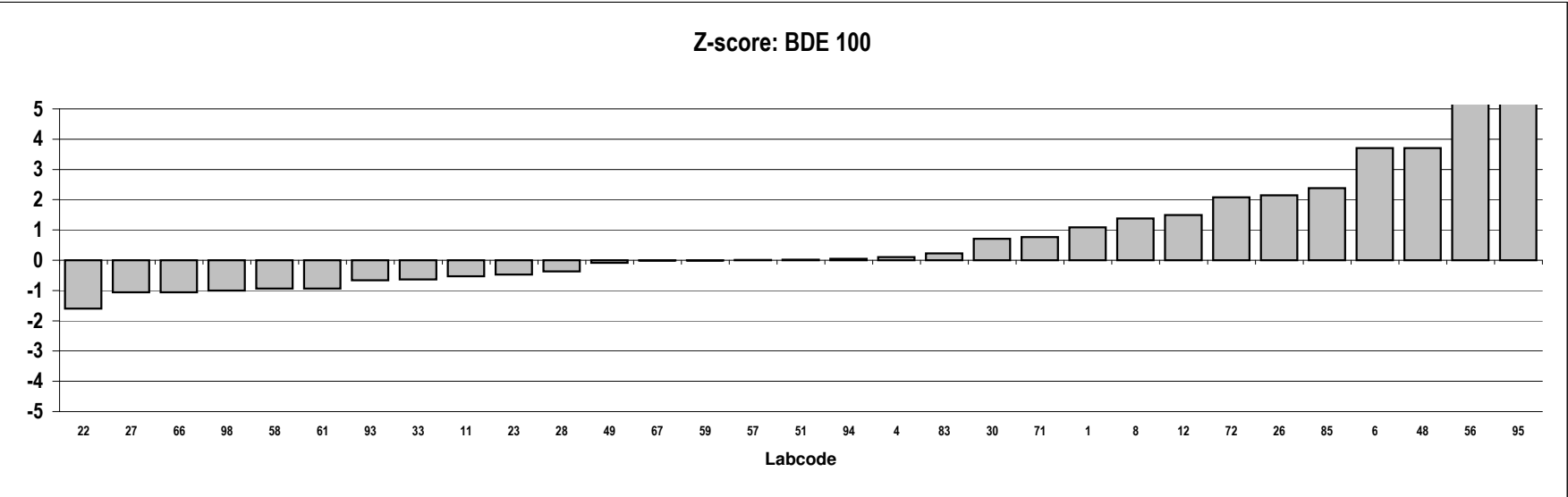
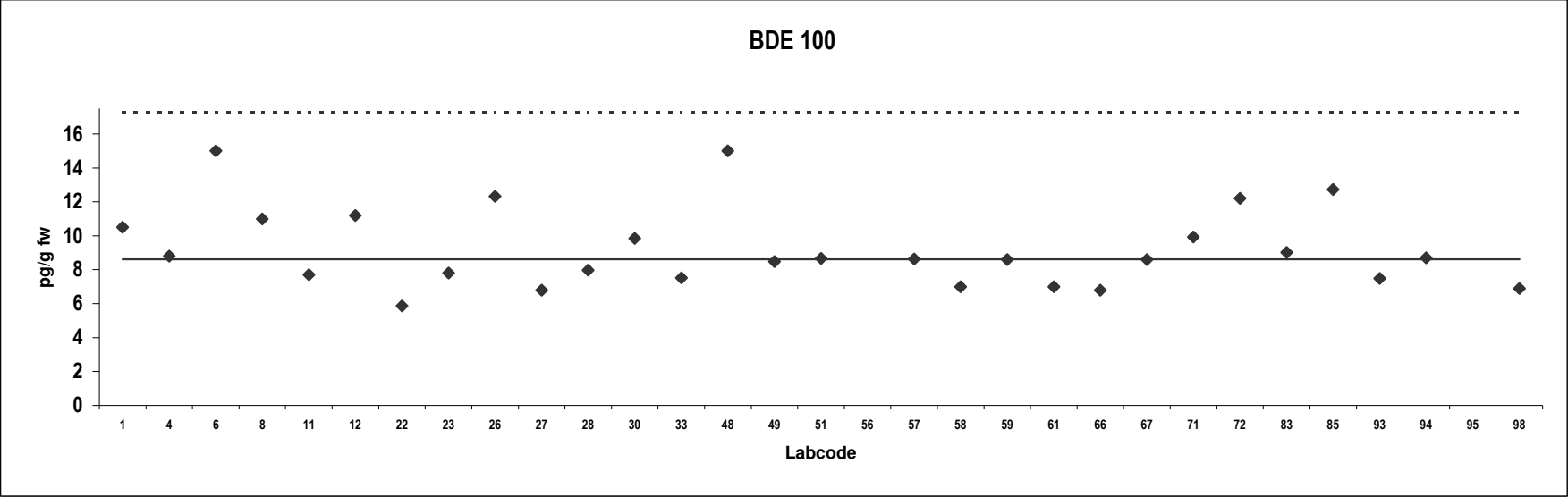


**Egg**  
Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11				
4	8.8				
6	15				
8	11				
11	7.7				
12	11				
22	5.9				
23	7.8				
26	12				
27	6.8				
28	8.0				
30	9.8				
33	7.5				
48	15				
49	8.5				
51	8.7				
56	19	Outlier			
57	8.6				
58	7.0				
59	8.6				
61	7.0				
66	6.8				
67	8.6				
71	9.9				
72	12				
83	9.0				
85	13	ND			
93	7.5				
94	8.7				
95	130	Outlier			
98	6.9				

**Consensus statistics**

Consensus median, pg/g	8.6
Median all values pg/g	8.7
Consensus mean, pg/g	9.2
Standard deviation, pg/g	2.4
Relative standard deviation, %	26
No. of values reported	31
No. of values removed	2
No. of reported non-detects	1



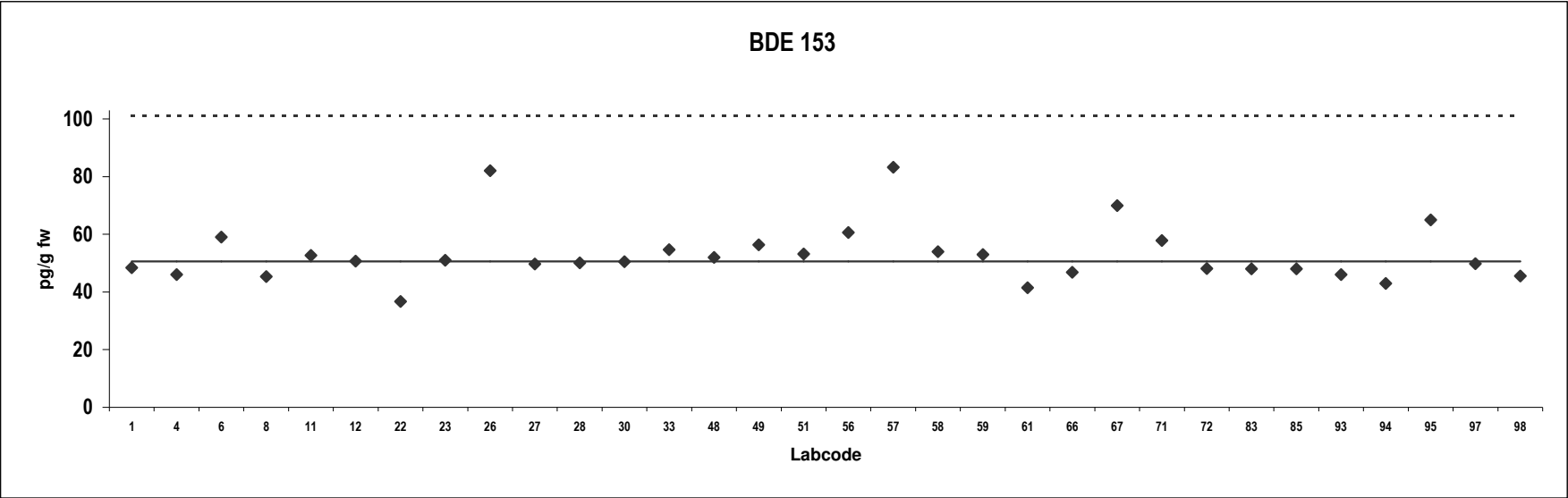
**Egg**  
Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	48				
4	46				
6	59				
8	45				
11	53				
12	51				
22	37				
23	51				
26	82				
27	50				
28	50				
30	51				
33	55				
48	52				
49	56				
51	53				
56	61				
57	83				
58	54				
59	53				
61	42				
66	47				
67	70				
71	58				
72	48				
83	48				
85	48				
93	46				
94	43				
95	65				
97	50				
98	46				

**Consensus statistics**

Consensus median, pg/g	51
Median all values pg/g	51
Consensus mean, pg/g	53
Standard deviation, pg/g	10
Relative standard deviation, %	19
No. of values reported	32
No. of values removed	0
No. of reported non-detects	0



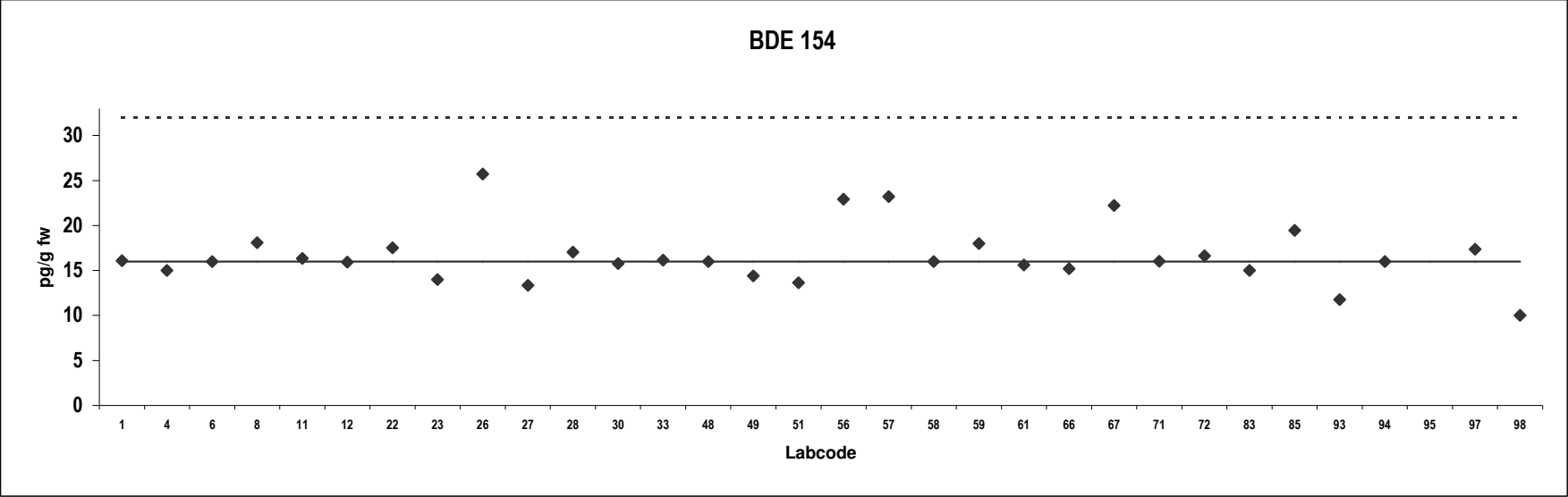


**Egg**  
Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	16				
4	15				
6	16				
8	18				
11	16				
12	16				
22	18				
23	14				
26	26				
27	13				
28	17				
30	16				
33	16				
48	16				
49	14				
51	14				
56	23				
57	23				
58	16				
59	18				
61	16				
66	15				
67	22				
71	16				
72	17				
83	15				
85	19				
93	12				
94	16				
95	100	Outlier,ND			
97	17				
98	10				

**Consensus statistics**

Consensus median, pg/g	16
Median all values pg/g	16
Consensus mean, pg/g	17
Standard deviation, pg/g	3.3
Relative standard deviation, %	20
No. of values reported	32
No. of values removed	1
No. of reported non-detects	1

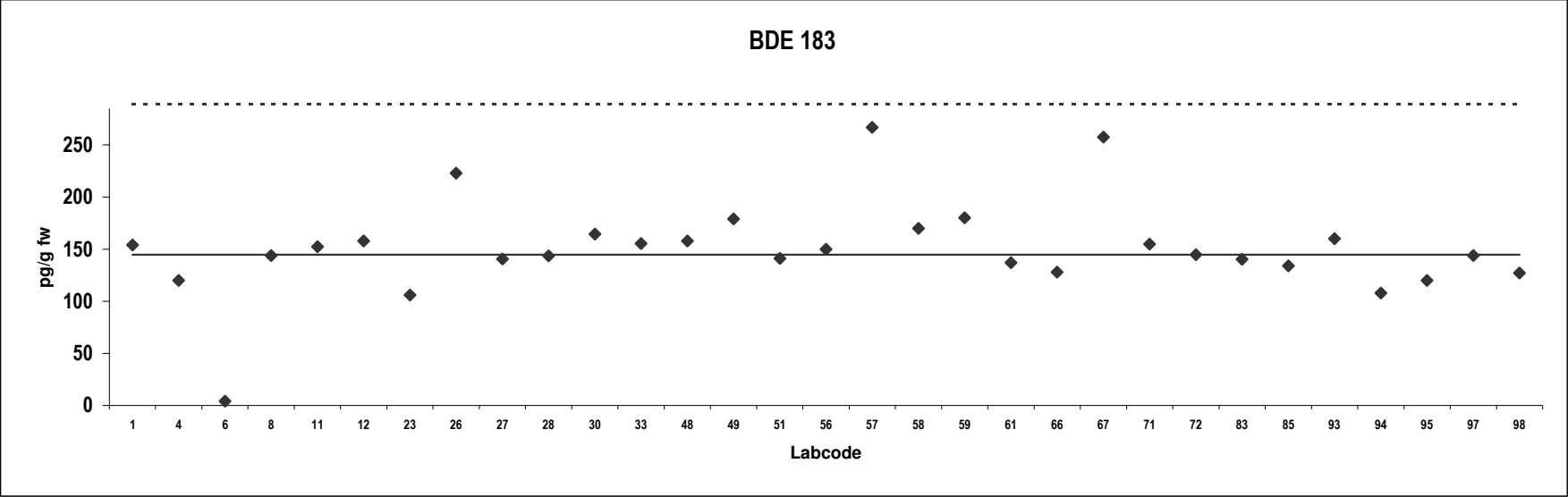


**Egg**  
Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	154				
4	120				
6	4.0				
8	144				
11	152				
12	158				
23	106				
26	223				
27	141				
28	144				
30	165				
33	155				
48	158				
49	179				
51	141				
56	150				
57	267				
58	170				
59	180				
61	137				
66	128				
67	257				
71	155				
72	145				
83	140				
85	134				
93	160				
94	108				
95	120				
97	144				
98	127				

**Consensus statistics**

Consensus median, pg/g	145
Median all values pg/g	145
Consensus mean, pg/g	150
Standard deviation, pg/g	45
Relative standard deviation, %	30
No. of values reported	31
No. of values removed	0
No. of reported non-detects	0

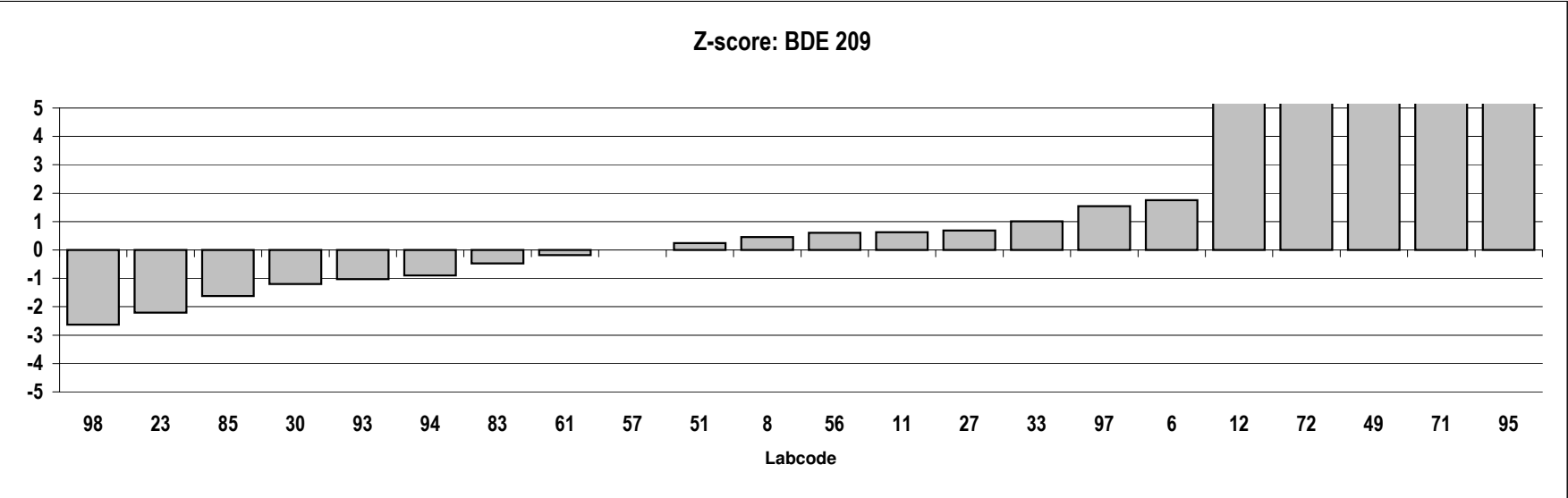
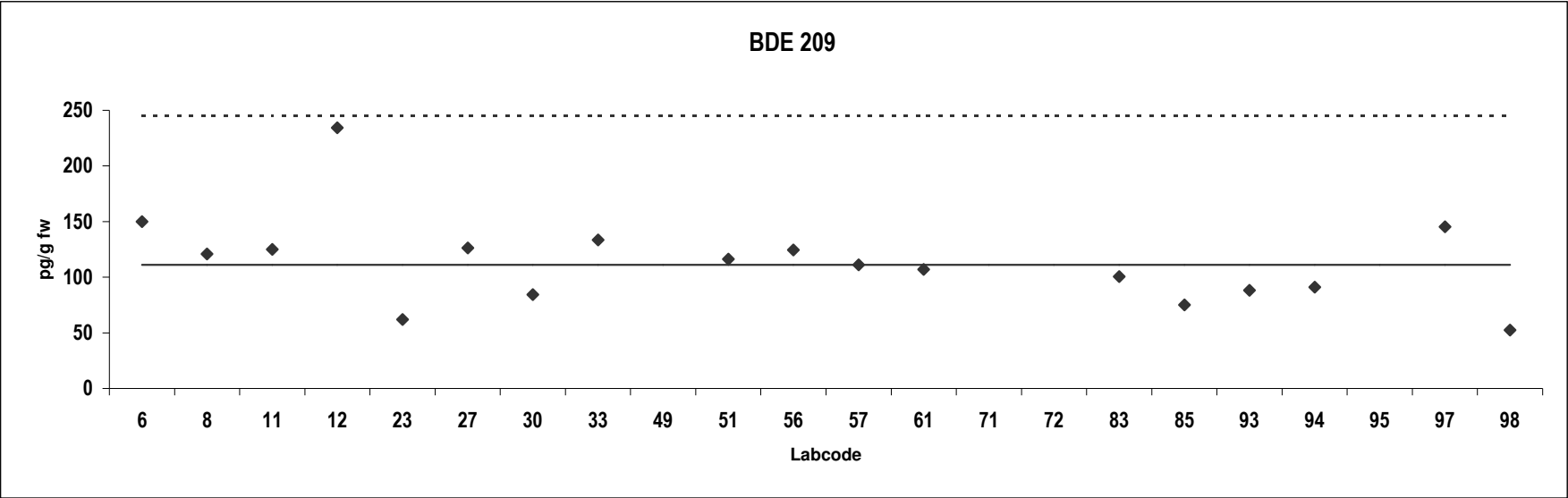


**Egg**  
Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	150	ND			
8	121				
11	125				
12	234				
23	62				
27	126				
30	84				
33	133				
49	1035	Outlier			
51	116				
56	124				
57	111				
61	107				
71	1633	Outlier			
72	282	Outlier			
83	100				
85	75				
93	88				
94	91				
95	5000	Outlier,ND			
97	145				
98	53				

**Consensus statistics**

Consensus median, pg/g	111
Median all values pg/g	123
Consensus mean, pg/g	114
Standard deviation, pg/g	41
Relative standard deviation, %	36
No. of values reported	22
No. of values removed	4
No. of reported non-detects	2



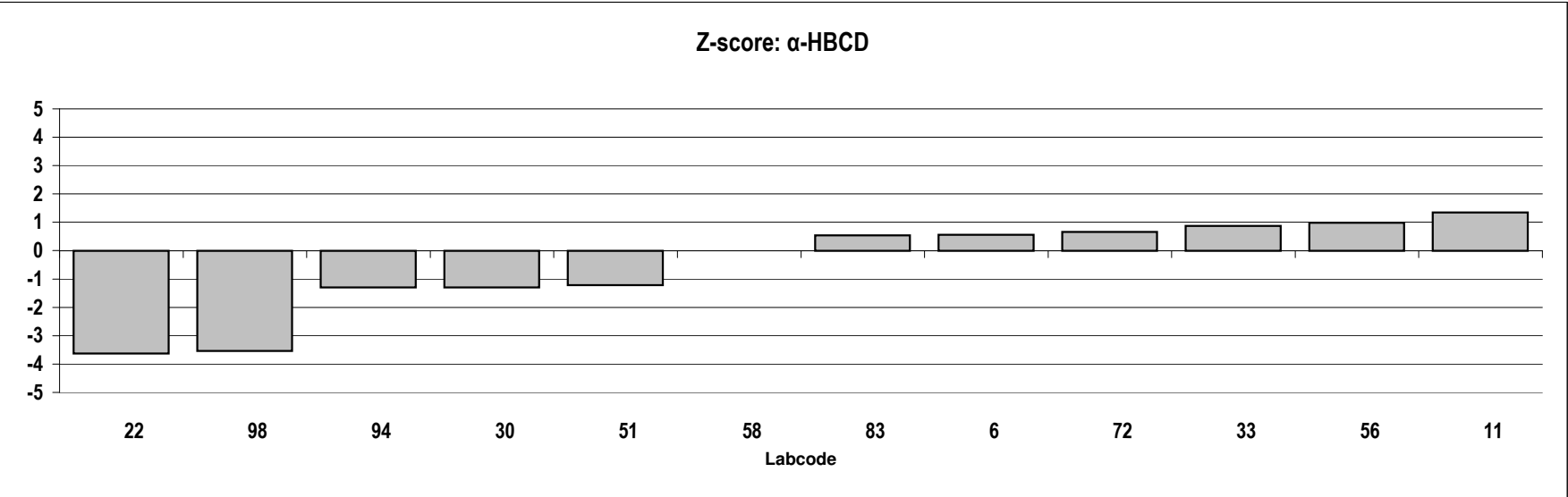
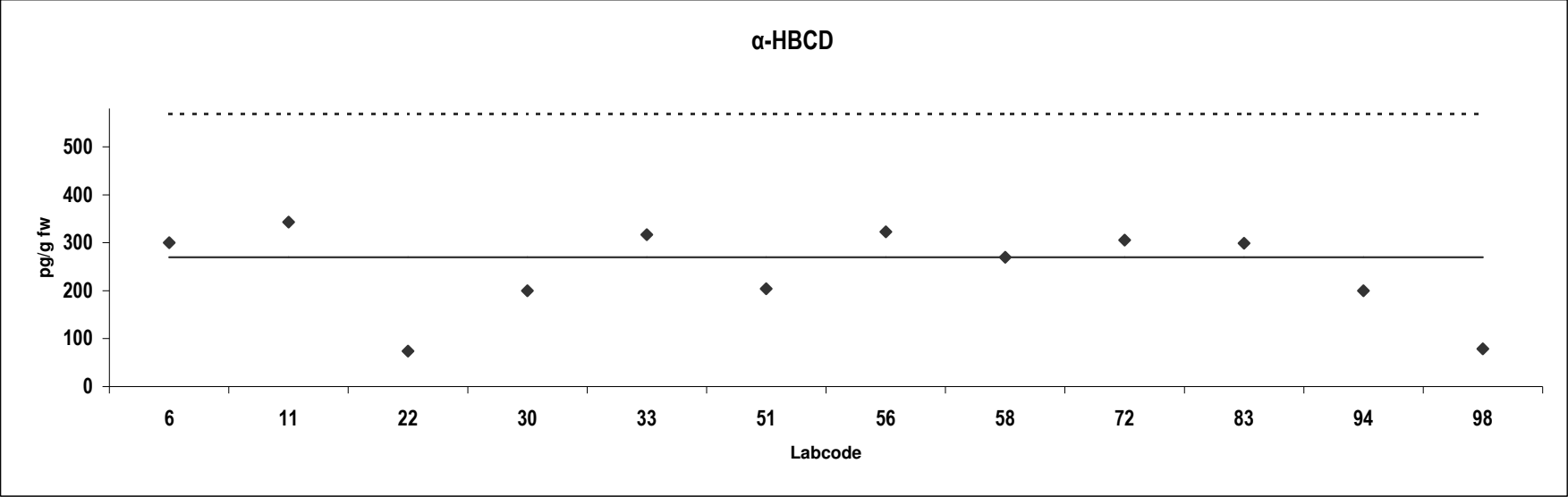
**Egg**  
Congener:  $\alpha$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	300	ND			
11	343				
22	74				
30	200				
33	317				
51	204				
56	323				
58	270				
72	306				
83	299				
94	200				
98	79				

**Consensus statistics**

Consensus median, pg/g	270
Median all values pg/g	285
Consensus mean, pg/g	243
Standard deviation, pg/g	92
Relative standard deviation, %	38
No. of values reported	12
No. of values removed	0
No. of reported non-detects	1



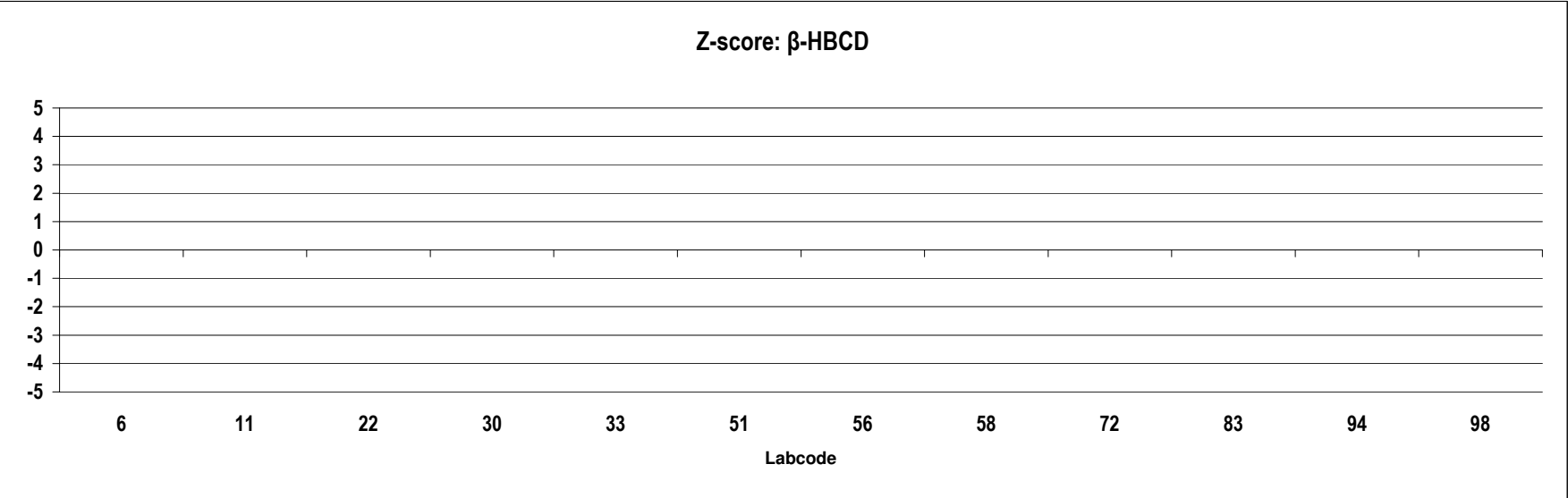
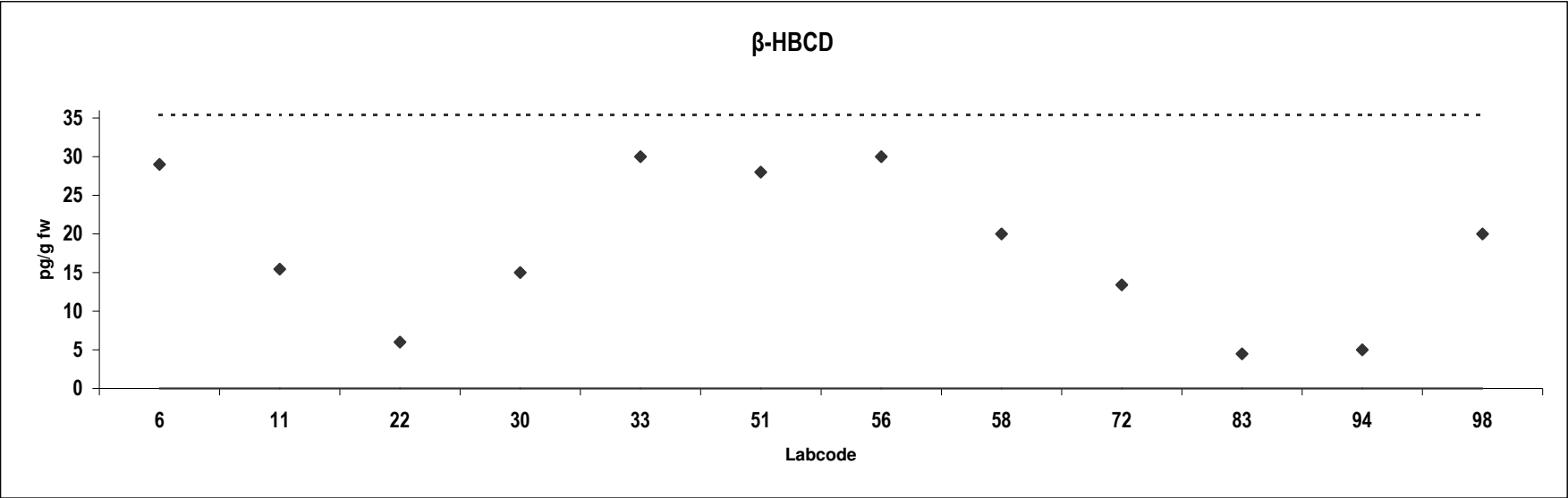


**Egg**  
Congener:  $\beta$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	29	ND			
11	15	ND			
22	6.0	ND			
30	15	ND			
33	30	ND			
51	28	ND			
56	30	ND			
58	20	ND			
72	13	ND			
83	4.5	ND			
94	5.0	ND			
98	20	ND			

**Consensus statistics**

Consensus median, pg/g	
Median all values pg/g	18
Consensus mean, pg/g	18
Standard deviation, pg/g	9.8
Relative standard deviation, %	54
No. of values reported	12
No. of values removed	0
No. of reported non-detects	12

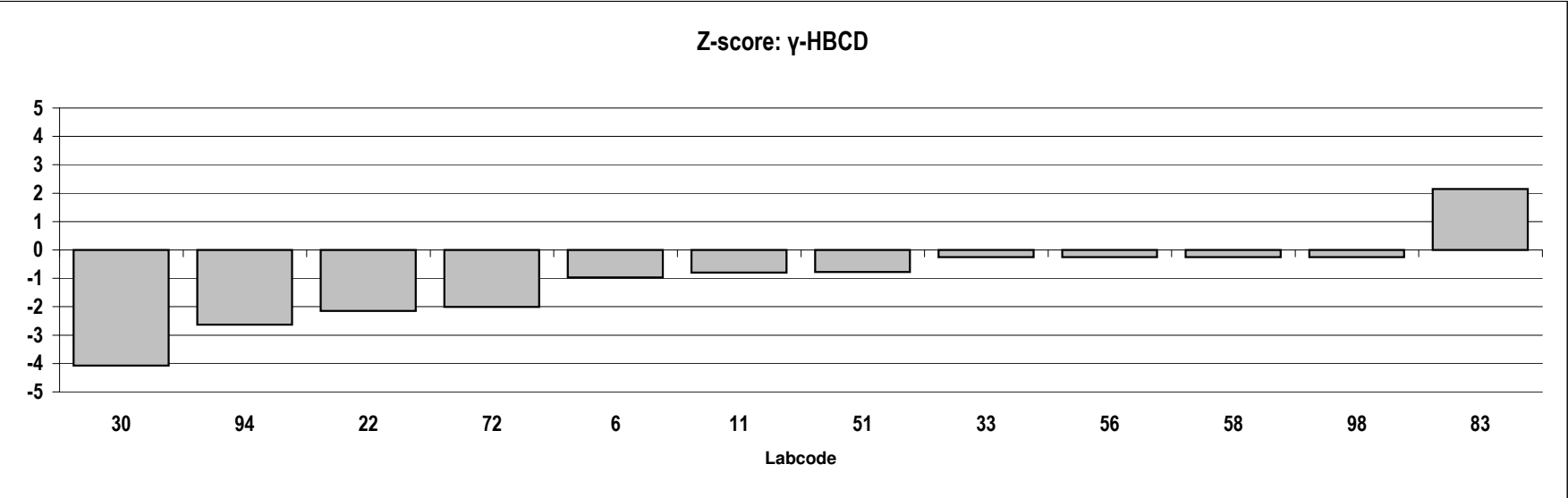
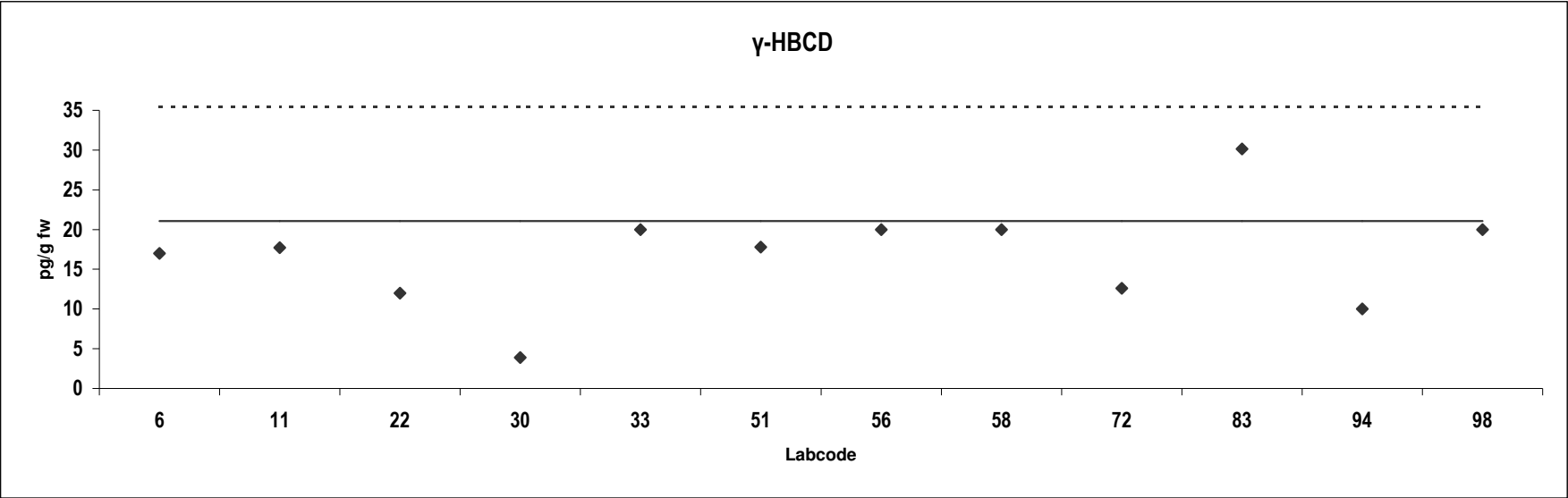


**Egg**  
Congener:  $\gamma$ -HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	17	ND			
11	18	ND			
22	12				
30	3.9	ND			
33	20	ND			
51	18	ND			
56	20	ND			
58	20	ND			
72	13	ND			
83	30				
94	10	ND			
98	20	ND			

**Consensus statistics**

Consensus median, pg/g	21
Median all values pg/g	18
Consensus mean, pg/g	17
Standard deviation, pg/g	6.6
Relative standard deviation, %	39
No. of values reported	12
No. of values removed	0
No. of reported non-detects	10

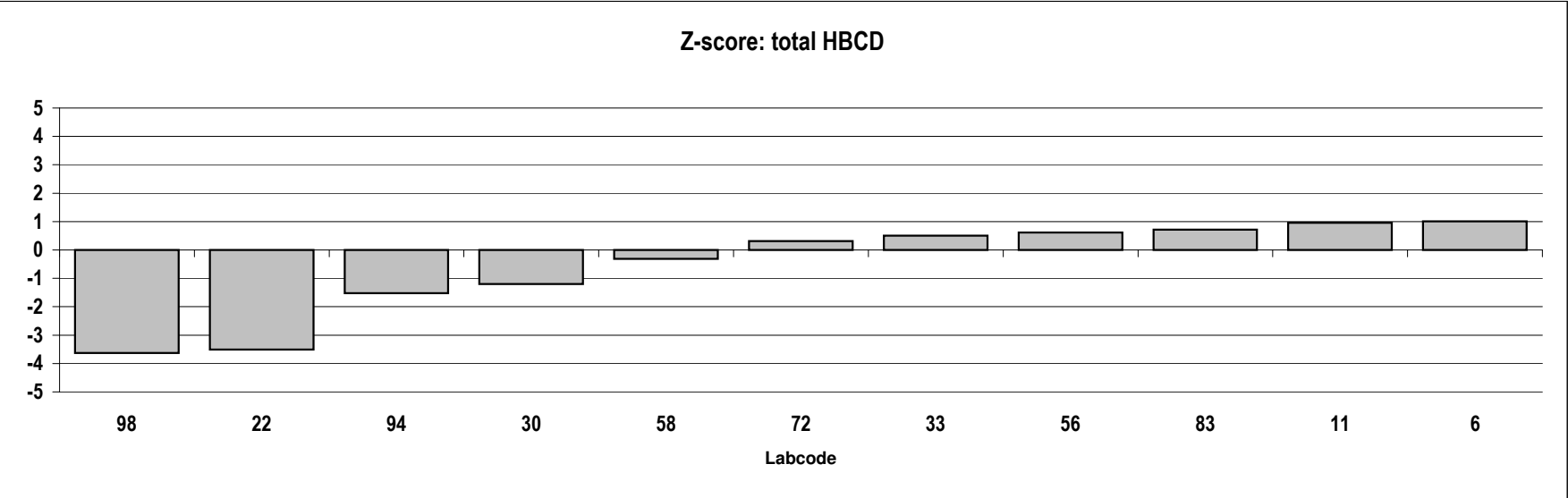
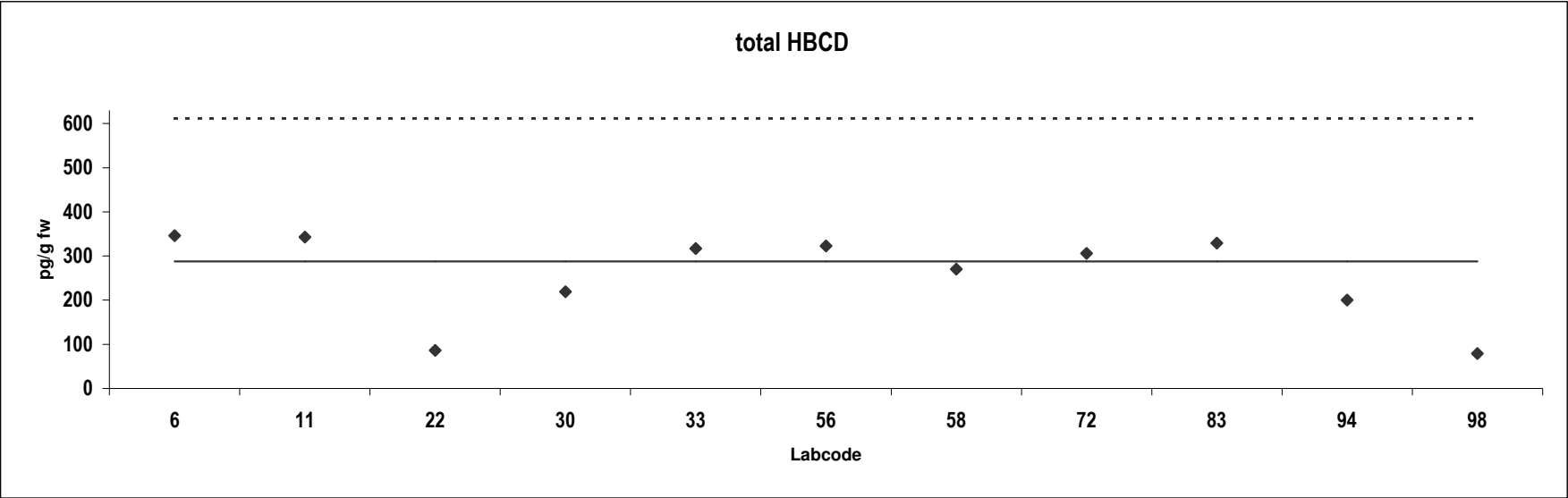


**Egg**  
Congener: total HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
6	346	ND			
11	343				
22	86				
30	219				
33	317				
56	323				
58	270				
72	306				
83	329				
94	200				
98	79				

**Consensus statistics**

Consensus median, pg/g	288
Median all values pg/g	306
Consensus mean, pg/g	256
Standard deviation, pg/g	98
Relative standard deviation, %	38
No. of values reported	11
No. of values removed	0
No. of reported non-detects	1









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